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Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Genetics and Plant Breeding	20	24
Plant Genetic Resources	07	11
Seed Science and Technology	08	11
Total	**35**	**46**

SCHOOL OF CROP IMPROVEMENT

Convenor: Dr. Monika A. Joshi, Professor, Division of Seed Science & Technology
Co-convenor: Dr. Shruti Sethi, Principal Scientist, Division of Food Science & Post harvest Technology

Chairperson: Dr. D.K. Yadava, ADG (Seed), ICAR, New Delhi

Dr Yadava was born in Chandawas (Rewari), Haryana, India on 10 April, 1966; and did B.Sc. (Hons) Ag. 1987; M.Sc. (Ag.) 1990; Ph.D. 1993 from College of Agriculture, Haryana Agricultural University, Hisar, Haryana. He is currently the Assistant Director General (Seed), Crop Science Division, Indian Council of Agricultural Research, New Delhi since 2017 to date. Dr Yadava initiated his career profile as Assistant Professor (Pulses and Brassica Breeding), Agricultural Research Station (Rajasthan Agricultural University), Sriganganagar, 1996-2003; Senior Scientist, Principal Scientist (Brassica Breeding), Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, 2003 to date and Head, Division of Seed Science and Technology, ICAR-Indian Agricultural Research Institute, New Delhi, 2014-21. As a Brassica Breeder and Seed Expert for last 27 years, Dr. Yadava has revolutionized brassica breeding and seed system in India. He has contributed in the development of 24 varieties of mustard (21) and pulses (3), which include very early juncea; timely and quality mustard varieties and has contributed in development of Pusa Double Zero Mustard 31, the country's FIRST Canola quality variety, branded as "INDOLA". Dr. Yadava is a Fellow of NAAS, New Delhi; NASI, Prayagraj and receipient Dr. Rafi Ahmad Kidwai Award and Dr. Rajendra Prasad Puruskar of ICAR; Dr. A.B. Joshi Memorial and Dr. B.P. Pal Memorial Awards of IARI; and National Academy of Agricultural Sciences Recognition Award-2018 and Dr. K. Ramiah Memorial Award 2021-22. He has guided three M.Sc. and eight Ph.D. students and published more than 100 research papers in high impact factor journals.

Genetics

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Prof. H. K. Dikshit

The Division of Genetics at IARI, widely regarded as the “Seat of Green Revolution” in India, is one of the important divisions of this institute that has been making significant contributions to basic, strategic, and applied research in genetics and plant breeding of various crops as well as model genetic organisms. The teaching and research activities of the division align well with the requirements of the farmers, and the diversified research activities include conducting basic and strategic research to development of varieties integrating both conventional and modern biotechnological tools. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Breeding for Higher Productivity

Genetic and molecular characterization of allocytoplasmic near-isogenic lines of Pusa Sugandh 5

WA cytoplasmic lines come with inherent problems like incomplete panicle exsertion, which negatively impacts production by causing sterility in spikelets. To address this, ICAR-IARI New Delhi has developed a collection of 50 allocytoplasmic Near-Isogenic Lines (NILs) of BC$_3$F$_3$, which has been further advanced to BC$_3$F$_4$ through cultivation at three different locations during *Kharif* 2022 in two replications. Significant variations were observed plant height, filled grain, total grain and plot yield. Traits like days to 50% flowering, plant height, panicle length, unfilled grain and total grain were influenced by both genotype and environment. GGE biplot analysis identified PS5-NIL-8, PS5-NIL-22, PS5-NIL-14, PS5-NIL-7, and PS5-NIL-43 as allocytoplasmic NILs with the highest and most stable panicle exsertion ratios. PS5-NIL-8 exhibited the highest panicle exsertion ratio. Similarly, PS5-NIL-1, PS5-NIL-6, and PS5-NIL-15 showcased consistently high total grain yield, while PS5-NIL-37, PS5-NIL-43, and PS5- NIL-49 demonstrated the highest spikelet fertility. For plot yield, PS5-NIL-8, PS5-NIL-15, and PS5-NIL-25 performed the best. A polymorphism survey was conducted using SSR markers between PS5 (recurrent parent) and Pusa 6B (donor parent). A total of 60 polymorphic markers were identified. Foreground analysis using RMS-SF21-5 (*Rf 3*) and RMS-PRR9-1 (*Rf4*) markers of all allocytoplasmic NILs showed positive with PS5. The recovery of RPG in the allocytoplasmic NILs averaged 97.73%. These allocytoplasmic NILs demonstrated comparable grain and cooking quality traits to the recurrent parent PS5. Based on the comprehensive analysis of phenotypic, molecular, and quality data, PS5- NIL-8, PS5-NIL-15, PS5-NIL-30, and PS5-NIL-43 consistently exhibited higher yields with improved panicle exertion than the recurrent parent.

Genome-wide association studies for stem sturdiness in rice (*Oryza sativa* L.)

The study was designed to understand the physical properties associated with stem sturdiness and to dissect it into component traits. A set of 280 indica rice germplasm lines evaluated in augmented RCBD were screened for mechanical strength, elasticity, and anatomical traits; and it revealed the presence of novel variability for stem sturdiness and component traits. There were 65 and 35 genotypes superior to that of positive check IET 28438 (SCM2) for bending force and cross-section modulus (CSM) respectively. Remarkably, all test genotypes, except MTU1010 and PB1847, exhibited low values in terms of BF and CSM. This observation emphasized the potential to prioritize the enhancement of this trait in breeding programs. K-means clustering categorized genotypes into three distinct clusters based on stem sturdiness. Correlation analyses indicated a significant positive correlation between anatomical traits and stem sturdiness parameters. Positive correlations were observed between BMAB and CSM. The top five novel sources were Daharnagra, ARC 13373, Dadkhani, ARC 15743, and ARC 18092. The study identified 49 significant marker-trait associations (MTAs) for stem-sturdiness-related traits which explained the phenotypic variation ranging from 2.4% to 31.8%. MTAs were found to be co-localized with important genes such as IPA1, FC1, OsGAE1, 4CL etc. A total of three haplotypes were identified for 4CL1 encoding 4-Coumarate: Coenzyme A Ligase 1. However, there was a significant difference between Hap2 and Hap3 only with Hap2 being the best haplotype. The integration of MTAs and significant haplotypes into breeding programs could yield rice varieties with enhanced stem sturdiness.

Genome-wide association study to identify marker-trait association(s) for morpho-physiological traits under contrasting production regimes in bread wheat

To dissect the genetic architecture of 19 morpho-physiological traits that could be involved in the enhanced adaptation and performance of genotypes under CA, we performed genome-wide association studies (GWAS) to identify marker-trait associations (MTAs) under four contrasting production regimes viz., conventional tillage timely sown (CT-TS), conservation agriculture timely sown (CA-TS), conventional tillage late sown (CT-LS) and conservation agriculture late sown (CA-LS) using an association panel comprising of 183 advanced wheat breeding lines along with 5 checks. The study identified ample variations for the target traits and assessment of genotype-by-environment (G × E) interaction for all morpho-physiological traits. The genotyping of the association panel was done using a 35K Breeders' Axiom array. The population structure and kinship analyses identified the presence of two sub-populations in the association panel. GWAS was performed using the BLINK model in R Studio. A -log10P value above 5.0 (Bonferroni threshold) was used as the significance criterion. In total, 80 MTAs were discovered for 19 morpho-physiological traits across the four production environments. The phenotypic variation explained by these QTNs ranged from 2.15 to 40.22%. A highly significant SNP AX94651261 (9.43% PVE) was identified to be associated with Phi2, while two SNP markers AX94730536 (30.90% PVE) and AX94683305 (16.99% PVE) were associated with NPQ. In addition, highly significant and informative SNPs were identified for DTH, DTM, PH, GY, and GL being linked to genes, the products of which have been reported to play pivotal roles in stress tolerance.

Phenotypic evaluation of genetic variability for productivity-related traits in a recombinant inbred population and molecular tagging of gene(s) for lodging resistance in chickpea (*Cicer arietinum* L.)

The primary objective of this study was to investigate genotypic variability for productivity-related traits in a Recombinant Inbred Line (RIL) population, identify molecular markers associated with lodging resistance genes, and pinpoint RILs displaying non-lodging characteristics with high yields. The research assessed genotypic diversity among 388 RILs and observed significant variations in various agronomic traits. High variations were noted for the number of pods per plant (NPP), number of seeds per plant (NOSP), and seed yield per plant (SYPP), whereas moderate values were observed for plant height (PH), hundred seed weight (HSW), number of seeds per pod (NOSPP), and low values for days to 50% flowering (DFF). Genetic advance (GA) was high for NPP, NOSP, and SYPP, moderate for PH, and low for DFF, HSW, and NOSPP. Notably, there was a significant positive correlation between seed yield per plant (SYPP) and NPP, NOSP, and HSW. Conversely, a negative correlation was observed with plant height (PH) and days to 50% flowering (DFF). Plant height and DFF exhibited negative correlations with NPP, NOSP, SYPP, and NOSPP but showed positive correlations with HSW and between each other. Among the RILs, LRRIL-308 was identified as the top performer, demonstrating both non-lodging characteristics and a high yield of 3424.33 kg/ha. Additionally, the SSR marker H3F08 was putatively linked to lodging resistance genes (*Sb1* and *Sb2*), as identified through Bulked Segregant Analysis (BSA). This represents the first instance of a marker associated with lodging resistance genes being reported.

Genetic diversity and association mapping of early vigor in aus rice (*Oryza sativa* L.)

To explore the genetic architecture of the genetically complex early vigour, encompassing both seed and seedling vigour, traits, a total of181 *aus* accessions from the 3,000 Rice Genome Panel were characterized to understand genetic diversity for early vigour traits in *aus* rice germplasm and to identify marker-trait associations (MTAs) using genome-wide association analysis (GWAS). We evaluated five seedling vigour traits along with seven seed vigour traits. GWAS was performed on seven early vigour traits using918, 863 SNPs. Significant variation was recorded for seedling vigour (Vg), chlorophyll content (CCI), biomass, and growth parameters. The germination percentage (GP), rate (MGR), and other seed vigour traits showed significant variations. Correlation coefficients indicated a positive association of grain yield with seedling vigour, CCI, and growth rate. GP showed a positive correlation with other seed vigour traits, except grain weight. Population structure analysis using 399K SNP markers revealed six *aus* sub-groups and indicated geographical structuring. The genome-wide linkage disequilibrium (LD) decay was ~140 Kbp. GWAS revealed 25 and 53 significant loci for four seeding vigour and three seed vigour traits, respectively. The post-GWAS analysis identified reported QTLs governing relative germination vigour, coleoptile length, low-temperature germinability, shoot dry weight, plant height, and chlorophyll content for seedling vigour. For seed vigour, genes like *OsMDP1* for enhanced seed germination, coleoptile elongation and mesocotyl length. These findings provide valuable information for understanding the genetic control of early vigour in *aus* rice and for further validation of identified MTAs is required.

Genetic analysis of kernel row number (*krn*) gene(s) in the manifestation of heterosis in maize (*Zea mays* L.)

This study undisclosed the pivotal role of kernel row number (KRN) in maize hybrids and investigates the genetic mechanisms that influence the manifestation of heterosis. A set of ten hybrids was developed through the crossing of five distinct lines (half-sibs) with two distinctive testers one characterized by high KRN (AI543) and the other by low KRN (PML 105). These hybrids were analyzed to examine the genetic understanding of KRN and its subsequent impact on yield. Significant influence of testers on various traits including plant height, 50% tasselling, 50% silking, ear height, ear length, ear girth, KRN, total kernels, grain yield, and test weight were observed. The investigation also unravels the intricate genetic interactions and explains that the KRN trait followed additive gene action. Based on GCA, the AI 5116 line and two testers as well as the resulting two hybrids viz., AI 5116 × AI 543 and AI 5116 × PML105) were selected for further molecular studies. Notably, the gene *fea2* exhibited a correlated expression pattern with KRN, subsequently expressing a distinguishable influence on hybrid yield. In contrast, *td1* demonstrated a negative correlation with KRN determination, however, expression of this gene influenced heterosis in hybrids. Genes *fea4* and *tsh4* showed positive correlations with KRN within the parental lines, but the expression of these genes was not correlated with the manifestation of heterosis in studied maize hybrids. These findings offer a deeper comprehension of the genetic regulation of KRN and its significant effects on maize yields in tropical and subtropical regions.

Ploidy-regulated trait expression in pearl millet (*Pennisetum glaucum*)

The research encompasses diploid strains of pearl millet (2n=2x=14), including a male sterile line (81A4) and its maintainer (81B). Additionally, induced tetraploid variants (2n=4x=28), viz. Tetra A4 (TA4, male sterile), and Tetra1 (T1, maintainer), were employed for inter-ploidy hybridizations. The study also introduced combinations of 2x and 4x lines having anthocyanin pigment markers (Red 2x and Red 4x), alongside other diploid instances (81A1) and tetraploids (T2, T4). Crossing experiments unveiled intriguing findings, with the cross TA4 × 81B (4x × 2x) yielding a higher seed set due to maternal excess in the endosperm (4m:1p), while the cross 81A4 × T1 (2x × 4x) exhibited paternal excess (2m:2p). Similar trends were observed for germination percentage and initial plant vigor, in favor of the TA4 × 81B cross. Reciprocal cross differences suggested endosperm imprinting effects supporting maternal excess. Biochemical assessments disclosed higher total protein content and total soluble sugars in tetraploids compared to diploids. Cytological characterization illustrated chromosome configurations, with diploid pearl millet lines featuring 0.9I + 6.55II on average, characterized by normal bivalent formation. In contrast, tetraploid pearl millet lines displayed an average configuration of 0.72I + 12.28II + 0.16III + 0.56 IV, including normal bivalents and higher chromosomal configurations such as quadrivalents. Red 2x consistently exhibited higher gene expression than Red 4x for all genes studied, warranting further investigation. In addition to the differential response of morphological, cytological, biochemical, and molecular traits dependent on ploidy levels, the present study also suggested a relaxed embryo-endosperm genome balance operating in pearl millet.

Assessment of morphological and genetic diversity using simple sequence repeat (SSR) markers in horse gram (*Macrotyloma uniflorum*)

The present study aimed at morphological and molecular characterization of 75 Horse gram genotypes along with 4 checks using ten agro-morphological traits and forty-five SSR markers. ANOVA under augmented design showed significant and exploitable variation for all the traits under investigation. High to moderate estimates of PCV, GCV, heritability, and genetic advance were observed for all the traits. At the phenotypic level, seed yield per plant had a significant and positive correlation with the number of pod clusters per plant, number of pods per plant, number of seeds per pod, and plant height. The genotypes showing maximum seed yield per plant were observed for IC-23440, Indira Kulthi, IC-22431, and IC-120826.). The genotypes IC-561031 and HPKM-317 were found to be early maturing as it takes fewer days to flowering and maturity. Total genotypes are grouped into 2 major clusters. Cluster 1 with local landraces Jalthanda, Dorma, HPKM-317, Birsa Kulthi-1, and some Indigenous cultivars. Cluster 2 with 2 sub-clusters having genotypes, TCR-636, Indira kulthi, and other Indigenous cultivars. Twenty-four polymorphic SSRs produced a total of 59 alleles, with an average of 2.5 alleles per locus. MUMS-10 was found to be the most informative marker with a PIC value of 0.55 and HUGMS-07 was found to be the least informative marker with a PIC value of 0.013. The high level of genetic diversity assessed in this study at both morphological and molecular levels emphasized the importance of its conservation which can be further utilized in future breeding programs of horsegram.

Development of SSR markers and their application in revealing genetic diversity in adzuki bean (*Vigna angularis*)

Assessing the genetic variation at the phenotypic and genotypic levels gives a clear idea about the distribution of genetic resources and the extent of variability among and within the available population. The present study characterized 50 adzuki beans (*Vigna angularis*) comprising indigenous and exotic accessions using newly developed 22 SSR markers and 15 quantitative traits. A wide range of variation was observed for quantitative traits.

Grain yield was positively correlated with plant height, leaf length, leaf width, clusters per plant, number of pods per plant, and 100 seed weight. Among accessions highest yield was observed in EC-87071, followed by EC-87815 and EC-34027. Fifty-nine alleles with an average of 2.68 alleles per SSR locus were detected. The polymorphic information content (PIC) value ranges from 0.09 to 0.59, with an average value of 0.36. The genotypes were grouped into two major clusters in neighbor-joining and STRUCTURE cluster analysis. The clustering pattern did not show a relationship between geographic distribution and the grouping pattern of genotypes. The results suggested that the high-yielding exotic accessions may be used as parents for further crop improvement strategies. The polymorphic SSR markers developed in the study would boost end-use-based improvement and conservation studies for the sustainable use of the adzuki bean.

Molecular characterization and utilization of matrilineal (*mtl*) gene for in-vivo haploid induction in maize (*Zea mays* L.)

The study attempted to develop locally adapted haploid inducer lines using marker-assisted back cross-breeding for introgression of favorable alleles for matrilineal (encoding phospholipase) with 4 bp insertion and DMP (encoding DUF679 domain membrane protein) with T to C transition in different heterotic groups. The inbreds were tested for haploid induction rate (HIR) by crossing with the Pusa Vivek QPM9-Improved Hybrid as source germplasm. Introgressed inbreds with favorable alleles were subjected to make crosses to obtain heterotic hybrids. The hybrids were tested for HIR (PMI-PV1-HI × PMI-PV2-HI: 11.53 to 5.07%, PMI-PV1-HI × PMI-PV3-HI: 12.83 to 5.20%, and PMI-PV2-HI × PMI-PV3-HI: 15.95 to 8.66%) by crossing with the Pusa Vivek QPM9- Improved Hybrid as source germplasm. Haploids with purple coloration in the endosperm only were separated from the diploids with anthocyanin pigmentation in both scutellum and endosperm using the R1-nj marker. In addition, the segregating generations used for inducer development were again screened for intense expression of R1-nj marker with wild-type alleles for haploid induction using the genetic dropout method. RGB-based vegetation indices were used for the classification of haploid seeds from the diploid progeny with 80% accuracy using discriminant function analysis and classification and regression tree (CART). Genome-wide methylation pattern with varying expression of the transcriptome in parental inbreds and their hybrids provides clues for explaining the complex phenomenon of heterosis. Overall, genetic information and stocks generated from this study provide an extraordinary platform for DH line development, mapping complex traits, and editing novel traits of agronomic importance.

Development of heterotic pools in Basmati rice

An attempt has been made to improve the parental lines of Basmati rice where a panel of improved parental lines including 107 putative restorers carrying restorer allele of *Rf4* or/and *Rf3*; and 59 maintainers were developed, and were evaluated for various agro-morphological, grain, and cooking quality traits. The improved lines showed significant G × E interaction for grain yield. Grain quality evaluation revealed 143 improved genotypes from both populations qualified the minimum Basmati quality standards. Genotyping the panel with gene-based/gene-linked markers confirmed the presence of one or more genes for both blast and blight resistance. Pollen fertility (PF) of testcross hybrids ranged from 77.7% to 99.2% while 11 of them were perfect maintainers. Genome-wide association study conducted on a population of 172 improved breeding lines revealed a total of 32 unique Marker Trait Association (MTA) including 11 robust MTAs for the agronomic traits and 25 unique MTAs including two robust MTAs for the grain and cooking quality traits. Testcross hybrids were evaluated and tested in three locations across the Basmati GI regions to detect nine parental lines including four PMP lines and five PRP lines possessing higher general combining ability (GCA). The SCA effects of the common hybrids tested across three locations were used to cluster the respective parental lines and obtained two clusters majorly accommodating restorers and maintainers. The PPLs were then grouped into two populations namely, Pop1 and Pop2 based on the structure analysis. The present study has laid a strong foundation for robust Basmati rice hybrid breeding.

Genetic mapping of flag leaf and panicle architecture in rice

In a comprehensive study involving a 175 recombinant inbred line (RIL) derived from PR126 (a green super rice cultivar) and Pusa NPT34 (a new plant type line), we present the mapping of Quantitative Trait Loci (QTLs) associated with primary branching and grain number utilizing a custom microsatellite linkage map designed specifically for this population, spanning a total of 2415.1 centimorgans and incorporating 103 markers. Among the 25 QTLs identified for various traits, 18 were clustered within five hotspots. Seven of these QTLs exerted major effects. Notably, two of the identified QTLs, namely qFGN9.1 for grain number and qPBN11.1 for primary branches are novel. To validate these QTLs, we employed $F_{2:3}$ families derived from a cross between Pusa Basmati 1509 and Pusa NPT34. We also report the discovery of QTLs for flag leaf length, flag leaf width, and flag leaf area. Seventeen QTLs were identified on chromosomes 2, 3, 4, 5, and 6 across multiple locations. Four markers, RM190, RGNMS2221, RM335, and nksssr04-11, were utilized for validation, and only one marker, RM190, was found to be polymorphic between the parental lines. Remarkably, we successfully validated three QTLs, namely qFLW6.1, qFLA3.1 and qFLA6.1, within the F2:3 lines of the PB 1509/Pusa NPT34 cross using single marker analysis during field trials at ADT. Intriguingly, both of these validated QTLs originate from 'Pusa NPT34.' Further refinement of marker intervals through fine mapping promises to narrow down the genomic regions and identify candidate genes for more precise marker-assisted selection aimed at shaping flag leaf characteristics.

Identification of heterotic genomic segment(s) in *Brassica carinata*-derived *Brassica juncea* introgression lines

Interspecific hybridization between *B. carinata* accession BC-4 and *B. juncea* cultivars, viz., DRMRIJ 31, Pusa Mustard 30, and Pusa Agrani, resulted in the generation of *B. carinata* derived *B. juncea* introgression lines (ILs). Sufficient genetic variability in *B. juncea* has been achieved through the introgression of genomic segments from *B. carinata*. To access the effect of the introgressed segments in heterozygous conditions, 153 hybrids were generated by inter-mating ILs in different combinations. Of these, 61 hybrids exhibited both significant heterobeltiosis and standard heterosis over their respective checks. To identify heterotic genomic segments that contributed to the hybrid vigor, ILs were hybridized with their respective recipient parents to generate introgression line hybrids (ILHs) and the common tester (SEJ 8) to generate test hybrids (THs). Ten ILs with significant mid-parent heterosis in ILHs and significant standard heterosis in THs for seed yield were used for the dissection of heterotic genomic segments. Representative SNPs from identified heterotic segments led to the discovery of potential candidate genes that were reported to regulate yield-related traits in previous studies. Statistical comparisons between ILs, ILHs, and recipient parents, on the other hand, classified heterotic phenotypes into different modes of inheritance, viz., dominant, over-dominant, recessive, and additive. A significant difference was observed for the overdominant mode of inheritance between the productive and non-productive groups of traits, indicating the preponderance of over-dominance in the expression of heterosis in IL-derived hybrids. The material generated also provided us with the opportunity to unravel the genetic basis of heterosis.

Understanding genetics and marker-trait associations for seed yield and quality in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]

To study the genetics as well as to map genes/QTLs for seed coat color and seed size, and to identify marker-trait associations for seed yield and quality. Populations developed by crossing DRMRIJ-31 (brown and bold-seeded) and RLC-3 (yellow and small-seeded), were studied. Reciprocal differences were observed suggesting the influence of maternal effect. Segregation analysis of seed coat color in the F_2 indicated digenic duplicate epistasis, with brown seed coat color dominating over yellow. For seed size, generation mean analysis was conducted, indicating the prevalence of additive, non-additive, and additive × additive gene action, suggesting selection and population improvement programs. *Bju.TT8* homologs were cloned and sequenced in DRMRIJ-31 and RLC-3, which had an insertion of 1279bp and Bju.BTT8 had SNP (C→T) at the 7th exon in RLC-3, cumulatively leading to yellow seed coat formation. Functional STS and allele-specific markers have been developed and validated in the F_2 population and a germplasm assembly. Subsequently, for seed size two stable 99 MTAs were identified through GWAS of TSW. By exploiting these SNPs, CAPS and gene-based (SAMBA) markers have been developed and validated in the F_2 population. The GWAS panel underwent phenotypic evaluation for 21 agro-morphological, seed yield, and quality traits, and was genotyped using the Brassica 90K Cons ABC SNP array (Illumina). Subsequently, GWAS analysis identified 25 MTAs for various seed yield, quality, and agromorphological traits. *In-silico* analysis of these stable SNPs revealed their association with candidate genes known to be involved in molecular, physiological, and biochemical pathways relevant to the studied traits.

Inheritance, molecular mapping of gene(s) for cream grain color, and gene action studies for some quantitative traits in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

Inheritance of cream grain color has not previously been reported in pearl millet and limited information on gene action for different traits, especially biochemical traits, is available. Significant genetic variation was found among thirty-five inbred lines used for characterization. Seed yield per spike demonstrated a significant positive correlation with number of productive tillers, 1000-seed weight, amylose content, and sucrose content while showing a significant negative correlation with oil content, total protein content, and phytic acid content. These lines have been categorized into four distinct clusters. In principal component analysis, the first two principal components explained 42.88% of the variation. Amylose, ash, and phytate content contributed the most to PC1, while starch content, spike girth, and total protein content contributed the most to PC2. Six crosses were evaluated during Kharif, 2021 and 2022 for inheritance and gene action studies. Cream grain color was found to be governed by a single dominant gene. The gene responsible for cream grain color was mapped to linkage group 2, positioned between two markers, *Xpsmp2089* and *Xipes0218* with a genetic distance of 17.9 cM and 16.9 cM, respectively. Since this is only preliminary mapping, fine mapping of the gene is needed for marker-assisted breeding. The majority of variables that affected yield were controlled by dominant gene action, indicating that heterosis breeding may be fruitful. Both additive and dominant gene actions affected iron and zinc content, whereas additive gene action predominated. Similarly, it was observed that both additive and non-additive gene action controls all biochemical traits.

Association mapping for agronomic traits influencing yield in mungbean

To dissect the phenotypic variability and the genetic basis of agro-economic traits, we investigated 153 diverse mungbean genotypes for eleven agroeconomic traits (days to 50% flowering, days to 100% flowering, days to maturity, number of primary branches, plant height, pod length, pod number, nitrogen status, seeds per pods, 100- seed weight and yield per plant under two environmental conditions. Significant phenotypic variability was observed and the genotypes were re-sequenced by the genotyping-by-sequencing (GBS) method. Genome-wide association studies (GWAS) with Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) model were carried out which identified 50 SNPs (highest p-value > 0.0001 (–log10(p)) to be significantly associated with eleven agro-economic traits. At the flanking region (30 kb) of each identified SNP, *in-silico* analysis deciphered nineteen candidate genes to indirectly regulate agro-economic traits. BLAST search was performed against the control Arabidopsis genome database to spot the Arabidopsis orthologue of the identified mungbean candidate genes. Further, the expression angler platform revealed that identified candidate genes are digitally expressed in different plant parts including root, seeds, leaf, shoot apical meristem, cotyledons, dry seed, and flowers. The identified candidate genes could play a vital role in regulating the agro-economic traits in mungbean. GWAS study in mungbean could assist in developing elite germplasm lines through marker-assisted selection and the dissected agroeconomic traits could have a significant contribution in fostering mungbean breeding and developing improved varieties.

Identification of genomic regions for nodulation traits through genome wide association mapping in chickpea (*Cicer arientinum* L.)

Here we evaluated a diverse core set of two association panels each consisting of 271 and 284 diverse genotypes including 4 checks and data recorded for chickpea genotypes in four different environments for morphological and nodulation traits. Wide genetic variation was observed and correlation analysis revealed that the number of nodules was positively correlated with seed yield in both the association panels. Further, seed yield was partitioned into direct and indirect effects at genotypic and phenotypic levels through path coefficient analysis. A subset of an association panel 1 consisting of 20 genotypes was evaluated in pots and studied to compare for the nodulation features in field and pot conditions. The genotypes ICC-6579 exhibited the highest level of nitrogenase activity, while ICC-9002 displayed the lowest activity and we found higher total nitrogen content in the genotypes ICC1172 with a nitrogen content of 4.32 and with a mean number of nodules were 59.32. ICC9002 had the lowest number of nodules with a low nitrogen content of 1.99% in their seed and genotyping of 20 genotypes with 128 nodulation primers identified 26 polymorphic markers. A total of 450 and 632 stringent marker trait associations among them 75 and 53 were found to be stable in association panel 1 and association panel 2 were identified. Validation of the two markers each presented in the same genomic regions for the number of nodules and nodule fresh weight can be used in the marker-assisted transfer of identified genes/QTLs to develop high nodulation varieties of chickpea.

Fine mapping and deciphering the basis of zebra leaf trait in Pusa Zebra 18

A novel zebra mutant, ‘Pusa Zebra 18’ derived spontaneously from F_2 intercross population of Pusa 44 NILs exhibit distinguishable yellowish cross bands across the green leaf blade, specifically expressing in the seedling stage from 6 DAT, which diffuses progressively leading to the recovery of the normal green leaf by 30 DAT. At 6 DAT, the net photosynthetic rate, fluorescence kinetic parameters, and photosynthetic pigment content reduced significantly in the yellow portion of the mutant leaves. Based on the characterization of Pusa Zebra 18, it was discovered that is triggered by transplanting. RT-PCR analysis among the candidate genes revealed that the gene encoding the Tetratricopeptide repeat-containing protein was involved in the manifestation of the seedling stage zebra trait. After transplanting Pusa Zebra 18 seedlings experience stress in roots which forms a signal for the production of Abscisic acid, a major factor for lateral root development and seedling emergence. Root morphological analysis shows a delay in lateral root as well as xylem development affecting iron uptake leading to a zebra leaf pattern in the mutant. qRT-PCR and proteomic analyses confirmed the involvement of gene (LOC_Os2g15660), in the manifestation of seedling stage zebra leaves in PZ 18. To date, no gene governing zebra leaf mutation has been mapped on chromosome 2, therefore the mutation was found to be a novel mutation. Functional validation of the gene encoding tetratricopeptide repeat-containing protein using genome editing will enable marker-assisted introgression of this trait into parental lines of rice for use in hybrid purity testing.

Theme 2: Breeding for Resistance to Biotic Stresses

Marker-assisted backcross breeding (MABB) integrating rapid generation advancement (RGA) for improvement of wheat variety HD3086

Leaf rust resistance genes *Lr52* identified from the Watkin collection show a broad-spectrum resistance against the prevalent leaf rust pathotype. HD3086 being one of the popular wheat cultivars that is susceptible to leaf rust has been improved for leaf rust resistance by transferring the gene *Lr52* through backcross breeding integrating the rapid generation advancement. The recurrent parent (RP) HD3086 and donor parent (DP) Lr52/Yr47/2*Mace were crossed to generate $F_{1,}$ that were backcrossed to RP to generate BC_1F_1. The BC_1F_1 plants with resistance to leaf rust, foreground positive, and maximum phenotypic similarity with RP were selected and advanced to BC_2F_1 and BC_1F_2. The BC_2F_1 and BC_1F_2 plants were advanced to BC_2F_3 and BC_1F_4 by selection for rust resistance, foreground positive, and similarity to RP in glass house under rapid generation advancement. Further, BC_2F_3 and BC_1F_4 plants were grown under field conditions by screening against leaf rust, foreground selection, and phenotypic background recovery. Six resistant plants/lines with high phenotypic similarity were selected for background analysis. The lines with the highest recovery and phenotypic similarity have been selected for nomination to AICRP trials. In addition, a rapid advancement protocol has been standardized using HD2932 and HD3086 wheat varieties at natural daylength conditions, they were sown at differential planting density. For forced maturity, irrigation was stopped at 15 or 25 days after anthesis and mature seeds were harvested post 20 days of irrigation withdrawal. Seeds were cycled in 90-95 days and germination of seeds was achieved through chilling treatment of 72 hrs at 4^{o}C.

Molecular cytogenetic analysis of gamma-ray irradiated derivative lines of the cross between bread wheat and *Aegilops speltoides*

Selection2427 (Sel. 2427) is a genetic stock developed at the Division of Genetics, that exhibited resistance (LrS2427) to prevalent leaf rust races in India but posed sterility issues when crossed with other bread wheat lines. This behavior is similar to that of gametocidal genes and suggests multiple gene introgressions during the distant hybridisation. To confirm these introgressions, genomic in situ hybridization (GISH) was employed using a fluorescently tagged whole-genome probe from *Ae. speltoides*. Sel. 2427's chromosomes displayed six fluorescence signals, while F_1 (Agra Local × Sel. 2427) showed three in the majority of the cells, confirming three introgressions between the species. Gamma irradiation was utilized to break the association between LrS2427 and the putative gametocidal gene(s). The gamma mutants exhibited meiotic stability with the normal 21 bivalent configuration in both parent and F_1 generation, ensuring good pollen fertility and seed set. These mutants displayed remarkable seedling resistance to various leaf rust races, including the virulent race 77-5, confirming the presence and activity of the broad-spectrum resistant gene LrS2427. Field studies revealed that the top-performing gamma mutants surpassed Sel. 2427 and its sister line Easy Thresh in critical yield parameters such as tiller count, spikelets per spike, and seeds per spike. Notably, gamma mutants T250-20-20-6, T250-20-20-16, and T300-64-51-28 emerged as promising candidates, carrying the leaf rust resistance gene LrS2427. These mutants offer valuable assets for disease-resistance breeding programs due to their resistance to leaf rust without the baggage of linkage drag common while using wild and related species.

Unfolding the complex regulatory network of rust (*Uromyces viciae-fabae*) resistance in lentil (*Lens culinaris* Medik.) using comparative RNA-seq analysis

The study investigated the intricate molecular mechanisms underlying lentil resistance to the harmful rust infection caused by *U. vicia-fabae*. Utilizing RNA-Seq, we examined two genotypes that had been inoculated with rust spores: rust-resistant L4147 and rust-susceptible LLS 18-109. The RNA-Seq method produced useful insights by comparing resistant control (RC), susceptible non-inoculated (SNI), resistant inoculated (RI), and susceptible inoculated (SI) samples. In six comparisons, differentially expressed genes (DEGs) were found, totaling 12,316 DEGs in all possible combinations. In rust-infected plants, functional gene classes related to defense were noticeably impacted. Highlighting metabolic pathways, biosynthesis of secondary metabolites, and plant-pathogen interactions, enriched KEGG pathways shed light on functions of DEGS across all combinations. Notably, several histone-coding genes, R genes, and genes related to ionic activity and metabolic processes showed differential expression, possibly strengthening defense. The number of DEGs was reduced to 34, which included LRR receptor-like kinases, transcription factors (WRKY, TIFY, AP2-EREBP, etc.), pathogenesis-related proteins (PR1-like protein), hormone signaling proteins (GH3 family protein, auxin-induced protein, ethylene-responsive factors, ABA receptors), R proteins (CC-NBS-LRR class), etc. Our protein-protein interaction analysis uncovered intricate connections among these proteins, encompassing cell cycle regulation, hormone signaling, MAPK signaling, suberin biosynthesis etc. and some other non-interactive genes putatively associated with defense responses. The significance of the genes identified in response was highlighted by the validation of 16 genes between RNA-Seq and qRT-PCR results, which confirmed credibility. The study has shed light on the molecular basis of lentil rust resistance.

Genetic studies on rice lines introgressed with multiple biotic stress tolerance genes

The study was conducted to generate rice lines containing multiple resistance genes against BLB, Blast, and BPH. A total of 5 resistance genes against Bacterial leaf blight (BLB) namely *Xa4*, *xa5*, *Xa7*, *xa13,* and *Xa21* and 3 genes against Blast namely, *Pi54, Pita,* and *Pib,* and two resistance genes against Brown Plant Hopper (BPH*) i.e. Bph3* and *Bph9* have been considered. Rice germplasm/ multiple stress gene introgressed lines previously generated in the lab containing resistance genes for BLB + Blast and BLB + BPH were used for bi-parental crosses to introgress the genes for multiple traits. Resistance gene-linked molecular markers were used that include RM224 for *Xa4*, RM13 for *xa5*, M5 for *Xa7*, xa13prom for *xa13*, pTA248 for *Xa21*, YL155/87 for *Pita*, RM206 for *Pi54,* NSb for *Pib*, RM589 for *Bph3* and RM28348 for *Bph9* were used for screening for the presence of genes in introgressed rice lines. Hybridization of the selected parental lines was carried out and about 40 crossed progenies were raised genomic DNA from each of the progenies was isolated and the presence of resistance gene was detected by foreground selection by using PCR PCR-based approach. A total of 14 gene-introgressed lines were found to contain multiple resistance genes for BLB, BPH, and Blast. Among them, 4 lines namely, BBLP2-1, BBLP2-2, BBLP6-1, and BBLP6-2 contain multiple resistance genes against the BLB, Blast, and BPH as confirmed by gene-linked molecular markers. Once these lines become stabilized, they can serve as the pre-breeding line for future breeding programs.

Role of microRNA mediated regulation in host-pathogen interaction during leaf rust infection in wheat (*Triticum aestivum* L.)

In the present study, a total of 675 miRNAs comprising 321 known and 354 novel miRNAs were identified from *Triticum aestivum* infected with *Puccinia triticina* pathotype 77-5, through high-throughput RNA sequencing. Among these, 21 unique miRNAs were differentially expressed among compatible and incompatible reactions. Results from the qRT-PCR study revealed that among fifteen randomly selected differentially expressed miRNAs, ten miRNAs were found to have similar expression patterns as obtained in qRT-PCR. Degradome sequencing which was used to capture the targets of known, novel, and differentially expressed miRNA revealed that malate dehydrogenase, phosphoglycerate kinase, aquaporin 7, dehydrin WZY1-2, peroxidase, NBS-LRR class RGA, serine/threonine protein kinase, pathogenesis-related protein precursor histone H2B.2, NB-ARC domain-containing protein, WRKY transcription factor etc. were some of the major genes involved in different biological functions as well as a defense response against pathogen targeted by wheat miRNAs. Results obtained from miRNA-target interaction showed that only 30 targets were identified for S96 while 93 for R96 unique miRNAs. The functional categories of the target genes predicted for S96 miRNAs were WD40-repeat-containing domain, armadillo-type fold, nucleic acid-binding, and OB-fold involved in various important functions in pathogen while in R96, the functional categories of the genes were important for virulence of the pathogen. Thus, leaf rust-responsive wheat miRNA-mediated regulation of wheat and *P. triticina* genes involved in the important biological process as well as in defense against phytopathogens and virulence suggest that miRNAs play an important role during leaf rust infection in wheat reinforcing the role of miRNA in host-pathogen interaction.

Genetics and mapping of leaf rust resistance gene(s) in *Triticum timopheevii* zhuk. introgression lines in wheat (*Triticum aestivum* L.)

In the current investigation, the leaf rust pathotype 77-5 was used to test a collection of 41 *T. timopheevii* introgression lines (ILs) for resistance to leaf rust. 33 of the 41 ILs displayed a resistance response to leaf rust. When tested further against 19 different leaf rust pathotypes, two ILs, TTmD638 and TTmD793, demonstrated a high level of resistance. Using 35K Affymetrix Wheat Breeders' Axiom® array, the genetic makeup of these two ILs was analysed to identify any introgression segments from two *T. timopheevii* accessions. Genomic analysis of ILs TTmD638 and TTmD793 indicated, respectively, 30.59% and 20.30% of introgression from *T. timopheevi* 191 and *T. timopheevi* 235. In the crosses TTmD793/AL and TTmD638/AL for leaf rust resistance against pathotype 77-5, genetic analysis showed that the segregation ratios were 1 resistant: 3 susceptible in TTmD793 and 9 resistant: 7 susceptible in TTmD638. The placement of the resistance gene on the 2D chromosome in the case of TTmD793/AL was confirmed by bulked sergeant analysis utilizing SNP data. The resistance gene LrTTm 793 was discovered to be linked to the PCR-based SNP marker SNP 7932DS. Additionally, BSA employing SNP data identified the potential location of the leaf rust resistance gene on chromosome 7D in the case of TTmD 638/AL. Five SSR markers were discovered to be associated with the leaf rust resistance gene LrTTm638. The leaf rust resistance genes identified from the study seems to be broad spectrum and can be further used to broaden the genetic base for leaf rust resistance breeding.

Marker-assisted improvement of wheat variety HD3086 for leaf rust and moisture deficit stress tolerance

In the present study marker-assisted backcross breeding approach is used to transfer gene/QTLs linked to the component traits of moisture deficit stress tolerance and rust resistance gene (*Lr24*) on the background of HD3086. The genotypes DBW43 and HI1500 were used as donors in separate backcross programs; donor variety HI1500 had leaf rust resistance gene *Lr24* which confers resistance against all the major pathotypes found in India. QTLs associated with Normalized Difference Vegetation Index (NDVI), Canopy Temperature (CT), Biomass (BIO), Thousand Kernel Weight (TKW), and Yield (YLD) were transferred. Foreground selection was carried out in BC_1F_1, BC_2F_1, and BC_2F_2 generations to identify the plants with positive gene/QTLs conferring leaf rust resistance and moisture deficit stress tolerance. The BC_2F_6 lines were subjected to evaluation against *P. triticina* pathotypes under artificial epiphytotic conditions. The identified lines were evaluated for two years for their tolerance to moisture deficit stress and resistance to rust. Background analysis was done to identify plants with maximum recovery of RPG in BC_2F_5 using 35k SNPs from Axiom wheat breeders array and obtained plants with recovery range from 78-94%. Finally, in BC_2F_5 best seven lines from HD3086*2/DBW43 derived cross and eight lines from HD3086*2/HI1500 derived cross were identified which showed resistance to rust and performed better than recurrent parent HD3086 for component traits of moisture deficit stress tolerance such as CT, NDVI, TKW and yield. Best-derived lines, named HD3470 and HD3471, with maximum RPG recovery with phenotypic similarity to HD3086, are nominated for national trials for testing and further release.

Mapping and transfer of rust resistance gene(s) derived from *Triticum turgidum* var. durum cv. Trinakria in bread wheat

The objective of the present study is to map the rust resistance gene(s) derived from *Triticum turgidum* var durum cv. trinakria in wheat. Genetic analysis was conducted in F_1, F_2, and $F_{2:3}$ generations, and validated the dominant nature of the *LrTrk* gene. Genetic analysis of F_1, and F_2 of the cross HD2932+YrTrk × HD2932 showed the presence of a single dominant gene, which was further validated in the $F_{2:3}$ population. The BSA results revealed that gene *YrTrk* is located on the short arm of chromosome 1B and the closest SNP to the *YrTrk* gene is AX-94978860. The study incorporated LrTrk, a leaf rust resistance gene, into HD3086. The population comprising F_1, BC_1F_1, BC_2F_1, and BC_2F_2 plants was developed by crossing and backcrossing Trinakria with HD3086. Foreground selection targeting *LrTrk* and background analysis for recovering the recurrent parent genome (RPG) were conducted in the BC_1F_1 and successive generations. The *LrTrk*-linked SSR marker, *Xgwm234*, was utilized for foreground analysis, while polymorphic SSRs were used to determine the background recovery. BC_2F_3 NILs displaying the highest background recovery (97.23-98.67%) also showed differential leaf rust response with pathotype 77-5 of *P. triticina*. The research investigates the transfer of the *LrTrk* gene into the HD3059 background, revealing no resistance in BC_1F_1 plants. This may be due to the presence of suppressor genes in HD3059 genetic background, which limit the expression of the leaf rust resistance gene, *LrTrk*. Incorporation of these new genes has the potential to enhance the genetic diversity of rust resistance in wheat cultivars.

Identification of QTLs imparting resistance to MYMIV infection and earliness traits in mungbean (*Vigna radiata* (L.) Wilczek).

Next-generation sequencing (NGS) was used to find the genetic regions governing MYMIV (Mungbean Yellow Mosaic India Virus) resistance, early flowering, and other morpho-biochemical traits in mungbean. For field screening and infectious clone development, 175 recombinant inbred lines (RILs; Pusa Baisakhi × PMR-1) were used. MYMIV was identified as the predominant virus in the fields of IARI, and New Delhi, and its evolution through intraspecific recombination. The infectivity and efficiency of various *Agrobacterium tumefaciens* strains identified EHA105 as the best. Both field screening and agro-inoculation have identified six RILs (RILs 10, 13, 21, 123, 131, 163) with consistent MYMIV resistance. Seasonal variations in key biochemicals, total phenolic content (TPC), and ascorbic acid, were observed. MYMIV-resistant genotypes displayed higher TPC levels over susceptible ones and similarly, ascorbic acid concentrations were also higher in resistant groups over susceptible. The linkage map was constructed with 1,730 high-quality SNPs, closely aligned with the mungbean reference genome with an average inter-marker distance of 0.345 cM. The map spans 11 chromosomes with variable marker counts and chromosome 9 features the longest linkage group (74.32 cM), while chromosome 3 has the shortest (45.959 cM). This study used 142 RILs spanning generations $F_{5:6}$, $F_{6:7}$, and $F_{7:8}$ from a larger pool of 166 RILs. A total of 22 QTLs were identified across 10 chromosomes, among these 09 were consistently stable. The findings hold significant promise for marker-assisted breeding to develop mungbean varieties with improved MYMIV resistance, optimized flowering time, and other essential morpho-biochemical traits.

Identification of candidate gene(s) for leaf rust resistance in *T. timopheevii* IL Sel.G12 and transfer to wheat variety HD2932

In this research, we assessed the response to leaf rust in RIL population derived from a cross between Selection G12 and Agra local and HD2932, including F3:4, and F6:7 recombinant inbred lines (RILs), over multiple seasons with two leaf rust pathotypes 77-5 and 106. Through the test of allelism and single race testing (SRT) involving 32 Indian leaf rust pathotypes, we determined that LrSelG12 shares an allelic relationship with a previously reported gene, Lr18. LrSelG12 and Lr18 are situated in the same region on chromosome 5B (Lr18 locus), however, LrSelG12 differs from the previously identified Lr18 as it imparts a high level of resistance to all Indian leaf rust pathotypes. Sequence analysis of candidate genes revealed InDels and cloning of fragments having these deletions showed deletion in TraesCS5B02G544800 and TraesCS5B02G544900 in susceptible parent Agra local. Additionally, an InDel-specific PCR marker was designed that co-segregated with leaf rust resistance in the RILs and backcross-derived population. Conventional cum marker-assisted transfer of the leaf rust resistance gene LrSel.G12 into the wheat variety HD2932 resulted in the development of Near-Isogenic Lines (HD2932+LrSel.G12), exhibiting resistance against Indian leaf rust pathotypes. Through a combined approach of foreground, background, and phenotypic selection, NILs of HD2932 with over 95% Recurrent Parent Genome (RPG) were developed that revealed variations in traits such as plant height, tiller numbers, test weight, number of seeds per spike, and yield per plant. Notably, several NILs displayed superior traits compared to HD2932, indicating the potential for improved performance in these agronomically important traits.

Theme 3: Breeding for Tolerance to Abiotic Stresses

Genetic Diversity Analysis for low phosphorus tolerance in mung bean germplasm

The present study aimed at screening 228 mung bean accessions collected from acidic zones of Jharkhand, Bihar, Odisha, West Bengal, Andhra Pradesh, and North-Eastern states to identify genotypes with greater PUE. Eleven traits related to phosphorus use efficiency (PUE) as well as yield were evaluated, revealing variations for all traits, except root-to-shoot ratio (RSR). Heritability assessments for various traits, including shoot fresh weight (SFW), root fresh weight (RFW), shoot dry weight (SDW), root dry weight (RDW), phosphorus content (PC), total phosphorus uptake (TPU), phosphorus utilization efficiency (PUE) and yield-associated attributes i.e., Days for bud initiation (DBI), days for 50% flowering (DF), Days for pod initiation (DPI), Days for 50% podding (DFP), Cluster/Plant (CPP), Total no of pods (TP), Total pod weight (TPW), Yield (Y) and Yield/Plant (YPP) unveiled high heritability, denoting the potential for selective breeding to enhance these traits. Principal component analysis (PCA) and cluster analysis illustrated the genetic diversity of 120 mung bean genotypes based on 21 traits, i.e., including all PUE-related and yield-attributing traits. Interestingly, correlations and PCA patterns for phenological and yield attributes were comparable under both low phosphorus (E1) and optimal phosphorus conditions (E2). Morphological diversity analysis, using the Mahalanobis D^2 values, grouped the 120 mung bean accessions into 17 clusters under both E1 and E2. This research offers valuable insights into the genetic diversity for low phosphorus tolerance and yield, laying the foundation for targeted breeding efforts to ensure sustained agricultural productivity under low phosphorus conditions.

Molecular characterization of *Oryza sativa* genotypes using candidate gene markers for nitrogen use efficiency (NUE) and phosphorus use efficiency (PUE)

Nitrogen and phosphorus availability are two major abiotic factors limiting rice productivity, particularly in acid soil environments. Donors with high phosphorus and nitrogen use efficiency may help achieve sustainable rice production in deficient soil conditions. The present study characterized 96 popular rice varieties and landraces using 17 and 12 gene-specific markers for nitrogen and phosphorus use efficiency, respectively. Karhani (10 genes) was found to have a maximum number of positive alleles for phosphorus use efficiency, followed by IRCTN-91-84, IIABL-6, and IET30244 (9 genes). Tulsiphul, (14 genes) was found to have the maximum number of positive alleles for nitrogen use efficiency, followed by CAUS124, Pusa1176, Chandanchoor, and Ṅ IET 29573 (13 genes). Three genotypes (CAUS124, IRCTN-91-84, and Tulsiphul) were found to be positive for 21 loci. Bhalum 3, Bhalum 5, Vardhan, and CAUS 107 performed well under field conditions despite testing positive for only a few candidate genes, suggesting the role of some other genes responsible for their superior field performance. In the field study, the rice genotypes showed significantly high genetic variability for low P tolerance and low N. A few genotypes revealed non-Pup1 type tolerance.

Molecular mapping of QTLs conferring drought tolerance in *Brassica carinata* derived *Brassica juncea* introgression lines

The present study revealed enormous genetic variability for eighteen agro-morphological and three physiological traits in the *Brassica carinata-derived B. juncea* introgression lines (ILs). The significant correlation and a moderate level of direct effects were recorded by seeds per siliqua, biological yield (g), harvest index (%), and 1,000 seed weight (g) on seed yield per plot (g) under moisture deficit stress conditions. In rainfed conditions, ILs and their respective parents had a higher mean WUE than in irrigated conditions. The means of ILs were higher than their respective parents for WUE. Using these ILs, the drought tolerance index (DTI) and mean relative performance (MRP) were reported to be efficient in the selection of productive lines under drought conditions. The present study established the phenomenon of "heterosis" for drought tolerance and water use efficiency by evaluating 105 hybrids developed from intermating 15 ILs. Traits under study were found to be governed by both additive and non-additive types of gene action. Eight QTL hotspots containing two or more QTLs governing agro-morphological traits, WUE, and drought-tolerant indices were identified under moisture deficit stress conditions. Seventeen candidate genes, viz., SOS2, SOS2 like, NPR1, FAE1-KCS, HOT5, DNAJA1, NIA1, BRI1, RF21, ycf2, WRKY33, PAL, SAMS2, orf147, MAPK3, WRR1, and SUS, that were already reported to be involved in different biotic-abiotic stress tolerance pathways in crops, were reported in the genomic regions of identified QTLs. This study demonstrated the utility of interspecific hybridization by introducing genomic segments from a related species for improving drought tolerance in Indian mustard.

Mining and validation of ERF family genes for salt tolerance in landraces of chickpea (*Cicer arietinum* L.)

A comprehensive study using a diverse collection of 138 landraces from the WANA (West Asia and North Africa) region along with 25 varieties was conducted for agronomic, morpho-physiological, and root traits both under field and pot experiments. The high salinity-induced reductions were observed for these traits viz., PPP, 100SW, SY, RWC, MSI, Chlorophyll, shoot and root Na+ /K+ ratios, TRL, SA, RV, and RLD. By evaluating these traits, certain landraces, including ILC11902, IG5980, and ICCV10, demonstrated salt tolerance. In contrast, IG5856, IG5857, and DCP92-3 were identified as salt-sensitive based on Cumulative Stress Tolerance Index (CSTI) scores. By utilizing 16K SNPs spanning across all the 8 chickpea chromosomes, we have identified 11 significant SNPs under salt stress conditions. Interestingly, one SNP Ca30675468 exhibits associations with multiple traits, signifying its significance as a superior SNP. Moreover, a total 3 polymorphic sites (SNPs) (transition and transversion) were identified in the *HKT1* gene coding region. One parsimony informative site (was found at 492nd position in the coding region of *HKT1* gene in salt tolerant landraces ILC11902 and IG5980. The expression pattern analysis unveiled significant changes. ERF109 was found to be upregulated in tolerant genotypes, while downregulated in sensitive genotypes. Similarly, the HKT1 gene showed upregulation in tolerant genotypes and downregulation in sensitive genotypes. The findings suggest that tolerant genotypes exhibit a more advanced and efficient set of physiological and molecular mechanisms for coping with salt stress. The present study provides valuable insights into the complex nature of salt tolerance in chickpea landraces.

Genetic mapping of iron toxicity tolerance in rice (*Oryza sativa* L.)

Iron toxicity poses a significant threat to rice growth, particularly in lowland acidic soils, affecting both vegetative and reproductive stages. This study was aimed to uncover tolerance variability to high iron levels in rice and map genomic regions controlling the tolerance. Using a hydroponic system, 16 rice genotypes were evaluated for their phenotypic response to induced iron levels. Results revealed 460 ppm of iron in the nutrient solution as critical for screening seedling stage responses. Excess iron impacted morphological and root system traits, leading to the classification of genotypes as tolerant or sensitive. Leaf bronzing emerged as a prominent indicator of iron stress, aiding in genotype categorization. Among the identified tolerant genotypes, ILS12-5 was a previously unrecognized variety, while popular varieties like BPT 5204 and Pusa 44 exhibited sensitivity. Root system traits, including root length, surface area,and volume, were severely affected by iron toxicity. Germplasm screening in hydroponic and field conditions highlighted trait variations, with panicle length being unaffected by iron toxicity. Despite a decline in flowering time and increased tillering under stress, yield remained compromised. Genotypic classification based on leaf bronzing and stress tolerance index categorized genotypes, yet a poor correlation existed between hydroponic and field conditions. Several genotypes, including IRG 81 and IRG 268, exhibited resilience across environments,while others like IRG 173 were identified as sensitive. The study identified 37 significant marker- trait associations (MTAs) for iron toxicity traits, explaining significant phenotypic variation. Notably, one novel MTA on chromosome 3 was linked with bronzing score. Field screening identified 19 MTAs, with novel associations for days to flowering under iron toxicity. A rigorous validation process revealed specific MTAs associated with flowering time, root length, and grain iron and zinc content. These findings offer valuable insights for managing iron toxicity in rice and enhancing tolerance through breeding programs. The integration of MTAs into breeding efforts holds promise for developing rice varieties with improved tolerance to iron toxicity, ultimatelycontributing to more robust and productive crops in stress-prone areas.

Genome-wide association mapping and genomic selection for drought and heat tolerance in wheat

A genome-wide association study followed by genomic selection for drought and heat tolerance was conducted. Multi-location phenotyping with irrigated, restricted irrigated and late sown conditions was conducted to impose drought and heat stress along with the control. Important agronomical, physiological and grain nutrition traits like Days to Heading (DH), Days to Maturity (DM), Normalized Difference Vegetation Index (NDVI), Chlorophyll Content (SPAD), Canopy temperature (CT), Plant Height (PH), Thousand Grain Weight (TGW), Grain Weight per Spike (GWPS), Plot Yield (PLTY), Biomass (BM), Grain zinc (GZnC) and grain iron content (GFeC) were phenotyped. Genome-wide SNP data was generated using 35K Axiom™ Wheat Breeder's Genotyping Array. GWAS panels were found to be structured. A total of 108 stringent marker-trait associations were identified, among them 24 were found under drought and 45 were found under heat stress conditions. *In-silico* search of the identified markers against the IWGSC ref genome revealed the presence of a majority of the SNPs at or near the candidate genes coding for various important metabolic activities. A comparison of prediction accuracy revealed that Random forest regression (RFR) is the best model for the calculation of genomic estimated breeding value (GEBV). A mean prediction of 44.7% was obtained for PH and 42.4%, 39.3%, 27.4%, and 26.6% was obtained for

DH, GWPS, TGW, and PLTY, respectively. Superior 25 lines each for drought, heat stress, and irrigated conditions were identified that can be used in the next cycle of genomic selection or can be evaluated for their potentiality in field conditions.

Allele mining of heat tolerance gene(s) in chickpea (*Cicer arietinum* L.) landraces

In this study, we conducted an extensive genetic investigation of chickpea, with a primary focus on traits associated with yield and their response to heat stress. Significant variations in these traits under both normal and high-temperature conditions were observed. Yield-related traits exhibited high heritability and AMMI1 analysis provided intricate insights into genotype-environment interactions. By employing a genome-wide association study (GWAS), we pinpointed 27 marker trait associations (MTAs) linked to yield-related traits among which five common MTAs displaying pleiotropic effects were identified after applying a stringent Bonferroni-corrected p-value threshold of <0.05 (–log10(p) > 4.95). Through an in-depth *in-silico* analysis of these markers against the CDC Frontier v1 reference genome, we discovered that the majority of the single nucleotide polymorphisms (SNPs) were located at or in proximity to gene-coding regions. These identified MTAs and associated candidate genes serve as valuable assets for breeding programs dedicated to crafting resilient chickpea varieties in the face of climate change. MTAs/genomic regions controlling pods/plants, yield traits, and phenological traits could be potentially incorporated in the high-yielding yet drought/heat stress-sensitive popular chickpea cultivars for improving drought and heat stress in chickpea. Genetic variation within the *CAP2* and *HSFA2* genes was explored by amplifying the entire gene length and sequencing the products. For *CAP2*, seven single nucleotide polymorphisms (SNPs) were identified, resulting in both synonymous and amino acid-altering mutations. For *HSFA2*, six SNPs were found, leading to synonymous and amino acid-changing substitutions. These insights gained pave the way for future breeding endeavours, contributing to global food security.

Mapping of QTLs for combined heat and drought tolerance in wheat (*Triticum aestivum* L.)

This study aimed to map Quantitative Trait Loci (QTLs) associated with key component traits of drought and heat tolerance, followed by the validation of these QTLs. The mapping population consists of two distinct sets of Recombinant Inbred Lines (RILs) derived from HD3086/HI1500 and GW322/KAUZ crosses. Analysis of variance revealed significant genotypic variation. Significant reductions in various traits were observed under combined stress followed by individual heat and drought stresses. Grain iron concentration increased under drought stress, while grain zinc concentration increased under heat stress. Traits like biomass, thousand-grain weight, and grain weight per spike showed significant positive correlations, while days to 50% heading showed negative correlations with yield. SNP genotyping was carried out using a 35K Axiom Breeders array. The linkage map indicated polymorphic markers were uniformly distributed throughout the genome. In the HD3086/HI1500 population, a total of 193 QTLs were mapped across different treatments with QTLs distributed across all chromosomes. Similarly, in the GW322/KAUZ population, 35 QTLs were detected for various traits under distinct stress conditions. A total of 39 stable QTLs were identified in the HD3086/HI1500 population along with 8 in GW322/KAUZ. Interestingly 8 QTL hotspots harbouring QTLs for multiple traits were found. Expression analysis unveiled 14 transcripts expressed under all stress conditions. Notably, 12 QTLs were successfully validated including those linked to grain weight, yield, NDVI, plant height, and days to heading. Overall, this study provides valuable insights into the genetic basis of drought and heat tolerance offering potential markers for crop improvement through marker-assisted selection.

Theme 4: Breeding for Enhanced Nutritional Quality

Molecular mapping of aroma in the improved Kalanamak rice (*Oryza sativa* L.)

The genetic basis of aroma in Kalanamak rice has remained largely unexplored and here we aimed to unravel the genetic basis of aroma in this prime rice cultivar. A set of 125 BILs derived from the cross of traditional Kalanamak and Pusa 1176, a short grain aromatic line derived from Bindli mutant 68 have been analyzed for their variation for aroma content through quantification of 2AP using GC-MS. The population depicted significant variation for the 2AP concentration which ranged from 263 ppb to 1997 ppb. Subsequently, two bulks contrasting for the 2AP concentration were constituted and the pooled DNA of the individual bulks, along with the parent Pusa 1176 were subjected to whole genome re-sequencing. The sequence data was analyzed using the QTLseq pipeline and this identified eight-grain aroma-associated novel QTLs (not reported in the previous studies), which are located in chromosomes 1, 3, 6, 7, 8, 10, and 12. The masking effect of the *badh2* locus on the QTLseq analysis was eliminated by ensuring the presence of 8 bp deletion of *badh2* in all the individuals of both the bulks. I*nsilico* analysis of the QTL regions uncovered potential candidate genes responsible for aroma synthesis and regulation. A total of 52 genes were identified as candidate genes for aroma, which includes LOC_Os01g37760, LOC_Os01g40190, LOC_Os03g13300, LOC_Os03g12290, LOC_Os06g08900, etc. These genes directly or indirectly regulate the 2AP metabolism and influence the aroma in Kalanamak rice and therefore, these QTLs and the underlying genes could be useful for rice breeding programs.

Assessment of genetic variability for yield components and nutritional quality in pigeonpea genotype

The selection of genotypes with high yield and yield-related characteristics, along with improved biochemical properties, is crucial for breeding programs aimed at developing better varieties/hybrids that can contribute to food and nutritional security in the current scenario. The experimental material comprised of 75 pigeonpea genotypes along with 5 checks was evaluated in randomized block design with 2 replications for studying the yield and its contributing characters. The observations were recorded on 7 agro-morphological traits. The top 30 high-yielding genotypes along with the 5 checks were subjected to nutritional analysis. Significant differences were observed for agromorphological traits such as plant height, number of branches, days to maturity, days to 50% flowering, 100 seed weight, yield per plant, and plot yield among the pigeonpea germplasm lines. This specified that there is ample scope for the selection of desirable genotypes in the present group of germplasm for yield improvement. Based on mean performance genotype ICP4715 exhibited the highest mean performance for grain yield per plot over the check TJT 501. As many as 15 pigeon pea genotypes were on par with checks for yield. The genotype ICP4715 was found to have a significantly higher yield than one of the check varieties TJT 501. Significant variations were also observed in the nutritional parameters. These genotypes with better yield and nutritional characteristics can be utilized in future breeding programs for developing better varieties/hybrids.

Genetic evaluation of black pericarp basmati rice genotypes

The present study was carried out to characterize the black pericarp Basmati rice genotypes developed through the introgression of high anthocyanin traits sourced from black rice with the desirable grain, cooking, and eating qualities of Basmati rice varieties. Significant differences in agromorphological traits were observed among the genotypes. As many as 23 black pericarp rice genotypes were found to yield on par with the popular Basmati varietal check such as Pusa Basmati 1121 and Pusa Basmati 1509, with two genotypes namely Pusa 3215-16-115-6-1- 5-1, Pusa 3214-16-30-13-2-2-1 significantly superior to the checks. Further, the black pericarp genotypes were classified into 17 black, 32 dark brown, 19 light brown, and 1 white-colored pericarp classes based on dehusked rice. TAC ranged from 167.88 to 2.897 mg/100g DW, and the specific components like C3G and P3G ranged from 2.897 to 167.88 mg/100g DW and 0.592 to 44.19 mg/100g DW, respectively. As many as 5 genotypes showed higher anthocyanin content retention with 15 seconds of milling than the check, Chakhao Poireiton. Molecular characterization using gene-specific markers revealed that 13 genotypes possess the resistance alleles of at least three genes for blast and BB genes in two combinations namely *xa13+Pi2+Pi54* or *xa13+Xa21+Pi2*. The research demonstrates the feasibility of combining the desirable attributes of both aromatic and Basmati rice varieties to produce grains with improved anthocyanin content for added health benefits. Overall, these developed improved provide base materials to meet the Basmati qualities along with enhanced anthocyanin content and resistance to both the BB and blast diseases.

Genome-wide association (GWAS) analysis of grain quality traits in emmer wheat (*Triticum dicoccum*) germplasm

A diverse set of 155 dicoccum wheat accessions from the Indian National Genebank were assessed for grain quality traits like grain iron, zinc, protein, and thousand grain weight; and a GWAS study was performed using 35 K Axiom SNP genotyping data. These accessions along with three checks were grown at three locations following alpha lattice design under optimum conditions. Significant variation was observed among the genotypes for the traits studied at all the locations. The heritability was highest for grain iron concentration and least in thousand-grain weight. A significant positive correlation was observed between grain iron and zinc whereas a significant negative correlation between grain protein and thousand grain weight. Following cluster analysis, the genotypes were grouped into six groups based on the Ward method, where clusters six and two had high and low mean performance for most of the traits. In principal component analysis, the major traits contributing for PC 1 were grain iron concentration and grain zinc concentration. Marker-trait association (MTA) analyses using maximum likelihood models revealed 125 significant MTAs for 4-grain quality traits with ($-\log_{10}(P) \geq 3$). We found 15 marker-trait associations (MTAs) for 4-grain quality traits with ($-\log_{10}(P) \geq 4$) and the phenotypic variation estimated (PVE) ranged from 3.44% to 73.10%. We identified 1 pleiotropic SNP regulating both TGW and GPC above the Bonferroni correction. The information generated in this study could be of potential value for improving the genetic base of grain quality traits in wheat using marker-assisted selection.

Genetic and molecular characterization of rice (*Oryza sativa*) germplasm for yield and nutritional quality traits

Phytic acid (PA) is a major source of phosphorus in grain and is essential for seed to germinate but at the same time is an anti-nutritional factor that reduces the bioavailability of micronutrients like Zn, Fe, Ca, etc. As a result, higher phytic acid content in major food grains such as rice leads to micronutrient deficiency affects human health. Breeding rice varieties with low phytic acid (LPA) is one of the effective strategies to overcome micronutrient deficiency in rice eaters. In this endeavor, a diverse set of 80 rice germplasm was evaluated for agro morphological traits and PA, Fe, and Zn content in grains. Genotypes were also screened with low phytic acid-associated candidate gene-based markers. The range of phytic acid in our study was 1.11mg/gm to 3.33mg/gm. The range of Fe was from 12.4mg/kg to 159mg/kg and Zn varied from 18.7 mg/kg to 49.7mg/kg. We got a significant difference for the SPDT gene and it showed a variance of 11.4%. There was no correlation among PA, Fe, and Zn content. The low phytic acid cultivar we found was BAU21802 which also has a good amount of Iron and can be used for donors or it can be released directly after validation.

Analysis of genetic variability, molecular characterization and marker-assisted enrichment of kernel oil in maize (*Zea mays* L.)

High oil maize (>6%) genotypes enhance the bioavailability of fat-soluble vitamins and higher calorific value of the grain. Allele screening by exploiting functional genomic regions of *dgat1*-2 and *fatb* genes in 292 diverse collections revealed the lower frequency of *dgat1*-2 (0.15) and *fatb* (0.12) mutant alleles and identified 10 germplasms with both the mutant alleles. Sequence characterization of *dgat1*-2 and *fatb* revealed wide variation within the genes. Gene-based InDel-markers developed here would facilitate the characterization of unknown germplasm. Multi-location evaluation of 48 diverse maize genotypes exhibited wide genetic variation for kernel oil content and fatty acid profile. Genetic dissection of embryo size and weight-related traits through generation mean analysis revealed the predominance of dominant and dominant × dominant epistasis. Marker-assisted introgression of *dgat1*-2 and *fatb* genes from IHO-donors into parental lines of four popular multi-nutrient-rich maize hybrids enhanced kernel oil content (>6.5%), a reduction (35%) in palmitic acid and an increment (50%) in oleic acid. Performance for other quality parameters (lysine, tryptophan, proA, and proE) and agronomic traits in introgressed inbreds and improved hybrids were similar to their original parents and hybrids. GWAS identified 64 significant marker-trait associations (MTAs) for tocochromanols and 20 MTAs for phenolic compounds with medium to high prediction accuracies across traits. These are first-of-its-kind genotypes developed with high oil content, better oil quality, and rich in lysine, tryptophan, proA, and proE contents due to the favorable alleles of six target genes (*o2, crtRB1, lcyE, vte4, dgat1-2* & *fatb*) in a single genetic background.

Genetic analysis, molecular characterization and enrichment of lysine and tryptophan in popcorn inbreds using marker-assisted selection.

In the present study, genetic variability studies on a diverse panel of 48 popcorn inbreds identified significant genetic variation for popping quality traits like total flake volume (TFV), popping expansion volume (PEV), single flake size (SFS), popping rate (PR), and grain yield (GY). Popcorn inbreds with desirable popping quality with higher grain yield were identified. The line × tester mating analysis on 15 lines and 5 testers employing 75 F_{1s} were subjected to multilocation evaluation for popping quality and agronomic traits. Additive genetic variance for the majority of popping quality traits, while dominant genetic variance for grain yield was predominant. Best general combiners and highly heterotic crosses with high specific combining ability for popping quality traits and grain yield were identified. Meta-analysis on popping quality QTLs identified 11 MpQTLs, of which MpQTL-1.1 (*umc2012*) was validated on diverse maize genotypes. We attempted genomics-assisted enhancement of protein quality in elite parental inbreds of superior popcorn hybrids viz., Pusa Popcorn Hybrid-1 and Pusa Popcorn Hybrid-2. A two-backcross generation marker-assisted backcross breeding for introgressing *opaque2* (*o2*) and opaque16 (*o16*) genes was employed for foreground selection and background selection using polymorphic SSR markers and phenotypic selection for vitreous kernel characteristics. The improved inbreds were selected for *o2+o2+*/*o16o1*6, *o2o2*/*o16+ o16+*, and *o2o2*/*o16o16* genotypes. The selected introgressed popcorn lines possessed 1.5- to 2.6-fold enhancement in lysine, and 2.3- to 3.7-fold increase in tryptophan (>0.087%). These newly derived quality protein popcorn inbreds would serve as valuable resources for the development of popcorn hybrids with higher lysine and tryptophan.

Assessment of the effect of compositional factors on chapati quality and marker assisted transfer of glutenin alleles to Indian wheat (*Triticum aestivum* L.) variety.

A set of 41 diverse genotypes including hard, soft, and *Sharbati* varieties of India was grown at three locations during and analyzed for forty-one traits including physicochemical, rheological, and gluten genes, for their relation with *chapati* quality components. *Chapati* with cream color, higher diameter, full puffing, easy to tear and retaining this pliability for a long time is highly desirable. Increased polyphenol oxidase (PPO) activity had a high positive correlation with the phenol reaction test and significantly contributed to undesired discoloration in dough and *chapati*. Allelic combinations, *PpoA1bPpoB2dPpoD1a (bda)* and *PpoA1bPpoB2dPpoD1a (baa)* produced the lowest PPO activity and are thus more desirable for superior *chapati* quality. Different subunits of glutenin were also found to have a significant impact on the *Chapati* Quality Score (CQS). The HMW-GS, GluA1-null coded by *Glu-A1*c, GluB1-20 coded by *GluB1e*, GluD1-2+12 coded by *GluD1a* and LMW-GS alleles, *Glu-A3f* and *Glu-B3i* were found to have significant positive association with CQS. Genotypes C273, C306, C518, HD2851 and HI1531 were found best and stable for *chapati* quality and C306 stood out as a variety with unique expression of many traits. It is recommended that the criteria for superior *chapati* quality flour be: High GHI, DaS, WA, DOS, P, P/L and low GI, SV, AC, PPO activity, DDT, Stability, FQN and L. Further, a successful attempt was also made to transfer the four glutenin alleles from C306 to the popular wheat variety HD2967 using the Marker Assisted Backcross Breeding method and seed of 59 BC$_2$F$_4$ homozygous plants (*GluA1cGluB1eGluD1aGluA3cGluB3i*) was obtained.

List of the students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Bajjuri Divya (21658)	M.Sc.	Genetic and molecular characterization of allocytoplasmic near-isogenic lines of Pusa Sugandh 5	Dr. Prolay Kumar Bhowmick	ICAR-IARI, New Delhi
2.	Kavya R (21659)	M.Sc.	Genome-wide association studies for stem sturdiness in rice (*Oryza sativa* L.)	Dr. Ranjith Kumar Ellur	ICAR-IARI, New Delhi
3.	Naman Raj (21660)	M.Sc.	Marker-assisted backcross breeding (MABB) integrating rapid generation advancement (RGA) for improvement of wheat variety HD3086	Dr. Shailendra Kumar Jha	ICAR-IARI, New Delhi
4.	Satyam (21661)	M.Sc.	Molecular mapping of aroma in the improved Kalanamak rice (*Oryza sativa* L.)	Dr. Harith Bollinedi	ICAR-IARI, New Delhi
5.	Ragini R (21662)	M.Sc.	Molecular cytogenetic analysis of gamma-ray irradiated derivative lines of the cross between bread wheat and *Aegilops speltoides*	Dr. Niranjana M	ICAR-IARI, New Delhi
6.	Jenia Roy (21663)	M.Sc.	Unfolding the complex regulatory network of rust (*Uromyces viciae-fabae*) resistance in lentil (*Lens culinaris* Medik.) using comparative RNA-seq analysis	Dr. Muraleedhar S. Aski	ICAR-IARI, New Delhi
7.	Amit Kumar Mazumder (21664)	M.Sc.	Genome-wide association study to identify marker-trait association(s) for morpho-physiological traits under contrasting production regimes in bread wheat	Dr. Kiran B. Gaikwad	ICAR-IARI, New Delhi
8.	Dharavath Hathiram (21665)	M.Sc.	Assessment of genetic variability for yield components and nutritional quality in pigeonpea genotype	Dr. Rama Prashat G	ICAR-IARI, New Delhi
9.	Roopa M N (50078)	M.Sc.	Genetic evaluation of black pericarp basmati rice genotypes	Dr. Gopala Krishnan S	#ICAR-IARI, Assam
10.	Udaya Bhanu Angirekula (50079)	M.Sc.	Genome-wide association (GWAS) analysis of grain quality traits in emmer wheat (*Triticum dicoccum*) germplasm.	Dr. Jyoti Kumari	#ICAR-IARI, Assam

11.	Harish Walikar (50080)	M.Sc.	Phenotypic evaluation of genetic variability for productivity-related traits in a recombinant inbred population and molecular tagging of gene(s) for lodging resistance in chickpea (*Cicer arietinum* L.)	Dr. Venkatraman Hegde	#ICAR-IARI, Assam
12.	Firos Basha T M (60107)	M.Sc.	Genetic diversity and association mapping of early vigour in aus rice (*Oryza sativa* L.)	Dr. Somnath Roy	#ICAR-IARI, Jharkhand
13.	Sayan Goswami (60108)	M.Sc.	Genetic diversity analysis for low phosphorus tolerance in mungbean germplasm	Dr. Anima Mahto	#ICAR-IARI, Jharkhand
14.	Kotte Bhargava (60109)	M.Sc.	Genetic analysis of kernel row number (*krn*) gene(s) in the manifestation of heterosis in maize (*Zea mays* L.)	Dr. Bhavana Patnayakuni	#ICAR-IARI, Jharkhand
15.	Chandana H S (80016)	M.Sc.	Genetic studies on rice lines introgressed with multiple biotic stress tolerance genes	Dr. Pankaj Koushal	**ICAR-NIBSM, Raipur
16.	Chaduvula Eshwar Sai Prasad (80017)	M.Sc.	Ploidy-regulated trait expression in pearl millet (*Pennisetum glaucum*)	Dr. Pankaj Koushal	**ICAR-NIBSM, Raipur
17.	Jaya Kothapelly (90011)	M.Sc.	Genetic and molecular characterization of rice (*Oryza sativa*) germplasm for yield and nutritional quality traits	Dr. Vijai Pal Bhadana	**ICAR-IIAB, Ranchi
18.	Adepu Priyadarshini (90012)	M.Sc.	Assessment of morphological and genetic diversity using simple sequence repeat (ssr) markers in horse gram (*Macrotyloma uniflorum*)	Dr. Sudhir Kumar	**ICAR-IIAB, Ranchi
19.	Mukesh Raj (90013)	M.Sc.	Development of SSR markers and their application in revealing genetic diversity in adzuki bean (*Vigna angularis*)	Dr. Avinash Pandey	**ICAR-IIAB, Ranchi
20.	Satya Sai Kumar Koppula (90014)	M.Sc.	Molecular characterization of *Oryza sativa* genotypes using candidate gene markers for Nitrogen use efficiency (NUE) and phosphorus use efficiency (PUE)	Dr. Avinash Pandey	**ICAR-IIAB, Ranchi
21.	Aalok Shiv (10828)	Ph.D.	Role of microRNA mediated regulation in host-pathogen interaction during leaf rust infection in wheat (*Triticum aestivum* L.)	Dr. Pradeep Kumar Singh	ICAR-IARI, New Delhi
22.	Sneha Nymagoud (10829)	Ph.D.	Genetics and mapping of leaf rust resistance gene(s) in *Triticum timopheevii* zhuk. introgression lines in wheat (*Triticum aestivum* L.)	Dr. Vinod	ICAR-IARI , New Delhi
23.	Suman Dutta (11268)	Ph.D.	Molecular characterization and utilization of matrilineal (*mtl*) gene for in-vivo haploid induction in maize (*Zea mays* L.)	Dr. Firoz Hossain	ICAR-IARI, New Delhi
24.	Abhijith K P (11269)	Ph.D.	Development of heterotic pools in Basmati rice	Dr. Gopala Krishnan S	ICAR-IARI, New Delhi
25.	Limbalkar Omkar Maharudra (11270)	Ph.D.	Molecular mapping of QTLs conferring drought tolerance in *Brassica carinata* derived *Brassica juncea* introgression lines	Dr. Naveen Singh	ICAR-IARI, New Delhi

26.	Nilesh Joshi (11271)	Ph.D.	Mining and validation of ERF family genes for salt tolerance in landraces of chickpea (*Cicer arietinum* L.)	Dr. Bharadwaj Chellapilla	ICAR-IARI, New Delhi
27.	Sunilkumar V P (11274)	Ph.D.	Marker-assisted improvement of wheat variety HD3086 for leaf rust and moisture deficit stress tolerance	Dr. Pradeep Kumar Singh	ICAR-IARI, New Delhi
28.	Ashvinkumar Katral (11275)	Ph.D.	Analysis of genetic variability, molecular characterization and marker-assisted enrichment of kernel oil in maize (*Zea mays* L.)	Dr. Vignesh Muthusamy	ICAR-IARI, New Delhi
29.	Suresh Yadav (11277)	Ph.D.	Mapping and transfer of rust resistance gene(s) derived from *Triticum turgidum* var. durum cv. Trinakria in bread wheat	Dr. Shailendra Kumar Jha	ICAR-IARI, New Delhi
30.	Nandakumar S (11521)	Ph.D.	Genetic mapping of flag leaf and panicle architecture in rice	Dr. Prolay Kumar Bhowmick	ICAR-IARI, New Delhi
31.	Sonu (11522)	Ph.D.	Genetic mapping of iron toxicity tolerance in rice (*Oryza sativa* L.)	Dr. K.K.Vinod	ICAR-IARI, New Delhi
32.	Prashant Vasisth (11526)	Ph.D.	Identification of heterotic genomic segment(s) in *Brassica carinata* derived *Brassica juncea* introgression lines	Dr. Naveen Singh	ICAR-IARI, New Delhi
33.	I Gopinath (11528)	Ph.D.	Genetic analysis, molecular characterization, and enrichment of lysine and tryptophan in popcorn inbreds using marker-assisted selection.	Dr. Vignesh Muthusamy	ICAR-IARI, New Delhi
34.	Manoj Kumar Patel (11530)	Ph.D.	Understanding genetics and marker-trait associations for seed yield and quality in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]	Dr. D. K. Yadava	ICAR-IARI, New Delhi
35.	Sunaina Yadav (11531)	Ph.D.	Inheritance, molecular mapping of gene(s) for cream grain color, and gene action studies for some quantitative traits in pearl millet [*Pennisetum glaucum* (L.) R. Br.]	Dr. Sumer Pal Singh	ICAR-IARI, New Delhi
36.	Nikki Kumari (11532)	Ph.D.	Identification of QTLs imparting resistance to MYMIV infection and earliness traits in mungbean (*Vigna radiata* (L.) Wilczek)	Dr. Gyan Prakash Mishra	ICAR-IARI, New Delhi
37.	Manjunatha P B (11534)	Ph.D.	Association mapping for agronomic traits influencing yield in mungbean	Dr. Harsh Kumar Dikshit	ICAR-IARI, New Delhi
38.	Narayana Bhat Devate (11535)	Ph.D.	Genome-wide association mapping and genomic selection for drought and heat tolerance in wheat	Dr. Pradeep Kumar Singh	ICAR-IARI, New Delhi
39.	Harisha R (11537)	Ph.D.	Assessment of the effect of compositional factors on chapati quality and marker-assisted transfer of glutenin alleles to Indian wheat (*Triticum aestivum* L.) variety	Dr. Anju Mahendru Singh	ICAR-IARI, New Delhi
40.	Chandana B S (11653)	Ph.D.	Identification of genomic regions for nodulation traits through genome wide association mapping in chickpea (*Cicer arientinum* L.)	Dr. Rajendra Kumar	ICAR-IARI, New Delhi

41.	Ramesh (11791)	Ph.D.	Identification of candidate gene(s) for leaf rust resistance in *T. timopheevii* IL Sel.G12 and transfer to wheat variety HD2932	Dr. Shailendra Kumar Jha	ICAR-IARI, New Delhi
42.	Danakumara T (11796)	Ph.D.	Allele mining of heat tolerance gene(s) in chickpea (*Cicer arietinum* L.) landraces	Dr. Bharadwaj Chellapilla	ICAR-IARI, New Delhi
43.	Karthik Kumar M (11799)	Ph.D.	Mapping of QTLs for combined heat and drought tolerance in wheat (*Triticum aestivum L.*)	Dr. Pradeep Kumar Singh	ICAR-IARI, New Delhi
44.	Amaresh (11800)	Ph.D.	Fine mapping and deciphering the basis of zebra leaf trait in Pusa Zebra 18	Dr. Gopala Krishnan S	ICAR-IARI, New Delhi

#IARI off campus

**Outreach Institute

Plant Genetic Resources

2

Prof. Sunil Archak

Management of plant genetic resources (PGR) requires multi-disciplinary expertise. Advancements in science and technology and increasing threats of genetic erosion call for research and development to support PGR conservation and utilization activities. In order to conserve, sustainably use and enhance the value of PGR, country requires trained human resource. Indian Agricultural Research Institute, New Delhi is the only organization offering post graduate teaching and research in PGR since 1997. The major thematic areas of post graduate research in PGR include: Ecogeography and Systematics, Genetic Diversity Analysis, Genomics of PGR and Germplasm Conservation. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Ecogeography and Systematics

Trait-specific diversity mapping and habitat prediction of cowpea germplasm conserved in the Indian National Gene Bank

In the present study 7,194 accessions of cowpea (*Vigna unguiculata*) and 175 accessions of Yardlong bean (*Vigna unguiculata* subsp. *sesquipedalis*) having locality information were analysed. The analysis revealed that the majority of the accessions (63.60%) were collected from the northern region, followed by the peninsular region (27.71%) and the north-eastern hill (NEH) region (8.69%). Out of the 9,289 collected accessions only 2,770 (29.82%) of cowpea are being conserved at the Indian National Genebank (INGB). Out of 175 accessions of Yardlong bean germplasm collected from 13 states only 53 accessions are being conserved in INGB. Diversity map of cowpea revealed that only two taxa are cultivated and distributed across the India. The GIS map showed that cowpea is widely distributed while Yardlong bean is distributed in hill and tribal regions of India. The study identified collection and conservation gaps that need to be prioritized for further exploration and germplasm collection. Trait-specific germplasm variability mapping was done using the Shannon-Weaver diversity index particularly for days to 50% flowering, days of maturity, 100 seed weight, number of primary branches, peduncle length, pod length, plant height (cm), seed per pod, terminal leaf length, and terminal leaf width. Trait-specific germplasm for high 100 seed weight accessions (H=2.9–3.9) were represented from Jharkhand, Kerala, Odisha, Telangana, and Andhra Pradesh. Habitat prediction studies showed that in the future cowpea taxa will face the challenge of increasing climate change and the loss of their habitats. The Eastern Ghats region of the India, which includes the states of Odisha, Andhra Pradesh, the Bastar region of Chhattisgarh requires immediate attention for the collection of cowpea germplasm through mission-oriented exploration programs because these areas are prone to tsunami and cyclone.

Chemotaxonomic approaches for the authentication of Citrus species

The genus *Citrus* L, belonging to the orange sub-family Aurantioideae in the family Rutaceae, is a significant component of India's citrus genetic diversity. Despite the country's abundant wild and cultivated citrus species across diverse landscapes and climates, this genetic wealth remains largely unexplored. A study was conducted on 19 species and 6 hybrids from 8 citrus groups including physio-chemical characterization and chemo-profiling of peel essential oils. Morphological characterization of the studied accessions was based on 18 qualitative and 12 quantitative traits, revealing clustering into three groups through a UPGMA dendrogram. While positive correlations among various fruit traits were identified, relying solely on morphological traits proved insufficient for precise citrus plant identification, emphasizing the necessity for supplementary tools. Biochemical profiling included assessments of ascorbic acid content, antioxidant activity, total titrable acidity (TTA), total soluble solids (TSS), TSS/TTA ratio, and peel essential oil yield (% v/w). Significant positive correlations were noted among ascorbic acid concentration, antioxidant activity, total soluble solids, and the TSS/TTA ratio. Conversely, total titrable acidity exhibited a significant negative correlation with the TSS/TTA ratio. Hierarchical clustering based on biochemical profiles formed three major clusters, further grouping the accessions. Peel essential oils, extracted through hydro-distillation, were characterized by gas chromatography (GC-FID and GC-MS), identifying 137 components across accessions. A dendrogram based on essential oil composition grouped accessions into three clusters. Positive and negative correlations among specific essential oil components were observed, leading to the identification of three chemotypes: limonene, 1,8-cineole, and Z-β-ocimene. Specific compounds like artemisia ketone, δ-cadinene, and α-thujone were found associated with particular citrus varieties and hybrids. This research offers potential for identifying and characterizing citrus cultivars at both inter-specific and intra-specific levels, though additional validation is warranted.

Genetic resources studies on melons (*Cucumis melo* L.) of India

An exploration undertaken in Tamil Nadu, gathered 17 local snap melon landraces and two wild types. Nine snap melon landraces (IC-0647724 to IC-0647732) were conserved National gene bank. Morphological markers were assessed in 49 melon accessions included six *C.melo* varieties namely *momordica, agrestis, conomon, melo, flexuosus,* and *alwarensis*. It is revealing significant variations in 17 qualitative traits major variation observed in ovary pubescence, ovary shape and fruit shape. Principal component analysis and cluster analysis grouped accessions based on their morphological traits, demonstrating geographical associations among snap melon accessions. The first two PCs revealed cumulative variance of 64.11% and cluster analysis divided 49 accessions into three main clusters mainly based on geographical location and taxonomic variety. Among the quantitative traits days to 50% flowering (D50) showed very strong positive association with days to first flowering (DFF; r = 0.92), earliness of male (EM; r= 0.87), days to first fruit (DFfrt; r = 0.45) but negatively associated with leaf petiole length (LPL; r = -0.64) and peduncle length (PL; r = -0.65).Furthermore, molecular characterization using ITS and *rbcL* sequences used for taxonomic delimitation and genetic distance calculation among snap melon accessions. Phylogenetic analysis revealed distinct northern and southern groups within snap melon based on ITS sequences the highest genetic distance of 0.028 is observed between "phut-30" and "IC 552458," the lowest genetic distance is observed between "IC 552488" and "IC 552470”. While *rbcL* sequences confirmed the identity of different melon accessions. Intermediate accessions (PP 19 and IC 552488) were aligned with the snap melon and Sothiarmelon (HCM-3) aligned with oriental pickling melon (*C. melo* var. *conomon*) accession.The high genetic distance 0.026 was observed between IC 526873 (*C. melo* var. *conomon*) and Arya melon (*C. melo* var. *alwarensis*).

Molecular phylogeny and cytogenetic characterisation of Indian *Musa* species

The present study employed cytogenetic and molecular phylogeny techniques as alternative tools for species identification and understanding evolutionary relationships within the *Musa* genus to facilitate sample identification. A total of 35 *Musa* accessions, representing 21 different species, were collected from the National Gene Bank. Flow cytometric analysis revealed small inter specific variation in nuclear DNA content. The average genome size (1C content) ranged from 462.6 Mbp to 886.1 Mbp. Cytogenetic analyses identified 29 accessions as diploid (2n=22), three as triploid (2n=33), and one as tetraploid (2n=44). The chromosome number showed a significant positive correlation with nuclear DNA content (R=0.74) and ploidy status (R=0.85). Cytogenetic localization of rDNA sites showed variations in the number of loci for 45S and 5S rDNA in different *Musa* species. Molecular phylogenetic studies using the Internal transcribed spacer 2 (ITS2) region constructed a Neighbor-Joining phylogenetic tree, confirming close relationships between *Eumusa* and *Rhodochlamys* sections.The analysis of the ITS region sequence was extended to identify unknown and uncertain species stored in the National Gene Bank. This work also revealed the taxonomic status of three specific species namely; *Musa puspanjaliae*, *Musa paramjitiana* and *Musa balbisiana* var. *andamanica* which were further studied using the chloroplast genome. Chloroplast genome analysis was conducted on four recently identified *Musa* species from the Indian region using Illumina sequencing technology. The entire length of the *Musa* chloroplast genome ranged from 169,485 to 169,861 bp. Maximum likelihood phylogenetic analysis based on chloroplast genome data revealed evolutionary relationships among 16 species highlighting the close relationship between *Musa paramjitiana* and *Musa balbisiana* var. *andamanica* with *Musa balbisiana*. This multi-faceted approach enhances our understanding of *Musa* species providing insights into their diversity, evolutionary patterns, classification, conservation and sustainable management of India's rich biodiversity.

Theme 2: Genetic Diversity Analysis

Assessment of genetic variability of diverse blackgram (*Vigna mungo* (L.) Hepper) germplasm conserved in Indian National Genebank for pre-harvest sprouting tolerance

Pre-harvest sprouting (PHS) is an environmental phenomenon that significantly reduces the yield of blackgram under humid weather condition. One of the major reasons behind the PHS in field under humid weather condition is loss of adequate seed dormancy during domestication. Deploying genotypic capacity for PHS tolerance might be a practical strategy for PHS, but it hasn't been tested in blackgram. In order to better understand the effects of different physical and physiological features on PHS, a laboratory-based study was carried out to evaluate the genotypic potential of PHS tolerance in blackgram. A total number of 112 different blackgram accessions were examined for seed and pod morphological characteristics, water imbibition patterns, fresh seed germination, alpha-amylase activity and seed dormancy or hard seededness to characterize the trait PHS. The use of alpha-amylase enzyme activity was done as an indicator of dormancy level. The lack of fresh seed dormancy (FSD) in blackgram seeds makes them susceptible to pre-harvest sprouting (PHS), which degrades the quality of the grain or seed that is produced even though the seeds are protected inside the pod. Therefore, it has become crucial to create blackgram cultivars with short (10–15 day) FSD periods in order to reduce PHS losses. In this work, we examined differences in PHS, fresh seed germination (FSG), and enzymatic activity among various blackgram accessions. The 112 accessions studied showed a wide range in PHS tolerance and FSG, and 13 accessions were found to be PHS-tolerant (10%). An indicator of PHS, seed germination in a pod, ranged from 2.75% in the accession IC0485641 to 95.85% in the accession Mash 479. Blackgram seeds were first germinated then activity of alpha-amylase was measured at 0, 24, 48, and 72 hrs of germination. In contrast to PHS-tolerant accessions, there was a significant rise in alpha-amylase activity in the accessions with high FSG and PHS, particularly at 48 and 72 h after germination. In dormant accessions, the activity of alpha-amylase was low while in non-dormant accessions, the activity of alpha-amylase was recorded significantly high. As a result, the biochemical marker alpha-amylase can be utilized to assess the FSD and PHS potential of a wide range of blackgram accessions. Additionally, the study's findings about the diversity in seed germinability may be applied to future blackgram improvement programs.

Morphological, biochemical and molecular characterization of *Abrus precatorius* germplasm conserved at National Gene Bank

The present investigation was carried out to characterize Ratti (*Abrus precatorius* L.) germplasm on the basis morphological traits, biochemical parameters and molecular markers. For morphological characterization, five qualitative and 14 quantitative traits were recorded inthe field trials conducted during 2019-20 in ABD design. The biochemical characterization was done for moisture content, total phenols, antioxidants, ash content, protein content, total monomeric anthocyanin and flavonol content. Association analysis revealed the positive association of seed colour with total phenols, antioxidant, anthocyanin and flavonols. Under RAPD analysis, OPA-04 marker revealed the highest PIC(0.256) out of 16 RAPD primers.The microsatellite transferabilitystudy using the primers derived from soybean, *Vigna* and chickpea showed that SSR primers of *Vigna* hadthehighest transferability.The grouping of Ratti accessions did not show any association with seed colour. The dendrogram did not exactly group the accessions based on the geographical locations from where they were collected.

Variability studies in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] accessions using phenotypic, biochemical and molecular parameters

Horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] is an underutilized pulse crop that has been cultivated in South Asian countries by tribal and rural communities since time immemorial. Numerous nutraceutical properties and resistance to several biotic and abiotic stresses make it an ideal crop for nutritional and food security in the era of climate change. In the present study, we characterized 150 landraces and 5 improved varieties of horsegram using 11 quantitative, 16 qualitative traits, and 46 SSR markers and evaluated a selected panel of 74 genotypes for sixteen biochemical traits. A wide range of variability was observed among the accessions, with seed color, seed yield, Fe, and phytic acid content being the most diverse traits. The principal component analysis (PCA) showed that seed yield, days to 50% flowering, and Cu and Zn content contributed to most of the variability. The hierarchical cluster analysis revealed that most of the accessions from north Indian states and Madhya Pradesh were superior for yield-contributing traits and early maturing types. These accessions had higher carbohydrates, dietary fibers, and anthocyanins. The population STRUCUTRE analysis revealed that 120 of the total 157 germplasm lines (77.40%) were pure, suggesting a low level of admixture among the three populations identified. The mean FST values of 0.14, 0.15, and 0.17, respectively, for the three populations showed moderate genetic differentiation. The seed yield was positively correlated with pod length (r = 0.54) whereas it was negatively correlated with days to 80% maturity (r = -0.72). Thus, simultaneous selection for the early-maturing and high-yielding types can be practiced. All three analyzed micronutrients (Cu, Zn, and Fe) had a positive correlation with each other, giving scope for their simultaneous improvement. These results may help in the genetic improvement of horsegram. To validate these results, multi-location trials should be undertaken.

Morphological and molecular analyses of genetic variation and population differentiation in wild rice species of AA-genome

Rice (*Oryza sativa* L) is a staple food crop and provides calories, nutrients and nourishment to the millions of human beings. Phenotypically and molecularly characterized germplasm of crop wild relatives is an ideal basic material for genetic enhancement programmes of rice. We characterized 96 accessions of eight *Oryza* AA-genome and one CC-genome species utilizing 20 qualitative and 17 quantitative traits. The morphological characterization revealed a large extent of phenotypic variation for all the qualitative and quantitative traits except anther colour. In principal component (PC) analysis, first five PCs revealed cumulative variance of 79.22%. Correlation analysis revealed strong and positive association of days to main heading with days to 50% flowering. UPGMA dendrogram based on quantitative traits grouped CWRs into three major clusters. Molecular analysis with 45 hypervariable markers amplified 676 alleles, which varied from 4.0 to 26.0 with mean of 15.24 alleles per locus. PIC values ranged from 0.676 to 0.931. UPGMA dendrogram based on SSR data grouped the *Oryza* accessions into four major clusters separated at 0.10 similarity value. Bayesian model-based structure analysis revealed four subpopulations. Nei's genetic distance showed least genetic distance was observed between subpopulation-2 and 3. AMOVA revealed huge variation among the accessions of different species. High gene flow (Nm = 1.53) and moderate level of genetic differentiation (F_{st} = 0.14) found in CWRs. DNA sequencing of partial region of seed shattering (*SHA*1) gene in aromatic landraces and wild rice species (*O. nivara and O. rufipogon*) revealed 24 mutated sites with 16 singleton variable sites and seven parsimony informative sites. The large amount of genetic variation found in the wild rice accessions of AA-genome and full gene sequences of *SHA*1 may help to discover novel SNP in wild rice accessions for seed shattering and other domestication traits for their utilization in rice genetic improvement programmes

Genetic diversity analysis of exotic & indigenous adzuki bean (*Vigna angularis* (Wild) Ohwi and Ohashi) collections of National Genebank of India

Adzuki bean, an underutilized legume, holds immense potential as a mainstream pulse crop due to its affordability, high protein content, and nutritional richness. Agro-morphological diversity analysis of 100 accessions revealed significant variations in ten traits. Accessions comprising EC15256 (47.2 g), EC000377 (23.5 g) and EC120460 (20.9 g) were found to be promising for the seed yield per plant. Accession EC340283 was found to be promising for multiple traits like days to 50% flowering (53.5 days), plant height (28.99 cm) and days to 80% maturity (93 days). Only five traits viz., leaf colour, stem pigmentation, plant growth habit, were showed variation within species. Molecular analysis using 22 primers identified genetic diversity, with 50 scorable fragments. The genetic diversity ranged from 0.569 to 0.030, reflecting substantial variability. Molecular variance analysis indicated high genetic variability within *V angularis* genotypes, supported by hierarchical cluster analysis and population structure analysis. Biochemical analysis showcased significant variations in all the eight nutritional traits. Certain accessions stood out for these traits, holding promise for high-value food and feed varieties. Positive correlations were observed between protein and antioxidant content. Accessions IC341955 (23.7%), EC15256 (23.6%) and IC360533 (23.4%) were found to be promising for protein content. The identified promising accessions will provide a foundation for breeding strategies to enhance economic value. Furthermore, there is a need to undertake multi-location evaluations and initiate pre-breeding programs. In India, the wild relative *Vangularis* var. *nipponensis* is widespread in the northeast hill regions, necessitating extensive survey and germplasm augmentation. The All India Coordinated Research Network on Potential Crop should popularize adzuki bean as a nutraceutical crop in the Western and Eastern Himalayas. Efforts should focus on collecting more accessions from Western Himalaya and the northeast hill region for breeding programs.

Study on morpho-nutritional diversity in grasspea (*Lathyrus sativus* L.)

Grasspea is a versatile cool season legume crop with an exemplary nutritional profile with a potential as climate-smart species. A total of 168 diverse accessions including four checks (Ratan, Prateek, Mahateora, and Narayangon) were evaluated for 14 quantitative and 20 qualitative traits at Pusa Farm, ICAR-NBPGR, New Delhi over two consecutive winter seasons (2019-20 and 2020-21). The promising accessions for important traits such as hundred seed weight– IFLA1439 (14.02g), IFLA432 (13.38g); early flowering- BANG31 (64.41days), IC525179 (63.34days); higher plant height- BANG285 (119.45cm); number of pods per plant- IFLA276 (87.08 pods); days to 80% maturity- BANG31 (112.35days) were identified. In SSR analysis, PIC value ranged from 0.02 to 0.67 and heterozygosity ranged from 0 to 0.5. Molecular diversity studies further categorized accessions into three principal clusters. Notably, the accessions with higher days to maturity and 100-seed weight were grouped in the same clusters of both the morphological and molecular cluster dendrogram. The sample selection is by the FOSS NIRS 6500 for biochemical analysis for both seeds and leaves for proximate parameters like protein, starch, sugar, phenol, moisture, ash, TDF, minerals like Fe, Cu, Zn, Ca and Mg along with amino acid profiling and β-ODAP estimation using UPLC with Agilent ZORBAX Eclipse Plus C18 and SB C18 column respectively. Significant difference was observed in ODAP content from 0.074 to 0.34 mg/kg in seed and 0.03 to 0.287 mg/kg in leaves. The identified Low β-ODAP in the seeds of IC525182 (0.074) and IC0634662 (0.078) and leaves of IFLA1193 (0.030) and IC208430 (0.040) was observed. The nutritional study revealed agronomically superior with a high range of protein, minerals and low β-ODAP in both seeds and leaves which include IC208430, IC0634654, IC0634662, IC0634674, BANG285, BANG31, IFLA143 and IFLA1193. These accessions can be used in further grasspea breeding programmes for the development of low ODAP and agronomically superior varieties.

Identification of physico-chemical and genetic factors for bruchid [*Callosobruchus maculatus* (fabricius)] resistance in cowpea [*Vigna unguiculata* (L.)]

Cowpea, scientifically known as *Vigna unguiculata* L. Walp, known by various names such as Lobia, Boda, cowpea gram, Cuba bean, and asparagus bean. This versatile legume crop serves multiple agricultural purposes, including consumption as a green vegetable, dal production, green manuring, and as a feed crop. Its significance lies in enriching soil with nitrogen, thereby enhancing soil fertility. However, the full yield potential of cowpea faces obstacles in production and storage, notably from insect pests and diseases. In the context of storage, the pulse beetle (*Calloso bruchusmaculatus*) emerges as a significant threat, causing both quantitative and qualitative losses. To address this, eco-friendly pest control methods, including host plant resistance, are crucial. In this comprehensive study, cowpea corset accessions were assessed for their reaction to *C. maculatus*, aiming to identify sources of resistance. The evaluation considered various parameters such as oviposition, development period, adult emergence, emergence holes, weight loss, and growth index. Accessions were categorized based on their resistance levels, ranging from highly resistant to highly susceptible. Furthermore, out of 372 cowpea core set accessions, 91 were selected for biochemical analysis, revealing correlations between various parameters such as total dietary fiber (TDF), starch, phenol, phytic acid, amylose, protein, total soluble solids (TSS), and insect resistance. The study researched into the genetic aspect through Genome-Wide Association Studies (GWAS), identifying significant Quantitative Trait Nucleotides (QTNs) associated with bruchid resistance. These findings offer valuable insights for crop improvement programs, including the development of bruchid-resistant varieties, Marker-Assisted Breeding (MAB), and enhancing the genetic diversity in national and international gene banks.

Theme 3: Genomics of PGR

Marker trait association analysis for component traits of seed longevity in wheat (*Triticum aestivum* L.)

A Genome-Wide Association Analysis was conducted to understand the mechanism behind wheat seed longevity and to identify the genomic regions associated with component traits of seed longevity using 104 wheat Germplasm accessions conserved in National Genebank, New Delhi and multiplied at ARI, Pune. Parameters for phenotypic evaluation included total antioxidant capacity, GSH-GSSG redox potential and mean germination time (MGT) after artificial ageing following two procedures- Accelerated Aging (AA) and Controlled Deterioration (CD). Genotyping was done with Axiom® bread wheat 35K array and 19090 SNPs were used for GWAS. The study identified ten significant MTAs with major candidate genes, for seed longevity. In K-net miner analysis, ATRAESCS5A03G0963300 gene was found on chr 5 which is an or thologue of *Arabidopsis Ats*1T1 gene that leads to accumulation of ROS, growth inhibition and cell death. On Chr 4B, TRAESCS4B03G0930800 gene was found, which is an or thologue of *Arabidopsis* AtRBOHB and rice OsRBOHB genes that modulates ROS accumulation and PCD. Candidate gene identified on chr 7B belongs to co-expression cluster of biological ageing process and that on chr 3A, has contributory role in ROS accumulation. This study complements the reports of other genome association studies that identified multiple loci and confirms the complex polygenic nature of the trait. The results also showed positive correlation with actual genebank conservation data. This information generated in this study could be of potential value for streamlining genebank conservation protocols and also can be utilized for improving the genetic base of seed longevity traits, using marker assisted selection.

Genome-wide association mapping for leaf rust resistance in a diverse germplasm collection of durum wheat

Leaf rust is one of the most damaging fungal diseases of wheat caused by the fungus *Puccinia triticina* Eriks. The phenotypic screening of 189 GDP (Global Durum Wheat Panel) for leaf rust resistance against the five pathotypes 77-5 (121R63-1), 77-6 (121R55-1), 77-9 (121R60-1), 12-5 (29R45), and 104 (17R23) categorized panel into immune, very resistant, moderately resistant, moderately susceptible, susceptible, highly susceptible, and heterogeneous and found good level of resistance for all five-leaf rust pathotypes. The publicly available genotype data of the 189 lines generated on Illumina iSelect 90K SNP array technology was used for population structure and association analyses. Population structure analysis categorized the population into three sub-populations. The neighbor-joining method also divided the durum germplasm into three subpopulations. The average LD decay distance for the A- genome, B-genome as well as the combined A and B genome was 1.45 Mb, 1 Mb, and 1.19 Mb respectively. The GWAS analysis used six different models. A total of 89 significant quantitative trait nucleotides (QTNs) were found to be associated with five rust pathotypes. Among these, 22 QTNswere considered reliable, detected in ≥2 models. We could also identify 20 expressed transcripts/candidate genes which are associated with 20 reliable QTNs/genomic regions. These transcripts encoded diverse functional groups of proteins that are responsible for resistance to this type of disease including Leucine-rich repeat (LRR) family protein, protein kinase family protein, receptor-like kinase, etc.

Genome wide association mapping of cowpea (*Vigna Unguiculata* (L.) Walp.) germplasm for key quality traits

Cowpea being a legume is a viable option for enhancing food diversity and eliminating malnutrition because of its rich nutritional composition. In the present study 202 diverse germplasm of cowpea both indigenous and exotic germplasm were taken up for assessment for 11 biochemical parameters i.e., protein, starch, amylose, TDF sugar, phenol, phytic acid, iron, copper, zinc & calcium using standard protocols. The results have exhibited a substantial variability in protein (20.2-29.7 g/100g), carbohydrates [starch (30-47.5), amylose (11.5-14.8), sugar (4.10-6.59) expressed as g/100g], TDF (15.6-24.5 g/100g), anti-nutritional factors [phenol (0.112-0.405 GAE g/100g), phytic acid (1.19-1.80 g/100g)] and in micronutrients [iron (51.1-124.8 ppm), copper (3.48-14.9 ppm), zinc (29.6-76.2 ppm) and calcium (215.6-738 ppm). Modified partial least squares (MPLS) regression-based NIRS prediction models were developed for the above given parameters to assess the above parameters rapidly and non-destructively. All of the traits have exhibited high RPD values >2.5 except phenols (1.78). High RSQ values and low SEP(C) values for all the traits indicates excellent prediction capacity for all the worked traits. To identify new sources of genes for nutritional quality in cowpea accessions GWAS (Genome-Wide Association Studies) have been performed. GBS (Genotyping by Sequencing) was done for SNP genotyping Amultilocus GWAS (ML-GWAS) approach was employed utilizing six different models, namely mrMLM, FASTmrMLM, FASTmrEMMA, pLARmEB, ISIS EM-BLASSO, and pKWmEB (LOD≥3). 42 significant QTNs along with four pleiotropic QTNs was found across 9 traits. Furthermore, gene annotations were exclusively conducted for the QTNs that exhibited a high level of significance and consistency. This decision was based on the notion that these QTNs were more dependable and likely to demonstrate strong performance across various environmental conditions. The findings of this study can be utilized variously in crop improvement programs viz., development of nutritionally rich varieties, MAB, and value addition to national and international gene bank.

Genome wide association studies on Yellow Mosaic disease resistance in cowpea germplasm

Yellow Mosaic Disease (YMD) poses a significant threat to cowpea production in India, primarily caused by the mungbean yellow mosaic India virus (MYMIV) and mungbean yellow mosaic virus (MYMV). This study systematically evaluated 1127 cowpea germplasm accessions from the National Genebank, conducting field screening at two distinct locations (Hyderabad and Delhi). Out of these accessions, 181 exhibited resistances to YMD. The top 100 resistant accessions were selected for whitefly-mediated screening, alongside 40 susceptible accessions. Whitefly-mediated transmission confirmed MYMIV resistance in 20 accessions, displaying a disease score of zero. Sequencing of YMD-associated begomo virus DNA-A genome of MYMIV, revealed a remarkable 99.02% genetic identity with the MYMIV isolate affecting cowpea in Pakistan. Genotyping by Sequencing (GBS) identified 17,703 high-quality Single Nucleotide Polymorphisms (SNPs) from a vast pool of 522,926 SNPs in the cowpea collections. The study assessed linkage disequilibrium across the entire cowpea genome, revealing an r2 value of 0.25. These analyses identified three significant Quantitative Trait Nucleotides (QTNs) associated with MYMIV disease resistance. the most significant and consistent QTNs were annotated. These findings offer invaluable insights for crop improvement programs, including the development of YMD-resistant cowpea varieties, Marker-Assisted Breeding (MAB), and the enhancement of national and international gene banks. Ultimately, this research contributes to safeguarding cowpea production against the devastating impact of YMD.

Theme 4: Germplasm Conservation

Effect of phytohormone Meta-topolin on *in vitro* propagation of *Rubia cordifolia* L.

The research presented in this thesis focused on the in vitro propagation of *Rubia cordifolia* L. (Indian madder), an important medicinal plant species native to India. Due to its exceptional therapeutic properties and commercial value, *R. cordifolia* has faced excessive collection from the wild, leading to its vulnerability and endangerment. To address this issue, in vitro propagation techniques were explored using the natural cytokinin, meta-topolin (mT), known for its efficacy in enhancing plant multiplication. Sixteen different media combinations were tested, including various cytokinins (BAP, Kn, 2-iP at 1.0 mg/L concentration) and mT concentrations (0.5-5 mg/L), for in vitro shoot multiplication. The results indicated that *R. cordifolia* demonstrated 100% shoot induction on all tested media combinations. Furthermore, the concentration of mT significantly influenced shoot production, with 2.0 mg/L concentration proving more effective, with the highest number of shoots (13.17±0.27) and nodes (28.44±0.71) after 16 weeks and 26.83±0.35 shoots, 48.73±0.70 nodes after 24 weeks. Best in vitro rooting was achieved using micro-shoots taken from plants grown on MS medium on half strength MS media supplemented with 2.0 mg/L IBA, which produced the most roots (13.17±0.27) after 8 weeks. The different cytokinins including mT, were evaluated for their effect on in vitro rooting. Meta-topolin at 2.0 mg/L displayed the favorable outcome, promoting a substantial number of roots (20.22±0.62). Following acclimatization, the rooted plants exhibited a 100% survival rate. Additionally, the genetic fidelity of the in vitro regenerated plantlets was assessed using 20 ISSR markers, demonstrating no discernible differences between mother plants and the in vitro propagated plantlets, confirming their genetic stability.

In vitro propagation and conservation of jackfruit (*Artocarpus heterophyllus* Lam.) – An underutilized indigenous fruit

The objectives of the present work were to standardize in vitro propagation protocol for *Artocarpus heterophyllus* Lam.,and to see the effect of different temperatures on the storage of in vitro shoots. Standardization of *invitro* propagation protocol included culture establishment using MS media supplemented with different concentrations of hormone BAP.Sterilization treatment of 0.1% $HgCl_2$ + 0.3% Bavistin for different timings 10 and 12 minutes were given to explants. After 4 weeks it was observed that 12 min sterilization treatment of explants obtained more clean cultures (45%). It was observed highest number of shoots (3 shoots per explant) were obtained on B20 media (BAP 2 mg/l). Highest shoot length(1.63 cm), higher number of nodes (2.31) and highest number of leaves (1.06) was observed in B10 media (BAP 1 mg/l).In TDZ media TDZ (0.4 mg/l) recorded maximum number of shoots (2.33), highest shoot length (1.54 cm), highest number of nodes (2.14) and leaves (1.00). In comparing BAP and TDZ for shoot multiplication it was observed that best results were obtained on media supplemented with BAP.½ MS + IAA at concentration 1 mg/l obtained highest number roots and highest root length. Hardening of rooted plants was carried out where, 85% of hardened plants survived.To standardize the temperature for storage of in vitro shoots three different temperature conditions were used which includedStandard Culture Room conditions(15˚C temperature; 16 h Light / 8 h Dark), BOD conditions(15˚C temperature; 16 h Light / 8 h Dark), Medium-term storage module(4˚C temperature; Dark). After 90 days of storage, it was observed that BOD conditions (15˚C temperature; 16 h light / 8 h dark) were suitable for storage of in vitro shoots.

Development of informatics system to document on-farm conservation: A case study

India is a megadiverse country and also holds diverse landraces of different crops being conserved on-farm. Though documentation, collection and conservation of landraces are in practice from 1970s in the country, still many landraces are undocumented and no platform is there to access the information on on-farm conservation status and diversity conserved in India. From the present study, it was evident that individual custodian farmers, community and NGOs, had a common goal *i.e.,* “protection of indigenous cultivars for future generations” but working through different ways to achieve this goal.The landraces diversity, determinants and constraints for conservation were documented in the Central Western Ghats and surrounding region in Karnataka, India. A total of 1,774 landraces belonging to 71 different crop species are recorded and grouped into eight different crop groups. The study also highlighted the critical factors that determine conservation like suitability to regional conditions, relevance in regional cuisine and the local medical system, cultural and traditional significance and critically the economic advantage was the main factor influencing conservation. A total of 93 tree species belonging to 75 genera and 41 families are being conserved *circa situm* by the farmers of this region solely depends on the farmers’ perception of the utilization of these species.The present database on on-farm conservation is one of its kind in India and probably the world, provides a user-friendly platform for documentation of status on on-farm conservation by the custodian farmers of India. The database also provides access to the diverse users for easy access to the landraces for germplasm exchange and access for utilization of landraces for varietal development to attain the food, nutrition and livelihood security by harnessing their potential.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Vivek Kumar (21685)	M.Sc.	Trait-specific diversity mapping and habitat prediction of cowpea germplasm conserved in the Indian National Gene Bank	Dr. D. P. Semwal	*ICAR-NBPGR, New Delhi
2.	Jyotsna Verma (21686)	M.Sc.	Assessment of genetic variability of diverse blackgram (*Vigna mungo* (L.) Hepper) germplasm conserved in Indian National Genebank for pre-harvest sprouting tolerance	Dr. Kuldeep Tripathi	*ICAR-NBPGR, New Delhi
3.	Sampa Saha (21687)	M.Sc.	Marker trait association analysis for component traits of seed longevity in wheat (*Triticum aestivum* L.)	Dr. Sherry R. Jacob	*ICAR-NBPGR, New Delhi
4.	Shradha Mahawar (21741)	M.Sc.	Chemotaxonomic approaches for the authentication of Citrus species	Dr. S.K. Malik	*ICAR-NBPGR, New Delhi
5.	Kunal (21742)	M.Sc.	Effect of phytohormone Meta-topolin on *in vitro* propagation of *Rubia cordifolia* L.	Dr. Sangita Bansal	*ICAR-NBPGR, New Delhi
6.	Guthi Likhitha (21751)	M.Sc.	In vitro propagation and conservation of jackfruit (*Artocarpus heterophyllus* Lam.) – An underutilized indigenous fruit	Dr. Sandhya Gupta	*ICAR-NBPGR, New Delhi
7.	Jitendra Kumar Yadav (21752)	M.Sc.	Genome-wide association mapping for leaf rust resistance in a diverse germplasm collection of durum wheat	Dr. Amit Kumar Singh	*ICAR-NBPGR, New Delhi
8.	Prabakaran S (11080)	Ph.D.	Morphological, biochemical and molecular characterization of *Abrus precatorius* germplasm conserved at national gene bank	Dr. Veena Gupta	*ICAR-NBPGR, New Delhi
9.	Manju Kumari (11081)	Ph.D.	Variability studies in horsegram (*Macrotyloma uniflorum* (Lam.) Verd.) accessions using phenotypic, biochemical and molecular parameters.	Dr. K. C. Bhatt	*ICAR-NBPGR, New Delhi
10.	Prabhu.P (11303)	Ph.D.	Genetic resources studies on melons (*Cucumis melo* L.) of India	Dr. Anjula Pandey	*ICAR-NBPGR, New Delhi
11.	Puneeth G M (11304)	Ph.D.	Development of informatics system to document on-farm conservation: A case study	Dr. Sunil Archak	*ICAR-NBPGR, New Delhi
12.	Aswin M. (11305)	Ph.D.	Morphological and molecular analyses of genetic variation and population differentiation in wild rice species of AA-genome	Dr. M.C. Yadav	*ICAR-NBPGR, New Delhi
13.	Deepika D D (11562)	Ph.D.	Genetic diversity analysis of exotic & indigenous adzuki bean (*Vigna angularis* (Wild) Ohwi and Ohashi) collections of National Genebank of India	Dr. K. C. Bhatt	*ICAR-NBPGR, New Delhi
14.	K R Ramya (11564)	Ph.D.	Study on morpho-nutritional diversity in grasspea (*Lathyrus sativus* L.)	Dr. K. C. Bhatt	*ICAR-NBPGR, New Delhi
15.	Siddhant Ranjan Padhi (11829)	Ph.D.	Genome wide association mapping of cowpea (*Vigna unguiculata* (L.) Walp.) germplasm for key quality traits	Dr. Rakesh Bhardwaj	*ICAR-NBPGR, New Delhi

16.	G J Abhishek (11830)	Ph.D.	Genome wide association studies on yellow mosaic disease resistance in cowpea germplasm	Dr. Celia Chalam V	*ICAR-NBPGR, New Delhi
17.	Rithesh B N (11831)	Ph.D.	Molecular phylogeny and cytogenetic characterisation of Indian *Musa* species	Dr. S. Rajkumar	*ICAR-NBPGR, New Delhi
18.	Chethan Kumar K B (11832)	Ph.D.	Identification of physico-chemical and genetic factors for bruchid [*Callosobruchus maculatus* (fabricius)] resistance in cowpea [*Vigna unguiculata* (L.)].	Dr. Kavita Gupta	*ICAR-NBPGR, New Delhi

*Sister Institute

Seed Science and Technology

3

Prof. Monika A. Joshi

The Division of Seed Science and Technology provides leadership in maintenance breeding, seed production, certification, quality evaluation, storage, physiology, pathology, variety identification, genetic purity evaluationand DUS testing for plant variety protection, development of seed quality assessment procedures and human resource development. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Seed Biology Studies

GWAS to identify marker trait associations for early seedling vigour in rice

In direct-seeded rice (DSR) cultivation, robust seedling establishment is crucial for crop success under less favourable field conditions. Early seedling vigor (ESV), encompassing lemma rupture (LR), radicle emergence (RE), and coleoptile emergence (CE), significantly influences uniform seedling establishment. Despite its importance, the genetic mechanisms governing ESV in early seed germination are largely unexplored. A genome-wide association study (GWAS) was conducted using a subset of the rice germplasm from the 3,000 Rice Genomes Project (3KRGP). Germination patterns were observed at four-hour intervals, and specialised software quantified key parameters: Time to First Lemma Rupture (TFLR), Time to First Radicle Emergence (TFRE), and Time to First Coleoptile Emergence (TFCE). GWAS identified six significant marker-trait Associations (MTAs) for TFLR across two seasons, with qTFLR3.1 and qTFLR6.1 stable in both. Fourteen candidate genes within MTA regions were associated with TFLR. For TFCE, six MTAs were identified, with qTFCE3.1 and qTFCE6.1 stable in both seasons. Seven candidate genes within MTA regions were proposed. Seven MTAs for TFRE were identified, with qTFRE8.1, qTFRE9.1, and qTFRE1.1 stable in both seasons, suggesting significant transcriptional changes during radicle emergence. In silico expression analysis validated the significance of the 24 candidate genes, emphasising their roles in germination-related traits. The study illuminates genetic mechanisms influencing ESV during rice seed germination, emphasising the importance of specific germination-related traits for crop stand establishment and seedling growth in direct-seeded rice systems. These insights offer valuable guidance for researchers and breeders aiming to enhance crop resilience and productivity in DSR systems.

Mapping of seedling vigour related traits for moisture deficit stress tolerance in wheat (*Triticum aestivum* L.)

This study investigates the genetic basis of crucial seedling vigour-related traits in wheat, essential for its resilience under climate-induced moisture deficit conditions. A genome-wide association study (GWAS) was conducted on 193 bread wheat genotypes, including elite varieties, breeding lines, and synthetic derivatives. Evaluated traits encompassed seed morphological traits, seedling vigour, and root attributes, with significant phenotypic variability observed in the association panel. The study identifies 37 marker-trait associations (MTAs) for seed morphological traits across 18 chromosomes. Notably, six stable single nucleotide polymorphisms (SNPs) consistently associated with area size, seed length, and thousand seed weight were identified. Additionally, 26 MTAs explain over 10% of phenotypic variation for seed morphological traits, with four stable MTAs identified for specific traits under various conditions. Forty-seven SNPs associated with seedling vigour and root traits were revealed, with 11 SNPs explaining over 10% of phenotypic variation. Significant associations include SNPs related to coleoptile length, seedling dry weight, and root diameter under both control and moisture deficit conditions. *In silico* analysis unveiled that the identified MTAs are located in genomic regions governing critical aspects of wheat development, such as stamen development, seed development, germination, root growth, and stress tolerance. Marker validation in a recombinant inbred line (RIL) population confirmed associations with key traits including AX-94773224 and AX-94918971 for coleoptile length, AX-94953183 and AX-94990696 for area under the curve and AX-94492491 for root diameter, further emphasizing their reliability. The Multi-trait Genotype-Ideotype Distance Index (MGIDI) was employed to select superior genotypes based on seed morphological traits, seedling vigour, and root traits. A total of 58 superior genotypes were chosen, emphasizing their potential for enhanced conservation agriculture and resilience breeding through marker-assisted selection. Overall, this study provides valuable insights into the genetic basis of wheat's response to moisture deficit stress, offering practical applications for targeted breeding efforts.

Studies on seed vigour traits in relation to flowering, harvest maturity, storage period and validation of QTL associated with seed vigour in rice (*Oryza sativa* L.)

Rice (*Oryza sativa* L.) is one of the important and the second largest food grain crop grown in the world both in terms of area and production. Seed vigour, an attribute of seed quality, significantly influences the early, rapid, and uniform germination, emergence, and growth of robust seedlings across varied environmental conditions. This study evaluated seed vigour in 44 Indian rice varieties, scrutinizing different seed vigour component traits. The assessment involved basic statistics, correlation analysis, principal component analysis (PCA), and cluster analysis to delineate genetic diversity among rice varieties, specifically concerning seed vigour traits and early seedling vigour. The varieties were grouped into five clusters based on average linkage and dendrogram analysis. Cluster-I, comprising 21 genotypes, was identified as a high vigour group, while cluster-IV exhibited the least seed vigour traits. The clustering of varieties based on seed vigour traits and their association with maturity periods indicated that early and medium maturity group varieties outperformed in seed vigour traits, while medium and late maturity group varieties displayed lower performances. PCA revealed the top five components explaining 77.01% of the total variation in seed vigour traits. Seed vigour index-I, seed vigour index-II, seed dry weight, shoot length, reserve mobilization, germination percentage, dehydrogenase, mean germination rate, speed of germination, and mean germination time contributed significantly to the variability among the varieties. The study also explored the application of thermal time models to understand the germination characteristics of rice varieties under varying temperatures. Genetic variability in seed vigour traits and their association with 41 SSR markers in 44 rice varieties were studied, indicating high genetic variability, heritability, and genetic advance. The identification of traits and markers namely RM 1353, RM 250 and RM 229 associated with seed vigour provides valuable insights for future rice breeding programs, aiming at enhancing the overall quality and productivity.

Genetic and molecular basis of protogyny, CMS and self-incompatibility system in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]

This study delves into critical aspects of *Brassica spp*. hybrid development, focusing on heterosis, cytoplasmic male sterility (CMS) systems, and the enhancement of seed production. Novel CMS and fertility restoration systems, utilizing cytoplasm from wild species (*Moricandia arvensis, Diplotaxis erucoides,* and *Diplotaxis berthautii*), offer promise for the future of hybrid mustard crops. Genetic diversity within the female line is highlighted as pivotal for success, with the synchronization of stigma receptivity during pollination identified as a means to boost hybrid seed production. Field experiments spanning two years investigated 30 new CMS lines derived from *Moricandia*, *Erucoides*, and *Berthautii* cytoplasm in Indian mustard (*Brassica juncea* L.). Two critical traits, percent siliquae set and seed set per siliquae, were evaluated for their impact on hybrid seed yield. Notably, CMS lines exhibited diverse responses attributed to cytoplasmic-nuclear interactions. These findings underline the complexity of hybrid development in *Brassica juncea*. Furthermore, this research explores the crucial post-pollination event of pollen-pistil interaction, emphasizing the significance of protogynous (PG) lines as self-incompatible (SI) alternatives in hybrid development. Fluorescence microscopy revealed the rapidity of intra-specific PG-SI interactions and the potential for self-reproduction, with treatments such as NaCl, GA_3, and Kinetin effectively breaking SI barriers in PG-SI lines. The study also sheds light on the genetics of PG-SI in Indian mustard, identifying digenic-duplicate gene action as responsible for the PG-SI trait. Genotype-by-sequencing (GBS) unveiled numerous differentiating SNPs between PG-SI and non-PG-SI genotypes, highlighting three consistently associated SNPs. Three putative candidate genes—calcium-binding protein PBP1, serine/threonine-protein kinase, and calcium-dependent protein kinase 5 were linked to these SNPs, deepening our understanding of the genetic basis of protogyny and SI in *Brassica juncea* L. These findings offer valuable insights for the selection of nucleo-cytoplasmic combinations in hybrid breeding programs, as well as the potential for marker-assisted breeding to transfer the PG-SI trait to different genetic backgrounds. In summary, this multifaceted research contributes significantly to the advancement of hybrid mustard production and the genetic understanding of critical reproductive mechanisms in *Brassica juncea* L.

Theme 2: Seed Production Technology

Studies on thermotolerance and its induction during seed germination and seedling growth in rice

Rice (*Oryza sativa*) is the staple food for about half of the world's population and is known to be susceptible to heat stress. In the present research, we have studied a range of phenotypic assays that can be used to characterize thermotolerance diversity i.e., basal thermotolerance (BT), short (SAT) and long term acquired thermotolerance (LAT) in rice during seed, radicle and early seedling stages and induction of heat tolerance by pre-acclimation treatments (thermopriming). Initially, BT was identified in seed (57°C, 30 min), radicle (48°C, 30 min) stage and early seedling stage (48°C, 30 min). Later, SAT technique has been identified to mitigate heat stress in seed (45°C, 75 min), radicle (38°C, 75 min) and early seedling stage (42°C, 60 min). Also, LAT technique was developed in seed (45°C, 75 min), radicle (38°C, 75 min) and early seedling stage (42°C, 75 min) and the methodologies was validated in known heat susceptible/tolerant genotypes. Better tolerance in thermotolerant variety was attributed to higher antioxidants, lower ROS and lower MDA compared to susceptible variety. Recovery during SAT and LAT could be due to increased peroxidase activity and reduced membrane degradation. For developing the chemical based seed priming technique to mitigate heat stress, seed priming technique was standardized for different factors. Phase II of imbibition curve with dry back temperature (26°C) was identified as most suitable, followed by selecting imbibition durations among different imbibition methods (direct soaking/blotter/PEG method) and effective concentration of spermidine (0.5/1/1.5 mM). Results indicated PEG (-1 MPa, 56 h) based method with a 1 mM spermidine effectively reduce heat stress compared to other methods. This can be attributed to higher antioxidants, available sugars and amylases and lower MDA. Overall, the study emphasizes the significance of thermopriming and spermidine priming in rice which offers valuable insights into effective mitigation strategies against heat stress.

Theme 3: Seed Quality Enhancement

Enhancing zinc use efficiency in mungbean (*Vigna radiata* L. Wilczek) through seed treatments

Zn-seed priming and coating treatments on short-duration mungbean variety Pusa Vishal were standardized to enhance the early seedling vigor characters. Among the Znprimed seeds at 300 ppm, 450 ppm, 600 ppm and 750 ppm, it was found that priming seeds with 450 ppm Zn2+ 1:1.5 (v/v) solution for 9 hrs at 25 ± 2°C has significantly enhanced the seedling growth. Among the seeds coated with Zn-fertilizers viz; Zn-NCPC (1:4; 1:2), Amino acid chelated Zn and EDTA chelated Zn, Zn-NCPC fertilizer + chalk powder in 1:4 proportion manifested in significantly higher in all seed quality attributes. Moreover, coating seeds with either Amino acid chelated-Zn fertilizer or EDTA chelated-Zn fertilizer did not have any beneficial effects on seed quality attributes as compared to the control. Secondly, the rate of Zn release from the total Zn loaded on/in the mungbean seeds through selected seed treatments was evaluated using a dialysis membrane and Flame Atomic Absorption Spectrophotometer. Various Zn-seed treatments viz; Zn-Primed, Zn-NCPC, AmZn, EDTA-Zn, were subjected to release kinetics experiment where Zn-NCPC (1:4)- coated seed treatment was found to be the slowest in Zn ion diffusion rate. With this controlled and slow-release property of Zn it would become available gradually to the plant's root zone for different metabolic events for a longer duration thus enhancing the Zn-use efficiency. It has been acknowledged that during storage, mungbean seeds decrease their viability very fast, especially in tropical areas kept without proper packaging thus the third objective was to assess the effect of Zn-treatments on seed longevity. Various Zn-seed treatments were subjected from 0 to 12 months duration at an interval of 3 months. At the end of the 12 months storage period, Zn-NCPC (1:4) fertilizer manifested in significantly superior performance. Hence, hydro-primed and Zn-primed seeds lose their viability at a faster rate and germination drops below IMSCS (70%) within 6 months of storage. In Zn- 1 seed treatments, Zn-toxicity tolerance of the seed decreases with aging which manifests in lower seed quality attributes. On the contrary, abnormal seedling % and dead seed % increase drastically with seed aging in mungbean. Conclusively, Zn-NCPC (1:4) seed coating fertilizer can be considered as significantly superior in terms of seed quality attributes, Zn use efficiency and storability.

Seed enhancement technology for quality seed production of chilli (*Capsicum annum* L.)

Chilli is an important high value vegetable crop, experience sub-optimum temperature during post-transplanting phase which affects seedling growth and crop establishment. Seed enhancement treatments play an important role in ameliorating detrimental effect of sub-optimum temperature. Chilli genotypes; namely Kashi Anmol (high vigour) and Arka Lohit (low vigour) were given seed enhancement treatments; namely hydropriming (24h), halopriming (2% NaCl for 24h), osmopriming (1.5 MPa PEG 6000 for 36h), solid matrix priming (vermiculite for 24h) and magneto priming (50 mT for 30 min) and their effect on physiological, physical, structural, biochemical changes and storability of primed seeds were studied. Seed enhancement treatments, apparently solid matrix and magneto priming showed significant improvement in seedling emergence, vigour and root growth parameters in both the genotypes under controlled conditions (15 and 20°C). Performance of primed seeds under field conditions showed improved seedling establishment, crop growth, fruit and seed yield and flowered 2 to 3.5 days earlier and the studied traits were more evident in first date of sowing (October 6, 2020) as compared to second sowing (January 14, 2021). Improved membrane integrity, seed water relation, elevated free radical and antioxidant levels and dehydrogenase activity are more evident in the primed seeds. Studies on X-ray showed free space existence and formation of micro cracks, pits and layer disintegration observed under SEM studies of solid matrix and magnetoprimed seeds. Storage studies showed that solid matrix and magneto primed seeds stored better at 10±2°C as compared to 30±2°C and in aluminium foil than 700 gauge packets and could maintain seed germination above seed certification standard (≥60%) for 12 and 9 months in Kashi Anmol and Arka Lohit respectively. Among the seed enhancement treatments, solid matrix and magnetopriming proved superior in enhancing germination, vigour, seedling establishment, plant stand, seed yield and quality both under sub-optimum and optimum temperature conditions.

Effect of chemical priming for improving early seedling vigour under salinity stress in lentil

Lentil (*Lens culinaris*) is the second most important annual, self-pollinated, herbaceous and winter-season grain legume crop mostly grown on marginal soils which hamper its productivity in India. Abiotic stress, particularly salt stress results in poor plant stand establishment, crop development and growth leading to yield losses.Seed priming is the simple quality enhancement technique for mitigating abiotic stresses in several crops. Keeping above facts in view, silicic acid, humic acid and their combination was used as a seed priming agent to enhance seed quality parameters under salinity stress. Among the various concentration and duration used, seeds primed with silicic acid @ 3mM for 18 hr, humic acid @ 600 ppm for 18 hr and their combination @ HA 100 ppm and 1mM silicic acid for 16 hr showed highest germination , seed vigour index I&II. Similarly, chemcial priming under salinity stress level (10, 12, 14 ds/m) also improved germination and vigour of lentil seed. Seed priming with combination of humic and silicic acid was found to significantly increase germination percentage ,seed vigour index I &II, speed of germination , germination rate index , germination index , chlorophyll content , relative water content, proline content , phenolic content, catalase activity ,peroxidase activity, superoxide dismutase content , total soluble sugar content, soluble protein ,carbohydrate content in IPL 316, PSL-9 and PDL 1 varieties under salinity stress condition. During storage of primed seed, the seed quality and physio-biochemical parameters significantly increase under both conditions. Seed priming with combination of humic and silicic acid increases seed quality and physio-biochemcial parameter till six months under normal condition in IPL-316 variety. Morover, it was observed that seed priming had a dual effect on seedling vigour, it not only increased the stress resistance capacity of susceptible lentil varieties (PSL-9 and PDL-1) but also improved the stress resilience of tolerant ones (IPL-316).

Studies on effect of salinity stress on seed quality parameters and its alleviation through seed priming in wheat species

The study assessed the impact of salinity stress on seed quality in four wheat species—bread wheat (*Triticum aestivum*), macaroni wheat (*Triticum durum*), emmer wheat (*Triticum dicoccum*) and Indian dwarf wheat (*Triticum sphaerococcum*). Seventeen genotypes, including salinity-tolerant wheat (KRL210), were evaluated to comprehend salinity stress effects and potential alleviation through seed priming. Different NaCl solution volumes (12.5 ml, 10 ml and 15 ml) in petri plates were tested, revealing increased seed quality parameters with 12.5 ml. The evaluation encompassed four salinity levels—0 dS/m (control), 3 dS/m, 6 dS/m and 9 dS/m. Across these species, increasing salinity from 0 to 9 dS/m significantly reduced seed quality parameters (germination percentage, root and shoot length, seedling traits, seedling dry weight, SVI I, SVI II), while increasing mean germination time (MGT). However, some parameters remained similar at 0 dS/m and 3 dS/m. Notably, at lower salinity (3 dS/m), improved seed quality suggested that NaCl acted as a beneficial nutrient, aiding tolerance mechanisms. Correlation analysis with salt tolerance index (STI) revealed substantial associations between STI and seed quality parameters at 9 dS/m. This aided in selecting resistant and susceptible genotypes for subsequent priming experiments. Priming with KNO_3 (1.5% and 3%)and ascorbic acid (50 ppm and 100 ppm) yielded diverse effects. Ascorbic acid (100 ppm) priming notably increased catalase, peroxidase and proline activity in bread wheat and *T. sphaerococcum*, particularly in the resistant genotype. Durum wheat responded favorably to 1.5% KNO_3 priming, while dicoccum wheat benefitted from 3% KNO_3 priming, especially in catalase and proline activity for resistant genotypes. In summary, salinity stress adversely impacted seed quality parameters across wheat species, with lower salinity levels occasionally displaying a positive effect. Priming experiments with KNO_3 and ascorbic acid unveiled differing responses among genotypes, underscoring the potential for targeted priming to enhance salinity tolerance in wheat, particularly in specific genotypes and under varying stress levels.

Effect of ZnO nano-particle based priming on seed quality enhancement in tomato (*Solanum lycopersicum* L.) under salt stress

The tomato crop is considered one of the most predominant horticultural crops in the world, but abiotic stress, particularly salt stress result in poor plant stands establishment, leading to yield losses. Recently, use of nanoparticles priming in agriculture, has received a lot of attention, due to their role in regulating seed metabolism and signaling pathways, germination and seedling establishment. Thus, zinc oxide (ZnO) nanoparticle (NP) was used as a seed priming agent to enhance seed quality of two tomato genotypes (QA001 and QA002) under salinity stress. The genotype, QA001 performed significantly better than QA002 genotype under both control and salinity stress condition. Among the various concentrations and soaking durations applied, tomato seeds primed with ZnO NP @ 750 ppm for 6 hour revealed significantly higher germination (92%), seed vigour index I (1399) and seed vigour index II (1813). Salinity stress (50 mM and 100 mM NaCl) remarkably affected the seed quality parameters as well as biochemical traits of 14 days old seedlings of both tomato genotypes. However, nanopriming with ZnO NP @ 750 ppm was found to notably increase germination percentage, seedling dry weight, total seedling length, seed vigour index I and II, speed of germination, chlorophyll content, phenol content, total soluble sugar (TSS) content, soluble protein content, proline content, superoxide dismutase (SOD), peroxidase (POD), catalase (CAT) activity and remarkably decrease the mean germination time, MDA content over the unprimed seed in both the genotypes under both control (no-stress) as well as salinity stress (50 mM and 100 mM NaCl) conditions. Overall, nano-priming with ZnO NP @ 750 ppm (6 h) significantly boosted the chlorophyll production, antioxidative mechanism and osmotic adjustment, which in turn lower the ROS accumulation and peroxidation of lipid in cell membrane thereby could be used for alleviating the detrimental effect of salinity stress in tomato.

Evaluation of seed coating with microbial formulations for enhancing seed yield and quality in chickpea (*Cicer arietinum* L)

Chickpea (*Cicer arietinum* L) is an annual legume from the Fabaceae family and it holds significant importance as a nutritious food source in different regions of world. Growing demand for food necessitates production of high-quality seeds. In the scenario of increased use of chemical inputs in intensive agriculture, environment friendly and organic approach is a viable option to achieve sustainable development. In this context, seed coating appears a dependable method to apply external substances (including biopolymers, colorants, biocontrol agents, and microorganisms) in proximity to germinating seeds which elevates seed quality, consequentlty yield. An experiment was conducted involving seed-coating with microbial formulations (e.g., *Anabaena torulosa-Mesorhizobiumciceri*; Cyanobacterial consortium BF1-4 comprising *Anabaena torulosa* BF1, *Nostoc carenum* BF2, *Nostoc piscinale* BF3, and *Anabaena doliolum* BF4; *Anabaena laxa*; An- Tr biofilm: *Anabaena torulosa-Trichoderma viride* biofilm). This was performed with 75% of the recommended nitrogen dose, comparing it against a control (seed treatment without microbial formulation) with 100% recommended dose of nitrogen in ICAR-IARI's research field during Rabi of 2021-2022 with an objective to assess the efficacy of these microbiological formulations in enhancing seed yield and quality, and explore whether these microorganisms could substitute chemical fertilizers in meeting nitrogen requirements. The experiment employed two chickpea varieties (Desi-Pusa 3062, Kabuli-Pusa 3022). A comparative analysis was also carried out to evaluate storability of coated seeds alongside their quality. The outcomes revealed enhanced field-emergence, field-stands, plant height, nodulation and enzymatic activity, caused greater microbial activity, availability of nutrients like nitrogen, phosphorus, potassium and organic carbon in soil. Additionally, the treatments resulted in increased pods per plant and yield. Application of microbial formulations through seed-coating exhibited a positive impact on seed storability. In conclusion, the study underscores the beneficial impact of seed coating with BF1-4 cyanobacterial consortium and biofilm (An-Rh) on crop performance with 25 % N savings.

Assessing the efficacy of seed coating with microbial formulations for quality enhancement in wheat (*Triticum aestivum* L.)

Wheat (*Triticum aestivum* L.) is one of the most widely cultivated cereal crops in India. Overuse of chemical fertilizer have resulted in the degradation of physical, chemical and biological health of the cultivable soil. Further, germination, field establishment and yield of wheat are often affected by environmental stresses, including nutrient limitation, which leads to decrease in crop productivity. In this context, the use of plant growth promoting rhizobacteria has been found to be an effective strategy to improve stress tolerance in plants and serve as a supplement to chemical fertilizers for increasing the plant growth and yield. As seed is the basic tool to transfer any technology to the field, therefore seed coating withmicrobial formulations has gained enormous importance to counter these constraints. Hence, an experiment was conducted with four leading wheat varieties among which two timely sown (HD 2967, HD 3086) and two late sown (HD 2851, WR 544) varieties in the research farms of IARI, New Delhi. Seeds of different varieties were treated with Vitavax and thiram and different microbial formulations, with treatments as: (Vitavax and Thiram (3 g/ kg seed) + 100% RDN; Vitavax and Thiram (3 g/ kg seed) + 75% RDN; Cyanobacterial Consortium (BF1 – 4) + 75% RDN; Bacterial consortium (PW 1+5+7) + 75% RDN; biofilm (An – Tr) + 75% RDN; biofilm (An - PW5) + 75% RDN). A comparative study was made to assess the efficacy of seed coating with microbial formulation based on field performance, seed quality attributes and the storability of coated seeds between treatments and control. Seed coated with different microbial formulations exhibited significantly higher values of field emergence, plant stand establishment, dehydrogenase and nitrogenase activity in soil, leaf nitrate reductase and glutamine synthetase activity, available soil nitrogen along with yield and yield contributing attributes. Seed coating with microbial formulation was found to save 25% nitrogen, with significantly at par yield, as recommended practices. Coating with microbial formulations led to better germination, seedling vigour and uniformity in germination throughout the storage period. Among all the treatment combinations, biofilm (An-Tr) and cyanobacterial consortium can be recommended for timely sown and late sown varieties respectively, as they were associated with an overall increase in crop growth, crop performance, seed yield and seed quality parameters.

Theme 4: Seed Pathology

Studies on stemphylium blight caused by *Stemphylium vesicarium* (Wallr.) on seed quality parameters in onion and its integrated disease management for quality seed production

Morpho-molecular characterization of *Stemphylium vesicarium* (Wallr.) for variability among 11 isolates of *S. vesicarium* isolated from different onion cultivars of four states namely, Delhi, Punjab, Karnataka and Maharashtra was done. Variable colony growth was observed as either cottony or velvety and pigmentation was recorded as whitish, light to dark grey to brownish with a filiform margin. The mean colony diameter ranged between 44.53 to 71.64 mm. Molecular detection by PCR assay using ITS1F/ITS4R primer amplified about ~550bp amplicon, whereas, β-tubf1 and β-tubr1 primer amplified ~1400bp amplicons. Two onion varieties namely Punjab Naroya (Susceptible) and Pusa Sowmya (moderately resistant) were used to for artificial inoculation of eleven isolates of *S. vesicarium* spore suspension at different conidial concentration to study the seed quality parameters and field emergence. Seed germination and vigour of Punjab Naroya was adversely effected at tested concentration with severe reduction at 5×10^4 conidia per ml. whereas, the seeds of Pusa Sowmya showed no decline in the seed quality parameters upto 4×10^4 conidia per ml and 11-14% reduction in germination at 5×10^5 conidia. In dual culture, *T.harzianum* exhibited better mycelia growth inhibition with 72.11% outperforming other biocontrol agents. A comparison is made between six fungicides (Mancozeb, Metiram + Pyraclostrobin, Difenoconazole, Zineb, Tebuconazole, and Kitazine) and two botanicals (*Lantana camara* and *Pongamia pinnata*) alongside *A. indica*. *In vitro* evaluation revealed superiority of *A. indica* in mycelial growth inhibition, outperforming other plant-based products and most fungicides, except Difenoconazole and Tebuconazole. Field trials demonstrate that three sprays of *A. indica* at 5 ppm reduce disease severity by over 50% and enhance seed yield, comparable to Mancozeb and Zineb. Seeds obtained from *A. indica* sprayed plants exhibit higher seed germination and vigour indices, at par with Mancozeb and Zineb, showcasing its effectiveness as an eco-friendly fungicidal strategy for minimizing economic losses in quality seed production.

Effect of sowing dates and planting seasons on the seed yield and quality attributes with special reference to Mungbean yellow mosaic India virus (MYMIV)

Mungbean (*Vigna radiata* (L.) Wilczek) is highly preferred legumes among vegetarians, extensively cultivated in Africa, South East Asia, including India due to its global popularity and demand. However, its cultivation is hindered by low yield potential and susceptibility to diseases in mungbean varieties. *Yellow Mosaic Disease* (YMD) in mungbean, caused by *Mungbean yellow mosaic India virus* (MYMIV) and *Mungbean yellow mosaic virus* (MYMV) among the most destructive diseases. Hence, the present study aimed to evaluate the effect of planting dates on incidence of MYMIV in mungbean. Treatments comprised of three planting dates, during *Kharif* (20th Jul, 30th Jul and 10th Aug) and S*pring-Summer* (20th Mar, 30th Mar and 10th Apr) and two mungbean varieties, Pusa 1371 (resistant) and Pusa 9531(susceptible) sown under field conditions. Plants showing typical symptoms were recorded at 15-60DAS at 15days interval, MYMIV detection using polyclonal antibodies in DAC-ELISA showed absorbance values of 0.32-0.66 at 405nm. Total DNA isolated from all MYMIV infected leaf samples, which were found to be highly positive in DAC-ELISA. MYMIV identified through PCR amplification, results obtained at 602bp and 850bp for the coat protein region of DNA-A and movement protein region of DNA-B, respectively. During *Kharif* season, minimum incidence of MYMIV and growth and yield parameters maximum in second and third sowing of Pusa 1371 as compared to first sowing. However, during *Spring-Summer* season, minimum disease incidence and the highest growth and yield recorded in first and second sowing of both varieties. During *Kharif* season, second and third sowing of resistant variety recorded enhanced seed quality, whereas in *Spring-Summer* season, all three sowings of resistant variety recorded highest seed quality. Hence, it is advisable to take sowing during second fortnight of March and first fortnight of August during *Spring-Summer* and *Kharif* season, respectively for better management of MYMIV under North Indian conditions.

Evaluation of organic seed treatments on seed quality and seed health status of chickpea (*Cicer arietinum* L.)

The study aims to evaluate the efficacy of organic compounds—specifically Beejamrit, Jeevamrit, and Kunapjal—in inhibiting mycelial growth of seed-borne fungi while examining seed quality across ten chickpea varieties. The *in vitro* assessment involved varying concentrations (3%, 6%, 9%, & 12%) of these products, alongside a chemical comparison using 0.2% Carbendazim 50% WP and a control group. Notably, Carbendazim 50% WP displayed over 90% inhibition of mycelial growth, standing out among the tested treatments. Among organic products, Beejamrit @ 12% showed maximum mycelial growth inhibition (81.82%) followed by Beejamrit @ 9% (72.71%) and Jeevamrit @12% (69.34%). Conversely, Kunapjal @ 3% exhibited the lowest fungal growth inhibition (41.54%) against *Fusarium oxysporum*f.sp. *ciceri*, *Alternaria alternata*, and *Ascochyta rabiei.* The concentrations (9% and 12%) of Beejamrit, Jeevamrit, and Kunapjal that showed relatively better performance were applied to seeds of 10 varieties, alongside untreated seeds and those treated with the recommended POP (0.2% Carbendazim 50% WP). Seeds treated with Beejamrit at 12% demonstrated better performance in terms of seed germination (93%), seedling length (26.66cm), and dry weight (0.396g), displaying robust seedling vigour indices compared to the control group. These findings contribute to the development of environmentally friendly approaches for managing seed-borne pathogens in chickpeas through seed treatments and potentially in other leguminous crops. Furthermore, understanding the impact of these organic seed treatments on seed quality offers valuable insights for farmers and seed producers, empowering them to make informed decisions to enhance crop production and overall productivity.

Theme 5: Seed Storability and Seed Longevity

Seed storability studies in quality protein maize genotypes

Maize stands as a vital cereal food crop globally, with Quality Protein Maize (QPM) addressing essential amino acid deficiencies in lysine and tryptophan. Despite its nutritional enhancement, QPM faces challenges in seed storability. In a recent study involving 28 QPM inbreds, seed morphological characters exhibited minimal variability, but significant variations emerged in vigour parameters. Mean germination time (MGT) displayed a negative correlation with germination at zero days of accelerated ageing (0 DAA), while radicle emergence (RE) correlated positively after 5 DAA and 7 DAA. Three QPM inbreds (MGU-QPM-16, 20, and 22) exhibited superior storability based on accelerated ageing and seed vigour parameters, earmarking them for QPM hybrid breeding programs. Further scrutiny involved an eighteen-month natural ageing study with two contrasting QPM inbreds (MGU-QPM-16 and PMIQ-3) and a non-QPM inbred (HKI-1128) as a control. Over storage periods, all inbreds exhibited a successive decline in seed viability and vigour, with PMIQ-3 being the least storable. Total protein content reduced uniformly, but storage protein components showed differential changes, notably in lysine and tryptophan. Poor storability (PMIQ-3) correlated with reduced non-reducing sugars, a 42% increase in fructose, and pronounced glycation of proteins. Reactive oxygen species (ROS)-mediated oxidation increased in poor storers, leading to higher protein carbonylation, malondialdehyde (MDA), volatile compounds, and electrical conductivity. Comparing deteriorative patterns in QPM and non-QPM versions during accelerated ageing revealed faster deterioration in QPM. The decline in viability and vigour, coupled with increased protein carbonylation and lipid peroxidation, indicated faster deterioration in QPM due to lower antioxidant activity (CAT and POD) and elevated ROS (H_2O_2) levels. This study highlights the physiological and biochemical distinctions between good and poor storers, providing crucial insights for improving QPM seed storability and ensuring food security.

Studies on seed longevity in rice seed lots using hyperspectral imaging and metabolomics

The study involved investigating germination of rice seed lots under natural and experimental storage conditions, establishing a relationship between germination parameters and the different ageing treatments. The research also aimed to assess the difference in seed viability in naturally stored lots by analyzing hyperspectral reflectance of 5 good and 5 poor storer varieties categorized based on P_{50} values. Furthermore, metabolomics analysis (HS-GC-MS) was performed on fresh seeds, 1-year, and 5-yearold seed lots of a poor storing genotype Shabhagi to understand biochemical changes with ageing. Seeds of 39 rice genotypes harvested in 2017, 2018, 2020, 2021, and 2022 and stored under ambient laboratory conditions were used for seed germination studies. The fresh seeds of all these genotypes produced in 2022 were used for controlled deterioration and accelerated ageing tests. The results of the studies showed that under ambient storage, aged seed lots in all varieties showed decrease in seed germination parameters. Correlation analysis indicated that seed storability under natural ambient storage was more related to CD storage than the AA storage. The kernels of rice grains used for hyperspectral technique showed that aged seeds had higher spectral reflectance than that of fresh seeds. A significant difference in spectral signatures, particularly in NIR and SWIR wavelengths showed high correlation with seed germination. Employing the multivariate technique, PLSR, proved effective in predicting seed viability with high accuracy (RPD>2) and significant R^2. Seed metabolomics identified unique and common volatile compounds in the headspace accumulated from the fresh and aged seed lots. The relative area of common volatile compounds was at higher levels in five-year-old seed samples compared to oneyear-old and fresh seeds. Few of these common volatile compounds showed highest negative correlation with seed viability. This study would be beneficial to efficiently manage long term storage of rice seeds, predicting marketable periods with accurate and rapid assessment of seed longevity using hyperspectral and metabolomics analysis.

Physiological and biochemical basis of seed deterioration in rice

Ensuring high-quality seeds is paramount for the seed and breeding industry, given its profound impact on crop productivity. Seed storage, a critical aspect, can lead to diminished germination and vigor, adversely affecting field emergence. This study delves into the dynamics of seed aging in rice, investigating 39 seed lots stored under ambient laboratory conditions for varying durations. The research unfolded with four main objectives. Firstly, it aimed to assess germination and longevity parameters in rice seed lots (n = 39) stored under ambient laboratory bench storage for different durations. The results revealed a progressive decline in germination over time, emphasizing the influence of storage duration on seed quality. Secondly, the study evaluated seed germination, vigor, and headspace ethanol content in selected rice genotypes from contrasting storage groups. Notably, significant variations were observed among accessions, with germination rates declining from 97% (fresh seeds) to 43% after 4 years of ambient storage and further to 25% after 5 years of ambient storage. . The seed half-viability period (P_{50}) estimated using the seed viability equation showed significant variation among genotypes. We performed cluster K means analysis based on seed germination and longevity parameters to differentiate (or select) genotypes with high resistance to aging (good storers) and high sensitivity to aging (poor storers). Pearson's correlation analysis indicated a strong relationship between seed vigor parameters and headspace ethanol content in good-storing rice genotypes. Thus, the headspace ethanol assay can be a simple, fast, and reliable assay to determine early seed vigor loss in rice seeds. The third objective involved utilizing near-infrared spectroscopy to differentiate seed quality among selected rice genotypes from varying storage groups. Pearson's correlation coefficients indicated a strong correlation with storage duration (degree of aging), seed germination, and vigor parameters at a specific spectral wavelength range (1200-1400nm). The final goal focused on understanding biochemical changes by studying fatty acid profiles in differentially aged seeds using GC-MS. Specific fatty acids, such as margaric acid (C17:0), exhibited strong correlations with storage duration and viability parameters, offering insights into the biochemical alterations during seed aging. In summary, this comprehensive study sheds light on the physiological and biochemical aspects of seed deterioration in rice. It introduces potential tools like headspace ethanol assay and near-infrared spectroscopy for efficient monitoring. These findings provide valuable insights for seed managers, equipping them with knowledge to ensure and maintain seed quality during storage.

Evaluation of seed physiological parameters of diverse rice genotypes under different experimental seed ageing methods

Damage during seed storage decreases vigor, germination, and seedling quality. The rate of seed deterioration depends on thestorage environment (RH, temperature, and oxygen), genetic makeup, and initial seed quality. Apparently, seeds of identical genetic background may show different response to storage conditions due to differences in seed cytoplasmic state. Thus, the present study aimed to evaluate germination variabilityin a diverse rice set after aging under different seed moisture regimes and compare germination data under dry CD and moist AA conditions. Initially, 20 rice accessions from a 283-accession panel were aged in hermetic container at 41°C with seed eRH of 66.9% (dry CD) and 95.4% (moist AA) for different durations. Viability declined progressively with time, rapidly in moist AA than dry CD storage. The moist AA storagetakesapproximately 14 days to reach 50% viability, while dry CD storage took about 56 days. Based on these results,maintests were conducted on all 283 accessions, aging them for 52 days under dryCD and 16 days under moist AA storage at 41°C. Upon aging, germination parameters varied significantly with initial 97% germination reduced to 56% under 52 days CD storage and 52% under 16 days moist AA storage. In both aging conditions, accessions showed tolerance, while others were sensitive, losing complete viability. Correlation analysis revealed a moderate positive correlation (r=0.49) in germination response to aging under dry CD and moist AA storage. In conclusion, diverse rice accessions exhibited varied responses to aging under different moisture regimes, emphasizing caution in interpreting moist seed aging results for dry storage decisions. Findings of our research are pivotal for enhancing seed longevity, influencing seed quality management in commercial seed warehouses and genebank storage.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the Student & Roll No.	MSc/ PhD	Title of the thesis	Chairperson	Institute
1.	Nan Khiang Khiang Soe (21378)	M.Sc.	Evaluation of seed physiological parameters of diverse rice genotypes under different experimental seed ageing methods	Mr. Manjunath Prasad	ICAR-IARI, New Delhi
2.	Sandeep (21707)	M.Sc.	Evaluation of organic seed treatments on seed quality and seed health status of chickpea (*Cicer arietinum* L.)	Dr. Atul Kumar	ICAR-IARI, New Delhi
3.	Tanya Singh (21708)	M.Sc.	Studies on seed longevity in rice seed lots using hyperspectral imaging and metabolomics	Dr. S. K. Chakrabarty	ICAR-IARI, New Delhi
4.	Shreya Patil (21709)	M.Sc.	Studies on effect of salinity stress on seed quality parameters and its alleviation through seed priming in wheat species	Dr. Monika A. Joshi	ICAR-IARI, New Delhi
5.	Tuhina Ghosh (21710)	M.Sc.	Effect of ZnO nano-particle based priming on seed quality enhancement in tomato (*Solanum lycopersicum* L.) under salt stress	Dr. Shiv K. Yadav	ICAR-IARI, New Delhi
6.	Yallavva Madar (21711)	M.Sc.	Physiological and biochemical basis of seed deterioration in rice	Mr. Manjunath Prasad	ICAR-IARI, New Delhi
7.	Mujtahida Khatun (60115)	M.Sc.	Evaluation of seed coating with microbial formulations for enhancing seed yield and quality in chickpea (*Cicer arietinum* L)	Dr. Priya Ranjan Kumar	#ICAR-IARI, Jharkhand

8.	Sayan Makur (60116)	M.Sc.	Assessing the efficacy of seed coating with microbial formulations for quality enhancement in wheat (*Triticum aestivum* L.)	Dr. Priya Ranjan Kumar	#ICAR-IARI, Jharkhand
9.	Mrinali Manohar Mandape (10670)	Ph.D.	Enhancing zinc use efficiency in mungbean (*Vigna radiata* L. Wilczek) through seed treatments	Dr. K.K. Singh	ICAR-IARI, New Delhi
10.	Niranjan Prasad H.P. (11328)	Ph.D.	Studies on stemphylium blight caused by *Stemphylium vesicarium* (Wallr.) on seed quality parameters in onion and its integrated disease management for quality seed production	Dr. Atul Kumar	ICAR-IARI, New Delhi
11.	Dilshad Ahmad (11332)	Ph.D.	Seed storability studies in quality protein maize genotypes	Dr. Vijay Dunna	ICAR-IARI, New Delhi
12.	Jayasri S. (11333)	Ph.D.	Seed enhancement technology for quality seed production of chilli (*Capsicum annum* l.)	Dr. Sudipta Basu	ICAR-IARI, New Delhi
13.	Preeti Sagar Negi (11334)	Ph.D.	GWAS to identify marker trait associations for early seedling vigour in rice	Dr. Arun Kumar M.B.	ICAR-IARI, New Delhi
14.	Archana H.R. (11598)	Ph.D.	Studies on thermotolerance and its induction during seed germination and seedling growth in rice	Dr. Vijay Dunna	ICAR-IARI, New Delhi
15.	Ramappa S. (11600)	Ph.D.	Mapping of seedling vigour related traits for moisture deficit stress tolerance in wheat (*Triticum aestivum* L.)	Dr. Monika A. Joshi	ICAR-IARI, New Delhi
16.	Shobharani M. (11601)	Ph.D.	Effect of sowing dates and planting seasons on the seed yield and quality attributes with special reference to Mungbean yellow mosaic India virus (MYMIV)	Dr. S.K. Lal	ICAR-IARI, New Delhi
17.	Shruti Kumari (11602)	Ph.D.	Studies on seed vigour traits in relation to flowering, harvest maturity, storage period and validation of QTL associated with seed vigour in rice (*Oryza sativa* L.)	Dr. S. K. Chakrabarty	ICAR-IARI, New Delhi
18.	Shahil Kumar (11860)	Ph.D.	Genetic and molecular basis of protogyny, CMS and self-incompatibility system in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]	Dr. S. K. Chakrabarty	ICAR-IARI, New Delhi
19.	Deepak Rao (11865)	Ph.D.	Effect of chemical priming for improving early seedling vigour under salinity stress in lentil	Dr. Sangita Yadav	ICAR-IARI, New Delhi

#IARI off Campus

Session II: School of Crop Protection

Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Agricultural Chemicals	06	06
Entomology	13	19
Nematology	04	02
Plant Pathology	11	12
Total	**34**	**39**

SCHOOL OF CROP PROTECTION

Convenor: Dr. Monika A. Joshi, Professor, Division of Seed Science & Technology
Co-convenor: Dr. Shruti Sethi, Principal Scientist, Division of Food Science & Post harvest Technology

Chairperson: Dr. Harikesh Bahadur Singh, FNAAS, Former Professor, BHU

Dr. Singh is currently working as Distinguished Professor, Biotechnology, GLA University, Mathura and Chairman, State Expert Appraisal Committee, Uttar Pradesh. Prior to this assignment he served as a Professor & Head at Banaras Hindu University. Dr. Singh has spent 40 years of committed service in the field of Plant Pathology at different institutions in different capacities; and has developed several formulations containing microbes viz., *Pseudomonas, Rhizobium, Bacillus* and *Trichoderma,* that can be used as biofertilizer, biostimulant and biopesticide. Commercial production of some of the biofertilizers (*Rhizobium*, PSB and *Azotobacter*) in 17 biofertilizer laboratories and biopesticides (*Trichoderma harzianum*, NPV and *Baeveria bassiana*) in 9 IPM laboratories of Govt. of Uttar Pradesh have been taken up using the technology developed by his group; for which he has was honoured by the Prime Minister of India with CSIR Award for Science & Technology Innovations for Rural Development in 2011. Prof.Singh has guided 24 Ph.D students, six Post-Doctoral, two Women Scientists and 29 M.Sc. (Ag.) students. He has obtained 19 patents (USA, Canada, PCT and 7 Indian patents published) and commercialized five technologies, published 296 research papers, 46 review articles, 96 book chapters and edited 44 books. Prof. Singh has served as member of DBT Task Force on Biofertilizers and Biopesticides DST WOS-A; DST WOS-B; DBT Task Force for Biotechnology Based Programme for SC/ST Population and Rural Development; DST NSTMIS Task Force; Chairman, Uttar Pradesh Council of Science and Technology Task Force on Agriculture and Allied Sciences and Member of RAC/ QRT of several institutes.

Agricultural Chemicals

4

Prof. Neera Singh

The Division of Agricultural Chemicals has proved a trendsetter in planning and execution of basic and applied research of national importance in multifarious domains of development, formulation and safety aspects of agrochemicals viz. pesticides and pesticide adjuvants, superabsorbent hydrogels and composites, nitrification inhibitors, hybridizing agents, nutraceuticals, plant growth regulators, smart agro-inputs delivery systems, nano products, new analytical methods for pesticide residues, etc. Significant research findings of post graduate students are enlisted under the following themes.

Theme 1: Development of Agrochemicals and Formulations

Appraisal of resin assisted purification mechanism of anthocyanins

Six macroporus resins (three adsorbent and three ion exchange) were screened for preferential adsorption of acylated (black carrot, purple cabbage) and non-acylated (rose, black rice) anthocyanins from crude extracts. Chemo-profiling of anthocyanin extracts through UPLC-TOF-HRMS revealed sixty anthocyanidins, anthocyanins and related compounds. Among adsorbent resins, XAD-16 and DIAION HP 20 and among ion exchange resins, OPTIPORE L 493 were best in adsorbing anthocyanins. OPTIPPORE-L 493 resin was the most effective resin due to its least desorption capacities and highest adsorption efficiencies (4.01 mg C3G eq g^{-1}). The scanning electron microscopy, high resolution microscopy, FT-IR spectroscopy and confocal microscopy-based characterizations confirmed the adsorption process occurred at pore spaces of macroporous resins. Pseudo 2nd order model better explained sorption kinetics while Freundlich isotherm best explained adsorption of anthocyanin, phenolics except sugars. OPTIPORE L 493 was the best resin in adsorbing acylated anthocyanin and as well as non-acylated anthocyanin and phenolics. Sugar was the weakly adsorbed on ion exchange resin and showed 62.2% desorption. The molecular simulation study for adsorption predicted that the thermodynamic stability was the highest for acylated anthocyanin [cyanidin 3-O-(6-O-p-coumaryl) glucoside - 760.432 kcal mol^{-1}] and least for phenolic compound (quercetin-3-glucoside - 467.677 kcal mol^{-1}). In general, adsorption of both type of anthocyanins on DIAION HP 20 and OPTIPORE L 493 resins was maximum at pH 6-7. Variation of temperatures didn't affect the adsorption process which was endothermic, spontaneous and random in nature. Ultrasonic assisted anthocyanin adsorption (36% amplitude, 90 min time, 1:45 resin to extract ratio) achieved 90.2% recovery at faster rate than conventional method. Process was optimized through response surface methodology and improved by genetic algorithm approach. Column assisted dynamic method for bulk purification yielded highest purity improvement in black carrot extract (243.6%) and lowest (43.9%) in black rice extract.

Development of EPN bio agent enriched powder formulation and evaluation for termite and white grub management in some field crops

Entomopathogenic nematodes (EPNs), a type of biocontrol organisms effective against insect pests have been established as potential biopesticides. However, the constraint of limited viability and infectivity under high temperatures and low moisture conditions limit their usage potential. The present study aimed to develop an easy-to-produce, out-scale, and apply EPN enriched powder formulation having sustained EPN survival and virulence against insect pests. A molecular docking simulation revealed the potential of three organic acids (OA-1, OA-2, and OA-3) in arresting the lipid metabolism of EPNs and wet lab experiments with OA-1 at 10 ppm was the most potential lipid metabolism arrestant for *Steinernema abbasi* IJs. The OA-1 led to enhanced IJ survival at 35°C and 40°C storage temperatures. Four EPN bioagents-enriched powder formulations were prepared using Katira gel and three types of aluminosilicate clays with varying moisture levels. Among all, the formulations, SaP-1 registered the highest nematode survival (92% on the 14th day at 37°C). Its bioefficacy assessment against subterranean termites (*Odontotermes obesus*) over three *rabi* seasons (2020-2021, 2021-2022, and 2022-2023) in infested wheat and chickpea fields revealed a significant reduction in plant damage due to pest attack in SaP-1 (20 kg ha^{-1}) treated plot(s) as compared to the control. Assessment of the biocontrol potential of SaP-1 against white grub (*Anomala dimidiata*) in sugarcane fields revealed the lowest white grub population in plots treated sequentially with SaP-1 @40 kg ha^{-1} and fipronil 40%+imidacloprid 40% WG application @ 75% of the recommended dose. Present work offers a novel method of developing an entomopathogenic nematode-based powder formulation that can withstand challenging storage conditions and effectively limit the damage to crops by soil-borne insect pests. The product developed can be effectively used in integrated pest management programs for termite and white grub management.

Phytochemical analysis and nematicidal activity of *Annona squamosa, Cymbopogon nardus* and *Pelargonium graveolens* against phytopathogenic nematodes

Present study aim to identify root-knot nematode control agents, either in crude form or pure bioactive compounds from the seeds of *A. squamosa*, and aerial parts of *C. nardus* (citronella) and *P. graveolens* (geranium) through phytochemical and bioassay guided pathways. Extraction of *A. squamosa* seeds with hexane and methanol gave 22.20% and 5.34% extract. Fresh leaves of *C. nardus* and aerial parts of *P. graveolens* contained 0.97% and 0.84% essential oils. GC-MS analysis of *C. nardus* and *P. graveolens* essential oils suggested that oil was rich in oxygenated monoterpenes and *C. nardus* oil contained citronellal (35.53%), citronellol (16.97%), and geraniol (23.6%), while *P. graveolens* oil contained citronellol (40.90%), geraniol (21.9%), citronellylformate (12.86%), menthone (5.14%) and geranyl formate (3.87%) as major compounds. Citronellal and citronellol were isolated from the citronella oil. Hexane extract of *A. squamosa* seeds mainly contained oleic acid (50.10%), linoleic acid (23.85%), stearic acid (11.81%), and palmitic acid (14.24%). Nine pure compounds were isolated from hexane-acetone extract while sucrose and stigmasterol glucoside were isolated from acetone insoluble portion of methanolic extract. Nematicidal activity (*in vitro*) of the essential oils, extracts, pure compounds and mixture against J2 of root knot nematodes, *Meloidogyne graminicola* and *M. incognita* showed LC_{50} of 9.23 – 130 ppm (*M. graminicola*) and 4.89 – 122 ppm (*M. incognita*), compared to carbofuran (3.95 ppm) and velum prime (13.7 ppm). The pot experiments after inoculation of J2 of *M. graminicola* using drenching and root dip methods (500 and 1000 ppm) showed reduction of number of galls and better seedling growth, similar to positive control. Drenching method showed better effect than root dip method. Similar results were found against J2 of *M. incognita* in brinjal seedling up to 60 days after inoculation. Microplots study in *M. graminicola* sick plots in direct seeded rice showed reduction in number of galls, similar to positive control.

Chemical analysis and pesticidal activity of *Azadirachta indica* and *Piper longum* against nematodes and sucking pest

Plants are rich sources of bioactive secondary metabolites and have emerged as alternatives to synthetic pest-control agents. Thus, phytochemical analysis and bioassay of extracts from leaves of *A. indica* and fruits of *P. longum* was carried out to identify the bioactive ingredients for management of nematode and aphid. *P. longum* fruits showed 0.49% essential oil containing (Z)-β-farnesene (25.08%), β-caryophyllene (13.57%), α-humulene (13.37%), 8-heptadecene (9.28%), heptadecane (7.07%), α-patchoulene (5.44%), 3-heptadecene (5.09%), γ-elemene (4.37%) and β-humulene (3.69%). Four pure compounds were isolated from different extracts of *P. longum* and identified as methyl piperate, piperine, guineensine, 1-methoxy-β-D-glucose. Eight pure compounds were isolated and identified in extract of leaves of *A. indica* (nimbolide, β-sitosterol-3-O-β D-glucoside, α-D-glucose, quercetin-3-O-β-glucopyranoside, azadirone, isorhamnetin-3-O-β-D-glucopyranoside, stigmast-5,22-dien-3-O-β-D-glucopyranoside, stigmasterol). I*n vitro* and pot evaluation of piper oil, extracts, and pure compounds for nematicidal activity against J2 of *Meloidogyne incognita* and aphicidal activity against *Lipaphis erysimi* (mustard aphid) showed promising results. Two compounds, quercetin-3-O-β-glucopyranoside (N-4) and nimbolide (N-1) exhibited potent nematicidal activity. The nematicidal activity of β-sitosterol-3-O-β D-glucoside, quercetin-3-O-β-glucopyranoside, nimbolide and azadirone was reported for the first time. The oil and extracts obtained from the fruits of *P. longum* were more effective than the extracts from the leaves of *A. indica*. This study suggests that essential oil, extracts, and pure compounds from fruits of *P. longum* and leaves of *A. indica* can be utilized for the development of new pest control agents for the management of root-knot nematode and mustard aphid.

Sustained release formulation of betalains for its application as natural food colorant

Betalains are a group of naturally occurring pigments in various plant parts including the dragon fruits (*Hylocereus* spp.). The peel, which constitute around 20% of the fruit's fresh weight and is discarded as wastes, contains large amounts of betalains. Thus, in quest for 'waste to wealth' generation and replacing artificial food colorants, optimized extraction of betalains from the peels of red dragon fruit (*Hylocereus costaricensis*) and developed its sustained release formulation with improved stability and bioavailability. Chemo-profiling of the pigments in *H. costaricensis* peels revealed the dominance of betacyanins (betanin, betanidin, phyllocactin, apiocactin, hylocerenin, etc.) over betaxanthins (indicaxanthin). Ultrasonic probe-assisted extraction (UPE) was better than conventional solid-liquid extraction, homogenization, and ultrasonic bath extraction techniques. Optimization of the process variables of the UPE technique (solvent-to-solid ratio, ultrasonication amplitude, and time) was carried out through response surface methodology (RSM) and genetic algorithm (GA). GA-coupled RSM model predicted the extraction yield of 286.27 mg g^{-1} of betalains (d.w.) by ultrasonication for 40 min at 50% amplitude with 111.5 mL g^{-1} solvent. Solid powder formulations of the extracted betalains were prepared by encapsulation through an ionic gelation technique with varying concentrations of chitosan and κ-carrageenan and were characterized. The loading capacity and encapsulation efficiency of the prepared formulations were 6.90-10.65%, and 70.38-97.08%, respectively. Encapsulated betalains were stable at freezing and ambient temperatures, while accelerated storage conditions (54±2°C for 14 days) led to a modest degradation (6.23-26.30%). A pH-dependent sustained release behavior of the encapsulated betalains from the formulations was observed with higher cumulative release at neutral than acidic pH. *In vitro* bioavailability study confirmed significant accessibility (30-73%) of encapsulated betalains in simulated gastric phase. The study presented a comprehensive exploration of sustained-release powder formulations of natural betalains from dragon fruit peels.

Phytochemicals from *Litsea glutinosa* for potential antifungal activity against storage fungal pathogens

Litsea glutinosa bark's sequential extraction using various organic solvents through conventional solid liquid extraction (CSLE) resulted highest yield of methanolic extract (6.74%), followed by $CHCl_3$ (3.87%) extract and EtOAc (3.12%) extract. Extracts were evaluated *in vitro* against *Aspergillus flavus*, *A. parasiticus*, and *Penicillium expansum* using poison food technique, highlighting maximum inhibitory action of $CHCl_3$ extract against *P. expansum* (EC_{50} 85.3 µg mL^{-1}) and *A. parasiticus* (EC_{50} 129.1 µg mL^{-1}). While, inverted plate antifungal assay revealed moderate effectiveness of $CHCl_3$ extract against *P. expansum* (EC_{50} 493.1 µg/mL), suggesting potential antifungal effect due to non-volatile components of the extract. A comparative analysis of four extraction techniques, CSLE, ultrasonic assisted extraction (UAE), microwave assisted extraction (MAE), and high-speed homogenization displayed UAE as the most efficient method. Therefore, UAE parameters were optimized to yield maximum $CHCl_3$ soluble fractions using response surface methodology (RSM) design. RSM results showed an impressive extraction yield of 582.15 mg $5g^{-1}$ sample, employing solvent to solute ratio of 54.43 mL $5g^{-1}$, employing power of 58.26 W and extraction time of 19.07 min. Fatty acid composition analysis of *L. glutinosa* bark resulted octadecanoic acid (11.69%) and 9,12-octadecadienoic acid (11.45%) as predominant. Untargeted phytochemical analysis using UPLC-QTOF-ESI-MS/MS revealed tentative identification of forty compounds in $CHCl_3$ extract. Likewise, analysis of hexane, EtOAc and methanolic extracts based on their accurate mass resulted tentative identification of nineteen, twenty-six and thirty-eight phyto-compounds, respectively. The effect of $CHCl_3$ extract on the treated fungi resulted reduction of cell wall ergosterol content 98.19% in *P. expansum* at 3000 µg mL^{-1} concentration. Molecular docking studies of the identified major compounds (ligands) and Cyt P_{450} sterol 1,4 α-demethylase (target protein, responsible for ergosterol biosynthesis) indicated litsealactone B as most prominent component due to its low distance conventional H-bonds and hydrophobic π-alkyl interactions.

Synthesis and evaluation of indazolylchromone derivatives against plant pathogenic fungi

A series of 2-indazol-1-yl-chromen-4-one derivatives was synthesized following condensation of substituted 2-hydroxy acetophenone derivatives with N, N-dimethylformamide dimethyl acetal to enaminones, cyclisation of enaminones with iodine to 3-idochromones, which on reaction with indazole resulted in the formation of 2-indazol-1-yl-chromen-4-one derivatives. A total of 20 indazolylchromones (6a-6t) were synthesized having yield of 76.35% - 93.86%. Among these, 19 compounds (6b-6t) were reported in the literature for the first time. All the compounds were characterized using infrared, nuclear magnetic resonance (^1H NMR and ^{13}C NMR). Indazolylchromones showed good antifungal activity against *Sclerotium rolfsii* and *Fusarium oxysporum*. Among the tested compounds, 6t and 6f exhibited very good antifungal activity against *S. rolfsii* with an ED_{50} of 10.10 ppm and 16.18 ppm, respectively. Compound 6f displayed good activity against *F. oxysporum* with an ED_{50} value of 27.82 ppm. *In vivo* evaluation showed that compounds 6t and 6f effectively controlled the disease at 1000 ppm with PDI values of 26.66% and 30%, respectively, and were at par with commercial fungicide, hexaconazole 5% SC, (PDI=25%). Compound 6f was found less active against *F. oxysporum* with PDI of 35% while commercial carbendazim 50% WP, showed PDI of 24%. A suitable formulation of these two compounds can be developed for effective management of *S. rolfsii*.

Synthesis of 1,3,4-thiadiazole derivatives and their antifungal evaluation against *Rhizoctonia solani* and *Macrophomina phaseolina*

The present study aimed to synthesize 5-substituted-1,3,4-thiadiazole-2-thiol derivatives and assess their fungicidal efficacy against two prominent agricultural pathogens, *R. solani* and *M. phaseolina*. A series of 25 derivatives was synthesized through multistep reactions, demonstrating yields ranging from 31% to 87%. Comprehensive spectral and analytical techniques confirmed the identity of synthesized compounds. Most of the compounds were effective as antifungal agents and their ED_{50} values were ranged from 3.6 to 196.56 µg mL^{-1} against *R. solani* and 2.66 to 181.44 µg mL^{-1} against *M. phaseolina*. The presence of halogen substituents in phenyl rings attached to 5 position of the thiadiazole moiety correlated positively with enhanced bioactivity. Detailed structure-activity relationship (SAR) analysis elucidated the influence of halogen substitution on the compounds' efficacy. Docking studies further affirmed the potential of these derivatives as antifungal agents. The findings highlight the potential of 5-substituted-1,3,4-thiadiazole-2-thiol derivatives as effective fungicides in agricultural pest management.

Theme 2. Assessment and management of contaminants

Dynamics of bisphenol A and triclosan in soil and water

Present study involved assessment and distribution of endocrine disrupting chemicals (EDCs) in soil and waters of India and persistence and leaching of these chemicals in two soils collected from IARI (Delhi) and Coochbehar (WB). LC-MS/MS method was optimized for detection and quantification of 11 EDCs in soil and water while QuEChERS method was used for the extraction of residues from the soil. Bisphenol-A (BPA), triclosan (TCS), triclocarbon (TrC), 4-nonylphenol (NP), 4-tert-octylphenol (OP), methyl paraben (MP), propyl paraben (PrP), butyl paraben (BuP), benzyl butyl phthalate (BBP), di (2-ethylhexyl) phthalate (DEHP), and di-n-butyl phthalate (DBP) were detected in river water, groundwater and agricultural soil samples collected from 26 sampling points of different agro-climatic zones. EDCs detection frequency varied from 45-100% in river water. DBP, BBP, DEHP, TCS, TrC, OP, NP, PrP and BuP were detected in 100% groundwater samples while OP, NP, BPA and DBP in 100% soils samples. EDCs detection frequency in IARI tubewell water and agricultural soils was 100% while BPA, TCS, TrC, OC, NP, MeP, PrP, DBP and DEHP were present in 100% drain water samples. Persistence (half-life, $T_{1/2}$) of BPA (47.0- 54.7 days) and TCS (68.3-73.3 days) decreased under UV-light exposure (BPA: 19.0-24.6 days; TCS: 36.2-40.1 days). Both compounds were more persistent in IARI soil than in WB soil (OC 1.98%). TCS ($T_{1/2=}$ 26.1 - 97.0 days), in general, was more persistent than BPA ($T_{1/2=}$ 4.5-85.9 days). Leaching studies suggested that major residues (>90%) were present in 0-15 cm soil core. Organic amendments reduced the downward mobility of BPA and TCS. Leaching of BPA and TCS was greater in IARI soil than in WB soil while BPA was more mobile than TCS. Organic amendments reduced the leaching potential of both compounds.

Method development for quantification of pesticide residues in processed foods and evaluation of pesticide residue kinetics during processing

An ultra-performance liquid chromatography-tandem mass spectroscopy method was developed for quantification of 103 pesticides. Instrumental limit of quantification (LOQ) for most of the pesticides was 0.001 µg g^{-1}. QuEChERS d-SPE clean-up suggested that anhy. $MgSO_4$ gave high recovery for maximum number of pesticides. This method was optimized and validated for identification and quantification of pesticide residues in mango juice, cookies, red chilli powder, tomato sauce and roasted soybeans. Dilution before extraction with 5 mL water, citrate QuEChERS and anhy. $MgSO_4$ cleanup was effective in recovering 100 pesticides in acceptable limits in mango juice. Pre-wetting with 4 mL water followed by QuEChERS clean-up using 25 mg C-18 + 150 mg anhy. $MgSO_4$ gave acceptable recovery of 98 pesticides in cookies. Pre-wetting with 10 mL water, followed by acetate QuEChERS extraction and 10 mg GCB+ 25 mg PSA+ 150 mg anhy. $MgSO_4$ clean-up yielded acceptable recovery of 95 pesticides in red chilli powder. Acidified water (2.5 mL) and QuEChERS dispersive clean-up using 25 mg C-18 and 150 mg anhy. $MgSO_4$ gave acceptable recovery of 93 pesticides in tomato sauce. Pre-wetting with 5 mL water followed by 10 mL acetonitrile extraction using QuEChERS with 150 mg anhy. $MgSO_4$ gave acceptable recovery of 94 pesticides from roasted soybeans. Most of the pesticides showed linearity in range of 0.001-0.005 $\mu g\ g^{-1}$ with LOQ of 0.01 $\mu g\ g^{-1}$. Mild to medium matrix enhancement was seen for majority of pesticides in all commodities except red chilli powder, which showed severe matrix enhancement (52.05-598.89%). Real sample analysis using developed methods showed that most of the market samples contained residues of >2 pesticides in red chilli powder and tomato sauce at/above LOQ. Processing of tomato into tomato sauce revealed concentration of 89 pesticides in sauce (processing factor >1). Residue kinetics study in red chilli showed concentration of 96 pesticides when dried for 7 days, with the processing factor ranged from 1.0-17.58.

Mesoporous silica and or its composites for the efficient removal of sulfamethoxazole (SMXZ) from water

Mesoporous silica composites were explored for removal of SMXZ from water. An analytical methodology using LC-MS/MS was standardized for detection and quantification of SMXZ. An extraction protocol optimized gave recoveries in the range of 80.45-90.66%. Eleven adsorbents were synthesized and characterized and among them mesoporous silica and graphene oxide composite (MPS-GO) showed highest adsorption. Optimum sorption of 96.56% was achieved using 20 mg of MPS-GO in 10 mL of SMXZ aqueous solution of pH 5.6 at a spiking level of 0.1 $\mu g\ mL^{-1}$ within 90 min. The adsorption kinetics data was fitted well to the pseudo 2nd order model (R^2=0.99). The satisfactory fitting of sorption data to Freundlich isotherm (R^2=0.954-0.999), indicated multilayer adsorption. Adsorption (K_d) was highest at 25ºC (2.64) followed by 35ºC (1.44) and 45ºC (1.37), indicating exothermic and spontaneous physical sorption process. A positive effect on the sorption of SMXZ on MPS-GO was observed when the humic acid (HA) concentrations exceeded 1 mg L^{-1}. The pre-equilibration of MPS-GO with HA for 24 h was the best for SMXZ removal. Among the different regeneration methods, highest antibiotic release was noticed using ethanol. Regeneration efficiency was 94.57-67.69% during 4 consecutive cycles with SMXZ removal efficiency of 96.4-65.25%. Regenerated SMXZ was efficiently degraded using UV radiation in the presence of H_2O_2. Removal efficiency of 88.56-90.84% was achieved in a jar test experiment. The decontamination method was validated in 0.1 $\mu g\ mL^{-1}$ spiked Yamuna River water with removal efficiency of 89.81-91.70%. The adsorption efficiency of MPS-GO was comparatively better than activated charcoal, and magnetic MPS-GO.

Molecular simulation-based synthesis and evaluation of biochar-metal organic framework (BC-MOF) composites for the removal of rice fungicide(s) residues from water

Five biochar-metal organic frameworks (BC-MOFs), *viz*. Cu-BTC@BC, Fe-BTC@BC, MIL-53(Al)@BC, MIL88b-Fe@BC, and ZIF-8@BC were prepared using sol-gel/solvothermal and hydrothermal synthesis methods. Grand Canonical Monte-Carlo (GC-MC) simulations and *in-silico* adsorption experiments indicated that MIL88b-Fe@BC, MIL-53Al@BC, and ZIF-8@BC composites exhibited exceptional sorption of rice fungicides namely tricyclazole, isoprothiolane, and carbendazim in single and ternary solute systems. Maximum adsorption of fungicides in single solute system was highest on MIL-53Al@BC (98.97-99.94%) and same trend was observed in ternary solute system. MIL-53(Al)@BC exhibited superior regenerative properties for tricyclazole (90%) and isoprothiolane (80%) compared to other BC-MOFs. Validation studies showed that MIL-88b-Fe@BC (99.4%) and

MIL-53Al@BC (98.6%) exhibited superior performance in removing tricyclazole, Cu-BTC@BC of carbendazim (90.8%) while MIL-53Al@BC exhibited a isoprothiolane removal efficiency of 99.09%. These findings highlighted the efficacy of MIL-88b-Fe@BC and MIL-53Al@BC composites in the purification of Hindon river water from these fungicides.

List of contributing students and Chairperson of advisory committee

Sr. No.	Name of the student, Roll No.	Degree	Title of the thesis	Chairperson	Institute
1.	Dipshikha Mondal, (21562)	M.Sc.	Sustained release formulation of betalains for its application as natural food colorant	Dr. Anirban Datta	ICAR-IARI, New Delhi
2.	Riya Kundu, (21563)	M.Sc.	Synthesis and evaluation of indazolylchromone derivatives against plant pathogenic fungi	Dr. Parshant Kaushik	ICAR-IARI, New Delhi
3.	Ashutosh Kumar Singh, (21564)	M.Sc.	Synthesis of 1,3,4-thiadiazole derivatives and their antifungal evaluation against *Rhizoctonia solani* and *Macrophomina phaseolina*	Dr. Rajesh Kumar	ICAR-IARI, New Delhi
4.	Sourabh Suman, (21565)	M.Sc.	Phytochemicals from *Litsea glutinosa* for potential antifungal activity against storage fungal pathogens	Dr. Aditi Kundu	ICAR-IARI, New Delhi
5.	Arindam Ray, (21566)	M.Sc.	Mesoporous silica and or its composites for the efficient removal of sulfamethoxazole from water	Dr. Neethu Narayanan	ICAR-IARI, New Delhi
6.	Chavali Saikumar Reddy, (21567)	M.Sc.	Molecular simulation-based synthesis and evaluation of biochar-metal organic framework (BC-MOF) composites for the removal of rice fungicide(s) residues from water	Dr. Abhishek Mandal	ICAR-IARI, New Delhi
7.	Anindita Paul, (10726)	Ph.D.	Appraisal of resin assisted purification mechanism of anthocyanins	Dr. Supradip Saha	ICAR-IARI, New Delhi
8.	Arka Deb Mukhopadhyay, (11155)	Ph.D.	Development of EPN bio agent enriched powder formulation and evaluation for termite and white grub management in some field crops	Dr. Anupama Singh	ICAR-IARI, New Delhi
9.	Ajith M., (11158)	Ph.D.	Phytochemical analysis and nematicidal activity of *Annona squamosa*, *Cymbopogon nardus* and *Pelargonium graveolens* against phytopathogenic nematodes	Dr. Virendra Singh Rana	ICAR-IARI, New Delhi
10.	Sutanwa Saha, (11159)	Ph.D.	Dynamics of bisphenol A and triclosan in soil and water	Dr. Suman Gupta	ICAR-IARI, New Delhi
11.	Vijay Kumar, (11376)	Ph.D.	Chemical analysis and pesticidal activity of *Azadirachta indica* and *Piper longum* against nematodes and sucking pest	Dr. Virendra Singh Rana	ICAR-IARI, New Delhi
12.	Madhu Tippannanavar, (11377)	Ph.D.	Method development for quantification of pesticide residues in processed foods and evaluation of pesticide residue kinetics during processing	Dr. Tirthankar Banerjee	ICAR-IARI, New Delhi

Entomology

5

Prof. Debjani Dey

The Division of Entomology has its origin as one of the five sections of the erstwhile Imperial Agricultural Research Institute. The Division has emerged as the torch bearer of research right from its inception and not only produced eminent entomologists but also played a key role in development of plant protection research, pesticide use policies and graduate and postgraduate education. The students of the school are trained with skill sets to identify/ characterize new pests and their natural enemies, their races/ biotypes; develop decision support system for early fore-warning; identify factors forhost plant resistance; biochemical and molecular diagnostics; developing bio-control strategiesfor effectiveand ecofriendly pest management, efficacy of insecticides / plant (botanicals) products and resistance management etc. Additionally newer upcoming areas are also being addressed. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Insect Systematics

Taxonomic studies of the family Tortricidae (Lepidoptera: Tortricoidea) of northern Kerala

The Tortricidae Latreille, 1803 under superfamily Tortricoidea Latreille, 1803, included 11,365 species under 1151 genera distributed across the globe. It is subdivided into three subfamilies, Chlidanotinae Meyrick, 1906; OlethreutinaeWalsingham, 1895; and Tortricinae Latreille, 1803. The objective of this study was to investigate the tortricid fauna of Northern Kerala, providing illustrated diagnostic keys, taxonomic treatments, and a checklist of Tortricidae species found in Kerala. Over 400 specimens of microlepidoptera were collected from ten different sites in nine localities of Northern Kerala. Through meticulous examination, we identified 37 species belonging to 34 genera, categorized into two subfamilies and eight tribes. The majority of species, 29 in total, were found in the subfamily Olethreutinae, with the highest number belonging to the tribe Olethreutini. Additionally, nine species were identified in the subfamily Tortricinae. Notably, this study proposed a species newto science, *Pseudancylis* sp. nov, along with 8 new species records to India *viz*., and 25 new species record to the state of Kerala. A comprehensive checklist of previously reported tortricid species along with the studied species in this study is presented. To facilitate identification, presented illustrated diagnostic keys for the subfamilies, tribes, and species, offering a rapid and accurate method for species identification.

Taxonomic studies on Superfamily Tortricoidea (Lepidoptera)

Tortricidae (Lepidoptera) is the sole family under Superfamily Tortricoidea and is one of the specious micromoth family with over 11,365 named species under 1151 genera. They cause substantial damage to agricultural and horticultural crops. The current study of the Superfamily Tortricoidea fauna in India, aimed to assess the species richness and endemism of Tortricidae in India while investigating the driving factors behind their diversity. Over 2000 specimens were collected from 37 localities across 5 states and a Union territory. The study revealed a total of 53 species in 37 genera under seven tribes from India. 13 species new to science *viz*., *Eucosmogastra* sp. nov., *Toonavora* sp. nov., *Blastesthia umngotana* sp. nov., *Rhopaltriplasia umiamensis* sp. nov., *Gypsonoma ovata* sp. nov., *Zeiraphera almoraensis* sp. nov., *Zeiraphera mussorriana* sp. nov., *Microsarotis* sp. nov., *Baburia chettalliensis* sp. nov., *Baburia tinsukiaensis* sp. nov., *Sycacantha* sp. nov., *Neocalyptis* sp. nov., *Trophocosta* sp. nov., including five genera and fifteen species as new records to India. DNA barcodes were generated for 31 species, among them, 27 species were submitted for the first time from India, and 14 species for the first time for the world. Molecular phylogenetic analysis revealed the paraphyletic nature of tribes. Further, species richness and endemic analysis of 423 Tortricidae species (151 genera with 2213 species distribution records of India revealed two species richness centers*viz*., Northeastern and western Himalayan region and three endemic centres *viz*., Northeastern, Western Himalayan and Western Ghats. Further negative binomial regression analysis revealed that species richness has positive correlation with mean annual precipitation, vegetation and negative correlation with mean annual temperature.

Biosystematic studies on ants (Hymenoptera: Formicidae) of central India

Ants are eusocial insects belonging to the family Formicidae (Hymenoptera: Formicoidea: Formicidae). They are ubiquitous, abundant and play significant roles in ecosystems as predators of agricultural and horticultural pests, scavengers, turning and fertilizing the soil, seed disperser, pollinators, etc. Ants can be distinguished from other Hymenopterans by the nodose metasomal segment; absence of felt lines; posterolateral portion of mesosoma with metapleural gland opening. Taxonomically ants are species rich with 14,863 valid species/subspecies worldwide grouped under 515 genera representing 22 subfamilies. India is home to more than 850 species/ subspecies belonging to 110 genera under 10 subfamilies. Central India with less than 50 ant species/subspecies is one of the least surveyed regions for ant fauna. The present comprehensive attempt to study the ant fauna of Central India resulted in compilation of a checklist with a total of 109 ant species/subspecies under 43 genera in 7 subfamilies. New distributional records of more than 60 ant species/subspecies, 14 genera *viz.,Mystrium* (1 species), *Chronoxenus* (1), *Lioponera* (1), *Agraulomyrmex* (1), *Plagiolepis* (3), *Prenolepis* (1), *Carebara*(1), *Cataulacus* (1), *Erromyrma* (1), *Lophomyrmex* (1), *Recurvidris*(1), *Anochetus*(3), *Ectomomyrmex* (1), *Hypoponera* (1), and one subfamily Amblyoponinaefrom Central India were established. Genus *Agraulomyrmex* Prins and *Cardiocondyla yemeni* Collingwood & Agosti, 19961983 were reported for the first time from India.Sixnew species *viz.,*with *A. damohensis* sp.nov. *Lepisiota binghami* sp.nov., *L. pusaensis* sp.nov., *L. satpuraensis* sp. nov., *L. wilsoni* sp.nov.and *Plagiolepis bhagwatiae* sp. nov.were described. A total of 85 species under 36 genera were studied and redescribed with more than 250 illustrations. Male genitalia of *L. bipartita* was described for the first-time. The DNA barcodes for 29 ant species were generated and deposited in public database. Phylogenetic analysis of important ant genera based on mtCOI sequences was done.

Biosystematic studies of leafhopper tribe Scaphoideini (Hemiptera: Cicadellidae: Deltocephalinae)

Leafhoppers are highly diverse economically important insects belonging to family Cicadellidae (Hemiptera). Tribe Scaphoideini with approximately 61 genera and 631 species, is the third largest tribe of the large leafhopper subfamily Deltocephalinae. Knowledge on Indian leafhopper tribe Scaphoideini is extremely fragmentary,therefore an attempt was made to study the Indian faunaof this tribe. Phylogenetic relationships of the members of this tribe based on morphological and molecular data was analysed. Specimens were collected and studied from 65 different localities across 17 states and one Union Territory of the country. An annotated checklist of the Indian leafhopper tribe Scaphoideini comprising of 109 species belonging to 24 genera was compiled. The present study included study of 82 species under 23 genera and led to the establishment of nine new distribution records for India in which three genera *viz*., *Neolimnus* Linnavuori, *Osbornellus* Ball and *Wanritettix* Vilbaste and six species, *viz*., *Neolimnus egyptiacus* (Matsumura) and *N. quadricornis* Khatri and Webb, *Wanritettix wanrianus* (Matsumura), *Phlogotettix fanjingshanensis* (Li), *Grammacephalus punjabensis* Shah and Duan and *Scaphoideus spiculatus*Viraktamath and Mohan along with 50 new locality records for 24 species. Taxonomic identification keys were formulated with emphasis on male characters for all taxonomic levels.Four leafhopper genera, *viz*., *Inagris* gen. nov., *Himachalanus* gen. nov., *Ramya* gen. nov. and *Shanaya* gen. nov. and 28 leafhopper species under following nine genera, *viz*., *Banus* (1 species), *Inagris*gen. nov. (4), *Himachalanus* gen. nov. (1), *Monobazus* (6), *Osbornellus* (4), *Ramya* gen. nov. (2), *Scaphoideus* (8), *Shanaya* gen. nov. (2) and *Univagris* (1) were described as new to science. All descriptions emphasized on the malegenetalic characters and included good quality illustrations. Thus about 15 and 25% of genera and species, respectively were described new to science from Indian fauna of the tribe Scaphoideini. NPC, New Delhi and and UAS, Bengaluru collections were augmented with 2000 identified specimens of 79 species including holotypes and paratypes of all the newly described genera and species.

Biosystematic studies on hymenopterous parasitoids associated with insect pests of vegetables ecosystem

Vegetables play a major role in Indian agriculture as they ensure food and nutritional security of the country, as well as enhance the per capita income of the farmers. Insect pests attack all plant parts at all stages of growthwith potential to cause huge losses if unchecked. Reliance on pesticides have led to issues of environmental contamination, pest resistance and resurgence. Generally, over looked, natural enemies often have an important role to play. The present study was undertaken with objectives of documentation of hymenopterous parasitoids associated with major vegetable croppests; their taxonomic diagnosis and formulation of a diagnostic key. Studies were carried out at ICAR-IARI vegetable fields during consecutive crop seasons of 2021-2020. Around 2000 specimens collected/ reared from various pest stagesbelonging to 18 families of Hymenoptera were recorded. A checklist of 109 species under 65 genera of parasitoids associated with important vegetables insect pests augmented with valid names, synonyms, details of their host/alternate host, stage parasitized, distribution was compiled. Identification of the collected specimens revealed numerous first record of species, six for India, 41 for New Delhi; 30 first records from any vegetable ecosystem ;seven new host records viz., *Apanteles hemara* and *Brachymeria hime* on *Leucinodes orbonalis*; *Apanteles mohandasi* on *Plutellaxylostella*; *Braconcarpomyiae* on *Bactroceratryoni*; *Opius indicus* and *Stenomesius japonicus* on *Liriomyzasativae*, and *Aphelopus indicus* on leafhoppers. Three hyperparasitoids were recorded *viz*., *Alloxysta pleuralis* on *Binodoxys indicus*; *Pachyneuron aphidis* on *Myzus persicae*, and *Aphanogmus fijiensis* on *Microplitis manilae* larvae. Taxonomic studies supplemented with new characters and morphometric ratios based on 39 diagnostic characters were conducted on 55 species under 41 genera. 65 plates with 325 Illustrations were included. Diversity and abundance of parasitoids was higher in organic compared to the conventional ecosystem leading to higher parasitism. However, parasitism significantly varied depending on the environmental conditions. A significant positive correlation was observed between parasitism and fruit infestation rate. Therefore, conservation and augmentation of these parasitoids will reduce reliance on insecticides in the IPM programs.

Biosystematic studies on Indian stingless bees (Hymenoptera: Apidae: Meliponini)

Stingless bees are widely distributed in Afrotropical, Australasian, Indo-Malayan and Neotropical regions of the world. Presently, 630 species were described globally while only 22 species are reported from India. Indian fauna of stingless bees is poorly known, with studies limited to only description of new species, with no collective information/diagnostic keys for their identification along with their nest architecture and foraging behaviour. An extensive exploration of stingless bees was undertaken in 37 localities of 19 states of in India during 2020 - 2023. The study recorded 20 species under 2 genera *viz*., *Lepidotrigona* (6), *Tetragonula*(14) including five species new to science *viz*., *Tetragonula kotagadensis* sp. nov., *Tetragonula navasariensis* sp. nov., *Tetragonula nisargae* sp. nov., *Tetragonula coimbatorensis* sp. nov., *Lepidotrigona ishanya* sp. nov. Male genitalia of three species, *Tetragonula ruficornis*, *T. bengalensis*, and *T. travancorica* were described in detail for the first time. Several new characters including genital characters with 43 coloured plates with >150 illustrations have been included in the study. An annotated checklist of Indian species was compiled with a total of 26 species under 3 genera *viz*., *Lepidotrigona*, *Lisotrigona*, and *Tetragonula*. Diagnostic keys for the genera and species studied have been prepared. A phylogenetic study for seven species of *Tetragonula* was done based on mtCO1 sequences. Further, detailed study on nesting habits, nest architecture and foraging behavior was carried out for *T. ruficornis*. Among 47 wild colonies recorded in Pusa campus, 27 were situated in the cavities of tree trunks and 20 in the cavities of building walls. The internal nest structure had centrally arranged brood cells which were encircled by pollen and honey pots. The bee foraging activity was limited to daytime from 0800 to 1800 hr with peak activity of foragers between 1000 and 1200 hr during all the seasons. Foraging activity when compared irrespective of seasons indicated that outgoing and incoming foragers were maximum at 1200 hr.

Theme 2: Insect Pest Management

Investigations on host plant resistance against brown planthopper, *Nilaparvata lugens* (Stal).

Rice (*Oryza sativa* L.) serves as a vital staple food, meeting the nutritional requirements of a significant portion of the global population. The brown plant hopper (BPH), *Nilaparvata lugens* (Stal) (Hemiptera: Delphacidae) causes substantial yield losses through hopper burn. To address this concern, host-plant resistance has emerged as an effective, environmentally friendly, and cost-efficient alternative. This study aimed to assess the biochemical basis of resistance of diverse rice germplasms, RP 2068-18-3-5, RP bio 4918-230S, Salkathi, IRG-309, IRG-221, IRG98, IR-64, and MTU-1010 against BPH, keeping PTB 33 and TN-1 as resistant and susceptible checks respectively. The study evaluated three types of responses: antixenosis (avoidance), antibiosis (inhibiting insect growth and development), and tolerance. Among the tested germplasms, RP 2068-18-3-5, and Salkathi showed least damage, on par with the resistant check PTB 33, indicating high resistance to BPH. The resistant rice germplasm showed higher nymphal settlement, feeding marks, and unhatched eggs of BPH compared to susceptible check (TN-1). However, susceptible genotype exhibited higher honeydew production and fecundity of BPH. IRG-98 had the highest number of feeding marks (36.80±0.86), lowest number of nymphal emergences (32.40±4.83) and a greater number of unhatched eggs (95.40±4.07). Nymphal survival was highest in IR-64, MTU-1010, which was on par with the susceptible check, TN-1, with shortest developmental period and higher growth index. Biochemical analysis demonstrated an increased superoxide dismutase (SOD) activity in all germplasms after BPH feeding over 96 hours. At 96 hours, PTB 33 showed highest SOD activity, followed by Salkathiand RP 2068-18-3-5 with no significant differences. Catalase (CAT) activity was lowest in resistant germplasm initially, while TN-1 consistently showed an increased CAT activity leading to reduced hydrogen peroxide content after infestation, indicating effective detoxification. Peroxidase (POD) and polyphenol oxidase (PPO) activities varied among germplasms, with IRG-98 followed by PTB-33 showing sustained increases up to 96 hours. RP 2068-18-3-5, Salkathi, and PTB 33 exhibited effective resistance against BPH. IRG-98 displayed antibiosis properties and strong defence against BPH. The correlation between biological and biochemical parameters suggest that oxidative stress influences growth and behaviour of BPH, providing valuable information for potential pest management approaches.

Assessing brown planthopper damage by using hyperspectral remote sensing

Remote sensing in glasshouse experiments during Kharif 2022 revealed brown planthopper (BPH), *Nilaparvata lugens* infested plants to have higher reflectance in the visible (VIS) region and lower reflectance in the near-infrared (NIR) region in comparison to un-infested plants. Correlation coefficient (r) estimation between rice plant reflectance and number of BPH/tiller resulted in the identification of sensitive bands for all rice varieties at 20 and 40 days after infestation with BPH. Based on rice plant reflectance values corresponding to the sensitive wavelengths from glasshouse experiments, BPH damage depicted a positive relationship with five spectral indices, *viz*., SIPI (Structure-insensitive pigment index), PSND CHL B (Pigment Specific Normalized Difference for Chlorophyll B), AIR1 (Anthocyanin Reflectance Index 1), PSSR A (Pigment Specific Simple Ratio for chlorophyll A), and PSSR B (Pigment Specific Simple Ratio for chlorophyll B). The Red edge value (REV) which is a highly sensitive wavelength region from 670-770 nm showed a high correlation with BPH severity in all the varieties studied. Different biochemical parameters like chlorophyll, carotenoid, protein, flavonoid, and relative water content were also estimated at a differential infestation of BPH in all varieties. The data generated were used for developing different models *viz*., spectral data Vs population model, spectral data Vs biochemical parameter model, and vegetative indices Vs population severity models for predicting BPH severity. The Partial Least Square Regression (PLSR) models were satisfactorily validated using the spectral and biochemical data collected from the field. These models developed through the study can facilitate the assessment of BPH severity and change in biochemical parameters using spectral signatures.

Quantification of the role of insect pollination on yield parameters of bottle gourd, *Lagenaria siceraria* (Molina) Standly.

Bottle gourd vine is a monoecious crop and pollination plays an important role in its production. In the Pusa Naveen variety of bottle gourd, during the summer season, staminate and pistillate flowers were produced at 58 ± 1.95 and 71.2 ± 7.67 DAS with a sex ratio and pollen-to-ovule ratio of 1:4.45 ± 1.42 and 93.15 ± 16.78:1 and blooming period lasted for 56.28 ± 2.55 and 44.28 ± 3.84 days under north Indian conditions. Anther dehiscence occurred between 1230 to 1330 hr. Anthesis of pistillate and staminate flowers occurred between 1630 to 1700 and 1730 to 1800 hr. Stigma attains receptivity at 28 hours before the anthesis and remain receptive until withering of the stigma. The maximum stigmatic receptivity and pollen viability were at the time of anthesis 1800 hr and after anthesis, both flowers remained for one day. Staminate flowers provide nectar and pollen with the maximum nectar production of 2.17 µl between 2200 to 0000 hr but pistillate flowers do not produce nectar. A total of 66 insect species belonging to Hymenoptera (40.9%), Diptera (16.6%), Lepidoptera (13.6%), Coleoptera (10.6%), Hemiptera (9%), Orthoptera (6%) and Dictyoptera (3%), visited bottle gourd flowers during both summer and Kharif seasons. During both the seasons and at different flowering conditions, *Haptonchus* sp was the most abundant and dominant floral visitor of the bottle gourd. Honey bees foraging activities were more on staminate flowers and less on pistillate flowers due to the floral rewards. *Aulacophora* sp and *Haptonchus* sp were most frequently observed on pistillate flowers. *Apis mellifera* exhibited less visitation frequency to pistillate flowers. Among the pollination treatments, the highest fruit set (67.50%), fruit width (9.125 cm), fruit length (31.69 cm) and fruit weight (1.453 kg) were recorded in hand pollination followed by open pollination (31.66% fruit set, 8.755 cm fruit length, 31.15 cm fruit length and 1.279 kg fruit weight). Nocturnal pollination contributed more to open pollination with observed fruit set of 19.16%, fruit width (8.755 cm), fruit length (31.15 cm) and fruit weight (1.279 kg).

Population dynamics and bio-intensive management of insect pest complex in high-density mango orchards

Mango, *Mangifera indica* L. (Family Anacardiaceae) is the national fruit of India and this fruit has developed its own importance all over the world due to its taste and aroma. The present study was conducted in the high-density mango orchard of National Germplasm Repository of Sub-tropical Fruit Crops at ICAR RCER, Farming System Research Centre for Hill and Plateau Region (FSRCHPR), Plandu, Ranchi from January to June, 2023 to study the insect pest population dynamics and formulate effective bio-intensive pest management strategies. A total of 24 species from 18 families of insect pestswith majority from the orders, Hemiptera, Lepidoptera, and Coleoptera were observed infesting mango flowers and fruits. The insect pests including, giantscale, *Labioproctus poleii* (Green), fog scale, *Aulacaspis tubercularis* (Newstead),scale, *Pulvinaria polygonata* (Cockerell), mango hoppers, *Amritodus atkinsoni* (Lethierry), *Idioscopus niveosparsus* (Lethierry), *I.nagpurensis* (Pruthi), Fruit flies, *Bactrocera zonata* (Saunders), *B. correcta* (Bezzi), *B. dorsalis* (Hendel) were observed major from flowering till fruit harvest period. Application of Imidacloprid 17.8 % SL @ 0.005 %, Clothianidin 50% WDG @ 0.03% and Dinotefuran 20% SG @ 0.006 % were found most effective against sucking insect pest complex at flowering stage whereas Spinetoram 11.7 % SC @ 0.012% was effective against fruiting stage pest complex and comparatively safer towards natural enemies. The treatment Clothianidin 50% WDG recorded the highest benefit:cost ratio (6.02) and was found to be the most economical among flowering stage treatments whereas Spinetoram 11.7 % SC was found as most economic (B: C ratio 3.91) at fruiting stage.

Allelochemical and antixenotic resistance traits of litchi fruits against *Conopomorpha* spp. complex

Litchi, *Litchi chinensis* (Family Sapindaceae), is highly popular throughout the world due to its captivating taste and aroma. The present study was conducted in the litchi orchard of National Germplasm Repository of Sub-tropical Fruit Crops at ICAR RCER, Farming System Research Centre for Hill and Plateau Region (FSRCHPR), Plandu, Ranchi to study the antixenotic and allelochemical fruits traits of litchi genotypes/cultivars associated with resistance against *Conopomorpha* spp. complex. A total of 11 litchi germplasms were screened and Swarna Madhu (CHL8) was found as highly resistant (2.5% fruit infestation) among all genotypes whereas Rose Scented was found as susceptible (39.17% fruit infestation) against fruit/seed borer complex. Seed size, fruit size, and number of protuberances showed positive correlations whereas fruit weight, and pericarp thickness showed negative correlations with the percent fruit infestation. The content of total phenols, total flavonoids, and total tannins was highest in resistant genotypes and lowest in susceptible genotypes. The correlation coefficients revealed that the total phenol content in pericarp (r = -0.82) and seed (r=-0.85) of litchi genotypes had a significant negative relationship with the percent fruit infestation. The total tannin content in litchi fruit peels also showed a significant negative correlation (r = -0.72) with percent fruit infestation. Phenolic fractions like gallic acid (r = -0.97), protocatechuic acid (r=-0.98), 4-HBA, vanillic acid (r=-0.86), and ferulic acid (r = -0.85) in the seeds of litchi genotypes showed significant negative correlations. The classified resistant genotypes Swarna Madhu and Bedana against *Conopomorpha* spp with marker traits could be used in future breeding programs as resistant sources.

Studies on silicon mediated management of insect pests of black gram (*Vigna mungo* L.)

Silicon (Si) has been recognized for its ability to confer tolerance to various biotic stresses in crop plants. For investigating the impact of Orthosilicic acid through both soil drenching and foliar application, a study was conducted on two black gram varieties, evaluating its efficacy against the incidence and damage caused by sucking pests in black gram under field conditions for two consecutive seasons. The influence of Orthosilicic acid on total sugars, total phenols, antioxidant and defense enzymes in black gram leaves were closely monitored including its effects on sucking pests damage, coccinellids activity and yield. Soil drenching and foliar application of OSA @ 2 ml/L resulted in a significant reduction in incidence of sucking pests of black gram during both the seasons, besides recording highest coccinellids activity and seed yield of 10.49 and 10.24 q/ha (rabi) and 11.22 and 11.02 q/ha (summer), respectively. Highest benefit: cost ratio (1.88 and 1.93) was recorded with soil drenching of OSA @ 2 ml/L surpassing the recorded ratio of recommended insecticidal check (1.65 and 1.72) during rabi and summer season respectively. All the OSA treatments significantly enhanced the activities of antioxidant and defense enzymes like polyphenol oxidase (0.87-1.14 change in absorbance/min/g), phenylalanine ammonia lyase (0.733-0.974 µM trans cinnamic acid/min/mg protein), peroxidase (15.73-19.02 nmol H2O2 reduced /min/mg protein), catalase (83.31-97.04 nmol H2O2 reduced /min/mg protein) and superoxide dismutase (85.28-92.38% inhibition rate). Elevated activities of antioxidants and defense enzymes and higher accumulation of total soluble sugars (3.86-4.72%) and phenols (3.84-4.94 mg/g) in response to OSA in black gram leaves significantly decreased the incidence of sucking pests. Soil drenching of OSA increased the plant available Si content in soil solution. Si content in leaves of black gram was highest due to soil drenching of OSA @ 2 ml/L (1.541%) followed by foliar application of OSA @ 2 ml/L (1.451%). The % Si content was positively correlated with yield, coccinellids activity and all the biochemical parameters and defense enzymes and negatively with sucking pests' incidences at significant levels. Both the application method of OSA proved significantly superior over insecticidal check on the management of sap feeders of black gram including improved seed yield, coccinellids activity as well as lowest cost of cultivation, which can be easily incorporated with other practices for eco-friendly, sustainable management of sucking pests in black gram. The present research convincingly demonstrated that silicon triggers a defensive response in black gram plants, effectively reducing the impact of sucking pests.

Studies on seasonal incidence and management of Fall armyworm, *Spodoptera frugiperda* (J. E. Smith) in Chhattisgarh plains

A field experiment was conducted on "Seasonal incidence and management of fall armyworm, *Spodoptera frugiperda* (J. E. Smith) in Chhattisgarh plains" at Research farm, ICAR-National Institute of Biotic Stress Management, Raipur during 2022-23. The seasonal incidence pattern of *S. frugiperda* was investigated for three seasons *viz*., Kharif, Rabi and Summer in Chhattisgarh plains on maize indicated highest incidence of *S. frugiperda* larva and damage on maize crop in Kharif season compared to Rabi and Summer seasons crops. Two larval population peaks were recorded during the early vegetative stage (V3-V5) and cob development stage in all the three seasons. S. frugiperda population showed a plant age-dependent response on maize, which will be crucial for developing effective management strategies in Chhattisgarh plains. A negative correlation between rainfall and incidence of *S. frugiperda* was found in all three seasons, while a positive correlation was found with temperature in the Kharif and Rabi seasons. Relative humidity showed a negative correlation during Kharif and Rabi and a positive correlation during Summer. All six insecticides evaluated were found significantly effective against *S. frugiperda* compared to control. Notably, Spinetoram 11.7 SC @ 0.3 ml/l exhibited exceptional effectiveness, manifested by highest reduction in larval population (86.30%) and leaf damage (64.70%) as compared to control. Further application of Spinetoram 11.7 SC @ 0.3 ml/lit. resulted in the lowest cob damage (10.28 %) and maximum grain yield (2480 kg/ha). Among biopesticides evaluated *Bacillus thuriengiensis* var. *kurstaki* 1% WG @ 3 g/lit. proved to be highly effective in reducing the per cent larval population (75.00 %) and leaf damage (61.18 %) compared to control. Additionally, this treatment resulted in the least cob damage (21.67%) and highest yield of grain (1942 kg/ha). Native strain of *Metarhizium anisopliae* 2% 1×10-7CFU @ 10 ml/lit. and Azadirachtin 1500 ppm @ 5 ml/lit. were found to be the next best treatments respectively.

Genotypic characterization and population dynamics of *Bemisia tabaci* in vegetable crops in Chhattisgarh

Whitefly, *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae) listed as one among the "100 of World's Worst Invasive Alien Species" by IUCN impacts vegetable yields significantly due to transmission ofbegomoviruses. Due to the presence of several genetic groups and their cryptic nature their differentiation through conventional taxonomy is often difficult therefore molecular diagnostics was used. 79 *B. tabaci* samples were collected from vegetable crops across 9 districts of Chhattisgarh, covering north, central, and south zones. DNA isolation followed by partial sequencing of the mitochondrial cytochrome oxidase I gene indicated that tomato (T2) exhibited the highest number of genetic groups, while okra (T4) had the lowest. Diversity of genetic groups increased towards the southern region of Chhattisgarh with record of six genetic groups namely Asia I, II-1, II-5, I-India, II-8 and IV in the southern region and only three genetic groups (Asia I, II-1, and II-5) from the northern and central areas. Asia I was the most widely distributed genetic group, accounting for 69.62% in Chhattisgarh. Asia IV, recorded on brinjal from the Kanker region is a first report from India. Further a field trial conducted at Baronda farm, NIBSM, for observing the population dynamics of *B. tabaci* and its relationship *vis-a vis* macro and microclimate indicated highest population of whiteflies on brinjal, followed by chilli, tomato, and okra. The pest appearance was first observed at 21 DAS, and population peaked at 72 DAS, 79 DAS, 72 DAS, and 58 DAS for chilli, tomato, brinjal, and okra, respectively. A positive correlation existed between whitefly population and relative humidity but a negative correlation with temperature. The distribution pattern found eggs predominantly on upper leaves in chilli (2.823±1.055), tomato (0.553±0.360), and brinjal (0.292±0.189), but were more on lower leaves in okra (0.461±0.398). Nymphs were mainly in the middle stratum in chilli (1.353±0.738), tomato (2.4±0.480) and okra (0.523±0.348) crops but in the lower stratum for brinjal (3.184±0.799). Adults, on the other hand, were primarily located on the upper leaves in all four crops, This study will help take specific strata-wise management strategy.

Studies on exogenous application of chemical elicitors for management of Lepidopteran pests of wheat and chickpea

Field and laboratory experiments were carried out at the research farm of ICAR-National Institute of Biotic Stress Management, Raipur, Chhattisgarh during rabi 2022-23 and summer 2023 to generate information comprehensively on the field efficacy of exogenous application of four chemical elicitors for the management of chickpea pod borer, Helicoverpa armigera and wheat pink stem borer, *Sesamia inferens*; detection of volatile profiles of chickpea and wheat, triggered by various extraneous stresses including herbivores' feeding, exogenous application of jasmonic acid, and combination of these two and mechanical damage; and identification of promising plant volatiles which are favourable to the foraging activity of *Trichogramma chilonis*. Exogenous treatment with chemical elicitors in field greatly decreased damage from chickpea and wheat borer pests while also significantly boosting the grain yield. Topical treatment of jasmonic acid @ 5 mM was found to be superior in reducing damage caused by the borer pests in both the crops. The volatile profiles induced by the chickpea pod borer (PB+) and wheat pink stem borer (PSB+) were detected and compared to the volatile profiles triggered by jasmonic acid treatment (JA+); herbivore feeding combined with JA treatment, and mechanical damage (MD+). In response to the combination of pod borer feeding and JA therapy, chickpea pot plants released a higher amount of volatiles. 1-Nonadecene ($C_{19}H_{38}$) appeared to be a significant compound under all kinds of external stresses. Similar to this, the wheat pot plants were made to release 21 volatile chemicals as a result of both pink stem borer feeding and JA treatment. In all profiles of wheat, the substances 1-Nonadecene, Oxirane, hexadecyl-, Eicosanoic acid, methyl ester and Benzenedicarboxylic acid, bis(2-methylpropyl) were commonly found. Thirteen different synthetic forms of volatiles were chosen, tested in a lab setting using a choice test, and compared to untreated and hexane-washed *Corcyra* eggs in an effort to find promising volatile chemicals that might be beneficial to *T. chilonis'* ability to forage. Eicosane, Octadecane, and n-Hexadecanoic acid were hallmark volatile chemicals from the volatile profiles of chickpea and wheat that were generated by various kinds of stressors to favour *T. chilonis'* foraging behaviour.

Effect of crop phenology and climate change on rice leaf folder (*Cnaphalocrocis medinalis* G.) incidence

The rice leaf folder (*Cnaphalocrocis medinalis*) is a major defoliator pest of rice in India, and may also survive on other hosts during rice off-season. Weather conditions may have an impact on its population thus, climate change could make things worse. Temperature significantly influences insect populations, making a thermal constant-based simulation model useful for studying the effect of climate change on pest population dynamics. Additionally, CO_2 affects the insect indirectly by altering the host plant chemistry. Understanding these interactions is crucial for pest management. Hence the present study was conducted to investigate various aspects of rice leaf folder incidence, including population dynamics, the impact of weather parameters, the influence of crop phenology, off-season survival, and the influence of climate change. The population dynamics analysis with life table data revealed varying survival rates across life stages, with the fourth-instar larvae exhibiting the highest survival. Among the weather parameters studied, temperature, morning relative humidity, and sunshine hours showed a significant correlation with *C. medinalis* population. The crop phenology and transplanting date also played vital roles, with peak infestation recorded during the heading and booting stages and the lowest infestation observed during the 3rd transplanting. The investigation into the off-season survival of *C. medinalis* highlighted maize as a highly suitable host, though the absence of field infestation may relate to the unavailability of suitable crop stages. Climate change simulations predicted a potential reduction in pest populations above a temperature rise of 1°C under New Delhi conditions, but adaptive strategies require further study. Elevated CO_2 (eCO2) benefited rice growth and yield but had a negative effect on insect survival and development. Further, the complex biochemical changes induced by eCO_2 levels in the rice leaf folder and rice were highlighted. These insights have practical implications for pest management and highlight the need for further research to address the multifaceted challenges posed by this pest. In conclusion, this study provides a holistic understanding of the various factors influencing rice leaf folder incidence. These insights not only contribute to the formulation of effective pest management strategies but also emphasize the necessity for further research to address the multifaceted challenges posed by this pest under changing environmental conditions.

Quantification of wheat aphid (*Rhopalosiphum padi* L.) damage through simulation and spectral signatures

Wheat (*Triticum aestivum* L.) is the major global staple food crop that meets the food security demands of various nations across the continents. Wheat production is subject to several biotic and abiotic factors especially, temperature and rainfall patterns, and pest occurrence. The present investigation identified a new association of *Macrosiphum euphorbiae* Thomas with the wheat crop. Life table parameters were studied for *M. euphorbiae* and *Rhopalosiphum padi*, which revealed the total nymphal duration and life cycle duration, respectively as 4.76±0.54 days and 9.71±1.38 days for *R. padi* and 5.84±0.69 days and 9.96±1.31 days for M. euphorbiae. The fecundity of *R. padi* and *M. euphorbiae* was observed to be 23.95±8.67 and 11.6±4.10 progeny/female, respectively, and was thus higher for *R. padi*. Similarly, the gross reproduction rate (GRR) was found higher in *R. Padi* (29.17 offspring/adult lifetime) compared to M. euphorbiae (19.58 offspring/adult lifetime). Spatial distribution indices viz., variance to mean ratio (ID), Green's index (GI), Index of mean crowding (IMC), index of patchiness (IP), and Index of mean clumping (IDM), and also the parameters of Taylor's power law and Iwao's mean crowding regression indicated an aggregated distribution of *R. padi* and *C. septempunctata* , however the distribution pattern of *C. sexmaculata* happened to be regular on wheat crop. The aphid damage on wheat was simulated with Infocrop, a generic simulation model. The model was calibrated and validated with two years', experimental data on differential aphid population, created through the application of Thiamethoxam 25% WG, and wheat yield and total dry matter (TDM). The simulated yield varied by 4.72 to 15.11% (R2=0.879, RMSE= 0.50) and by 2.85 to 17.55% (R2=0.886, RMSE= 11.22) from the observed yield, while simulated TDM differed by 0.92 to 11.69% (R2=0.90, RMSE= 0.91) and 6.83 to 13.01% (R2=0.932, RMSE= 1.22) from the observed TDM during two years. Simulated yield and TDM losses were also proximal to respective observed losses, thus indicating the proper validation of the damage mechanism of wheat aphids during both years.Two insecticidal foliar applications at 70 & 80 days after sowing (DAS) were found to be optimum to prevent the aphid population increase in wheat crop and after 90 DAS no spraying was needed as the prevailing temperature exceeded 300C, resulting in quick disappearance of aphid population from the field. Further, the aphid damage on wheat was recorded through hyperspectral remote sensing by developing its spectral signatures that were characterized as the leaf spectral reflectance decreased in the visible range (350 to 700 nm) and in the NIR range (700 to 1300 nm). When the plants were in different levels of aphid damage severity, the reflectance was substantially different in the blue, green, red, NIR, and SWIR band regions. In the NIR region (775- 1138 nm) as well as in the MIR region (1668 and 2159nm), reflectance decreased with an increase in aphid damage and 526nm, 724nm, 1391nm, and 1986nm were identified as sensitive bands for the aphid damage stress. The REV (Red Edge Value) spectral reflectance from 670 – 770nm showed a high correlation with the aphid infestation. Three new aphid-sensitive vegetative indices were developed through regression analysis out of which two indices showed a positive relationship of aphid damage with *R. padi*, index I (RPI-I) (R2 = 0.783), and *R. padi*, index II (RPI-II) (R2 = 0.698).

Assessment of crop losses due to multiple pests and development of decision support tools in wheat

Biotic stress, including insect pests and diseases, poses a significant constraint to the cultivation of food grain crops including wheat, which is affected by several pests. The present study was, therefore aimed to assess the yield loss in wheat due to occurrence of multiple pests in a holistic manner. Field experiments were conducted during rabi seasons of 2020–21 and 2021–22 with wheat variety HD 3086 (Pusa Gautami). Infestation of bird cherry-oat aphid (*Rhopalosiphum padi*), potato aphid (*Macrosiphum euphorbiae*) and disease incidence of Karnal bunt (*Neovossia indica*) and black point disease (*Alternaria alternata, Bipolaris sorokiniana*) were observed during both the seasons. Estimated avoidable yield loss due to higher aphid infestation(pooled mean 27.50 aphids/ tiller and 20.48 aphids/tiller) and minimum disease incidence of Karnal bunt(0.11% and 0.10%) and black point disease(0.91% and 0.87%) was observed to be 7.79% during 2020–21 and 6.10% during 2021–22. Incidence of these diseases was thus minimal in both the seasons, thus attributing the estimated avoidable losses largely to aphids. InfoCrop-Wheat V2 was calibrated and validated with differential aphid density and crop data observed during two rabi seasons. Satisfactory validation of the model was reflected by proximal values of simulated and observed yields (R2= 0.87-0.89) and simulated and observed TDM (R2= 0.88-0.93) with an acceptable level of deviations between simulated and observed yields (0.88-5.18%) and TDM (0.55 – 2.24%). Simulated Economic Injury Levels (EILs) of aphids during 50-70 DAS ranged between 15-16 aphids per tiller and between, 11-13 aphids per tiller during 80-90 DAS. Decision support tools (EILs), thus indicated that late tillering and heading stage of wheat cv. HD-3086 crop to be more vulnerable to aphid damage than initial vegetative phase under Delhi weather conditions. Seed treatment with *Trichoderma harzianum* before sowing and three foliar sprays of imidacloprid 17.80% SL (ETL based) were observed to facilitate production of highest grain yield. However, neem seed kernel extract (NSKE) formulation proved as effective as imidacloprid 17.80% SL in controlling aphids on wheat. Therefore, considering ecological risks associated with chemical insecticide, neem seed kernel extract seemed to be the most promising measure against aphids in wheat.

Elucidating biological and biochemical interaction between popular cultivars of *Brassica juncea* (L.) Czern & Cross. and *Lipaphis erysimi* (Kaltenbach)

The current investigation revealed significant differences for host selection, population buildup, developmental and reproductive biology, and bionomics of *Lipaphis erysimi*, and constitutive and induced nutritional, anti-nutritional, photosynthetic pigments and the defense enzymes in buds and siliquae of the test *Brassica juncea* cultivars. The aphid preference and resistance index were significantly lower on RH 0406, RLC 3, DRMR 150-35, Pusa Mustard 25, NRCHB 101, Pusa Mustard 26, and Pusa Mustard 27, Pusa Mustard 30 and Pusa Tarak, except in a few cases. Further, the developmental periods, mean generation time and doubling time were significantly longer, while fecundity, survival, intrinsic and finite rates of increase, and net and gross reproductive rates were significantly lower on Pusa Mustard 27, NRCHB 101, RLC 3, RH 749, RH 725, DRMR 150-35, Pusa Mustard 26 and Pusa Mustard 25, except in a few cases. Further, the constitutive and induced levels of different phytochemicals were significantly greater in NRCHB 101, RLC 3, RH 749, DRMR 150-35, Pusa Mustard 26, Pusa Mustard 27, DRMR 1165-40, Pusa Mustard 30 and RH 725 except in a few cases. The aphidinduced levels of total sugars, tannins, total chlorophyll, total glucosinolates, FRAP, AP, APX, PAL and TAL levels in *B. juncea* cultivars showed significant association with host preference, intrinsic and finite rates of increase, net and gross reproductive rates, and mean generation and doubling time of *L. erysimi*. However, the regression analysis revealed that the total sugars, phenols, antioxidants, FRAP, chlorophyll B, total chlorophyll, catalase, TAL and myrosinase content in buds and siliquae of test *B. juncea* cultivars contributed to 40.11 to 85.30% variability for host preference, multiplication rate and developmental biology, indicating their defensive role against *L. erysimi*, thus could be used as biochemical markers for identifying aphid-resistant mustard genotypes. Overall, DRMR 150-35, RLC 3, NRCHB 101, Pusa Mustard 27, RH 749, Pusa Mustard 28, Pusa Mustard 25 and RH 0406 have shown adverse effects on host preference, population build-up, development, survival and reproductive potential of *L. erysimi*, have greater induced plant biochemicals and defense enzymes, thus could be used in Brassica improvement program for sustainable crop production.

Studies on conservation of natural enemies in cabbage crop ecosystem (*Brassica oleracea* L. var. capitata) ecosystem

Cabbage (*Brassica oleracea* var. *capitata* L.) is an important winter vegetable crop for growers in India and it ranks second in production. The effect of selected intercrops sweet alyssum, calendula, cineraria, cornflower, marigold, dill, chenopodium, white mustard, mix of flower crops and monocrop of cabbage on the incidence of insect pests and their natural enemies was studied during Rabi 2020-21 and 2021-22 at the research field of Division of Entomology, ICAR- IARI, New Delhi. The mean data of both the years indicated that intercropping with Chenopodium recorded lower number of aphids (563.75±36.3 and 61.00±6.28/plant) and diamond back moth (1.87±0.16 and 8.00±0.18 larvae/plant) population and highest number of coccinellid predators (5.62±0.36 and 11.97±0.30/plant). The cabbage intercropped with white mustard resulted in lowest infestation of cabbage butterfly (2.73±0.13 and 11.06±0.30 larvae/plant). Sweet alyssum intercropping attracted the maximum number of syrphids (5.13±0.14 and 4.05±0.27/plant). The maximum population of predatory spiders (1.97±0.31and 2.10±0.26/plant) and aphid parasitoid, *Diaeretiella rapae* (69.13±0.24 and 55.54±0.65/plant) were recorded in cabbage intercropped with calendula. The percent increase in the yield over control was highest in intercropping with Chenopodium

(93.95) followed by dill (88.38). The B:C ratio was highest in calendula (12.00) followed by cineraria (11.35) and lowest in the monocrop of cabbage. The different diversity indices indicated chenopodium, white mustard and dill intercropping systems had more diversity of insects compared to the other systems. The effect of different floral and prey diet on longevity of *C. sexmaculata* concluded that grubs lived longer on Chenopodium (3.83±0.30 days) than on other flower and pollen diets. Whereas, the adults of *C. sexmaculata* lived longer on Chenopodium (14.93 ± 1.53 days) followed by white mustard (11.20± 1.37) and dill (10.40 ± 2.29 days) flowers. Volatile Organic Compounds (VOCs) from un-infested and infested cabbage plants by *Brevicoryne brassicae* was recorded by GC-MS. Volatile compounds released in case of DCM extract were Cyclohexasiloxane tetradecamethyl, followed by Cyclopentasiloxane decamethyl and 3-Hexen-1-ol. In case of DEE extract, the volatile compounds released were 3-Hexen-1-ol, (Z) followed by Cyclohexasiloxane, dodecamethyl. Y-tube olfactometer study showed that the response of males and females of *C. sexmaculata* was significantly more to DCM-WA and DEE-WA extracts.

Theme 3: Toxicology

Bio-efficacy of carvacrol and underlying enzymatic activity for the management of pulse beetle, *Callosobruchus maculatus*

Storage of pulses faces critical challenges from insect pests, notably pulse beetle, *Callosobruchus maculatus*. Alternative strategies were explored to manage storage insects due to development of resistance against conventional insecticides. Carvacrol, a natural phenolic compound found in various plants, exhibits diverse anti-insect properties. Our study evaluates carvacrol's efficacy against *C. maculatus* and its impact on enzyme activities, aiming to offer a potential alternative for pest management in pulse storage. Fumigation toxicity evaluation of carvacrol and phosphine displayed dose-dependent reactions in both egg and adult stages of *C. maculatus*. Furthermore, increased exposure duration led to reduced carvacrol and phosphine concentrations needed for 50% and 90% mortality. The lethal concentration (LC50) against adult in the absence of food grains (LC50 1.08 µl/L air) was lower than that with grains (LC50 2.32 µl/L air), whereas for phosphine it was 32.45 ppm, for 24h exposure. In contact toxicity, Carvacrol LC50 was 0.8% while that of deltamethrin 2.5% WP was 0.0002% for the same 24h exposure. Carvacrol also exhibited oviposition inhibition with ED50 values ranging from 0.03 to 0.02 µl/L air for 24-72 hours and ovicidal attributes with an LC50 of 3.2- 1.64 µl/L air for 24-72 hours exposure. Exploration of orientation behavior indicated the repellent action of carvacrol on *C. maculatus*. Biochemical analysis indicated relatively lower resistance of pulse beetle to carvacrol compared to phosphine based on activity of detoxification enzymes. Our study concluded carvacrol to be a promising phenolic monoterpenoid with fumigant, ovicidal, oviposition inhibitory and repellent activity against pulse beetle *C. maculatus*, contributing to our ongoing search for effective pest management strategies.

Toxicity of phosphine and carbon dioxide against Drugstore beetle, *Stegobium paniceum* (L.)

Exploration of pest mitigation techniques, emphasizes phosphine as a residue free fumigant for trade. Safer carbon dioxide also gains attention, bolstering pest control. When combined, carbon dioxide enhances the insecticidal impact. Study assesses their efficacy against *S. paniceum*, highlighting synergistic effects. Experiments involving different concentrations and exposure durations revealed the synergistic effect of combining carbon dioxide and phosphine. The mixture demonstrates significantly increased toxicity compared to phosphine alone, with up to a 6.25-fold increase at 24h exposure, 3 times increase at 48h, and 2 times increase at 72h. Examining four populations from various Indian states, the study found differences in tolerance levels. The Maharashtra-Kolhapur population exhibited slightly higher tolerance, with 0.25mg/L, 33.5% and 0.03mg/L on exposure to phosphine, carbon dioxide and the mixture respectively while other three populations displayed almost similar LC50 values for all fumigants. Detoxification enzyme activity was also explored in response to the fumigant treatments. Phosphine-treated insects showed higher enzyme activity compared to carbon dioxide or phosphine-carbon dioxide combinations. Activity of enzymes such as Glutathione-S-transferase, Cytochrome P450 monooxygenase, Carboxylesterase, and Acetylcholinesterase which are key contributors to pesticide detoxification was found to be higher in phosphine treated insects. Factorial analysis underscores the interplay of fumigant type, exposure duration, and population on enzyme activity. In conclusion, this research revealed the complex relationship between fumigant treatments, enzyme activity, and insect responses, highlighting the need for meticulous pest management strategies.

Temperature-toxicity relationship studies of label claim insecticides against whitefly, *Bemisia tabaci* (Gennadius) in Tomato (*Solanum lycopersicum* Mill)

Whitefly, *Bemisia tabaci* Gennadius is a notorious pest, a cryptic species complex and a super-vector, causing havoc in tomato agro-ecosystems. In general, farmers rely heavily on chemical interventions, and among several recommended label-claim insecticides, six were singled out for screening: dimethoate 30%EC, malathion 50%EC, imidacloprid 17.8%SL, thiamethoxam 25%WG, diafenthiuron 50%WP, and cyantraniliprole 10.26%OD. Their bio-efficacy against *B. tabaci* Asia II-1 (genetic group identified with NCBI GenBank accession no.: OQ402683, OQ402684 and OQ402685) using 'leafdip' bioassay was tested, which was upgraded with 'agar-cube method' making it convenient and practical, followed by dose-comparison and cost-analyses. Results revealed that above specified formulations of cyantraniliprole, thiamethoxam, and diafenthiuron were recommendable at current field recommended dosage on rotation-basis. Conversely, malathion and dimethoate proved unsuitable for managing *B. tabaci*, while imidacloprid essentially requires re-evaluation and revision for its field level dosage. Additionally, an economically viable and easy-to-handle laboratory protocol was developed for assessing temperature toxicity relationship on *B. tabaci*. Utilizing lab-generated LC20, LC50, and LC70 values, temperature-toxicity assessments were conducted at 23°, 27°, 31°, and 35°C with varying temperature pre-treatment periods (15-min, 45-min, 1.5-h, and 3-h). Notably, a nonlinear trend in mortality was observed with increase in temperature (from 23° to 35°C) for testinsecticides (dimethoate, malathion, imidacloprid, and thiamethoxam) with a significant dip in mortality at 31°C. In contrast, diafenthiuron and cyantraniliprole demonstrated gradual increase in mortality rates. Further exploration involved studying detoxifying enzyme activity *vis-à-vis* temperature and insecticidal (=toxicity) stress. Tolerance at 31°C was in line with elevated detoxifying enzyme activityfor carboxylesterase, cytochrome P-450 monooxygenase, and glutathione S-transferase. This interesting comprehensive investigation sheds light on effective insecticides for managing *B. tabaci*, inculcates a cost-effective laboratory approach for temperature-toxicity investigation, reveals how test-insecticides react under prevailing temperatures, and unravels the detoxifying enzyme activity in relevance.

Host specific comparative toxicity studies in whitefly *Bemisia tabaci* (Gennadius) against selected safer insecticides

Bemisia tabaci, a major sucking pest that affects tomato and brinjal crops, is predominantly managed through the application of conventional insecticides. For the current study, five available green labelled insecticides *viz*., clothianidin 50%WDG, spinetoram 11.7%SC, cyantraniliprole 10.26%OD, azadirachtin 1%EC, novaluron 10%EC, and one yellow labelled insecticide, imidacloprid 17.8%SL as check were selected. Bioefficacy was assessed on eggs, nymphs, and adults using the leaf-dip bioassay (IRAC, 2016). The results revealed that four out of six insecticides showed higher median lethal concentration (LC50) values on brinjal compared to those on tomato.The potential influence of the test-leaf on LC50 values was evaluated reciprocally, i.e. test populations grown on tomato were subjected to a brinjal leaf bioassay, and *vice versa*. This resulted in non-significant difference in LC50 values, implying that the test leaf had no effect on the observed difference between tomato and brinjal population LC50 values. Spinetoram demonstrated promising nymphicidal and adulticidal effects on both hosts. Novaluron, an insect growth regulator (IGR), proved quite effective against nymphal stages, while it was very poor in managing egg and adult stages. The feeding potential (as indicated by honeydew excretion) and reproductive potential (oviposition rate and egg hatchability) were recorded higher on brinjal in comparison to tomato, indicating that brinjal is a more suitable host. The brinjal reared population exhibited the higher activity of detoxification enzymes, *viz*., Cytochrome P450 monooxygenase, Glutathione S transferase, and Carboxylesterase, compared to the tomato population. It was observed that all the three enzymes increased with rising insecticide concentration in both hosts. It is inferred that selected greenlabelled insecticides are more effective in managing whiteflies as they exhibit superior ovicidal, nymphicidal, and adulticidal properties compared to imidacloprid. While spinetoram, clothianidin, and novaluron are not currently registered for the management of whiteflies both in tomato and brinjal, but they show promising nymphicidal and/or adulticidal effects. They may therefore be considered for label claim extension with further field evaluations.

Toxicological investigation on effect of recommended pesticides on the brinjal shoot and fruit borer *Leucinodes orbonalis* Guenee

Leucinodes orbonalis, a highly damaging insect-pest, poses a significant threat to brinjal production. Seven field populations of *L.orbonalis* were collected from various locations *viz*., Delhi, Pantnagar, Hapur, Coimbatore, Ganjam, Anand and East Godavari and reared in the laboratory. Bioassays were conducted on first instar larvae using six selected insecticides *viz*., chlorantraniliprole18.5% SC, flubendiamide 39.35% SC, cypermethrin 25% EC, chlorpyriphos 20% EC, Spinosad 45% SC and emamectin benzoate 5% SG. Spinosad and emamectin benzoate were found to be most toxic to *L.orbonalis* larvae. The population from East Godavari, exhibited the highest tolerance to chlorpyriphos, while the population from Pantnagar, was the most susceptible. Similarly, Coimbatore strain was most susceptible against cypermethrin, and Hapur strain was most tolerant one. Likewise, Coimbatore strain was most susceptible for the insecticides *viz*, flubendiamide, chlorantraniliprole and emamectin benzoate. However, East Godavari, Delhi and Hapur populations were tolerant to these insecticides. Anand population was found to be tolerant to spinosad insecticide compared to the susceptible Pantnagar population. This study indicated a significant variability in insecticidal susceptibility in *L. orbonalis* populations, indicated by increased expression levels of detoxification enzymes during the larval stages. Esterase, cytochrome P450 (cyt P450), and Glutathione-S-transferase (GST) activities varied among the populations. A significant positive correlation was found between the activity of esterase, cyt P450 and GST with the susceptibility levels of *L. orbonalis* populations towards the evaluated insecticides with a few exceptions. Study of the sublethal effects of insecticides on *L. orbonalis*indicated decreased egg hatchability, prolonged larval and pupal duration, reduced adult emergence and longevity, and altered fecundity in response to sublethal concentrations of all the tested insecticides. The effects varied between resistant and susceptible populations indicating complex interactions between insecticide exposure, population characteristics, and reproductive outcomes. This study investigated the induction of digestive enzymes (amylase, protease, and lipase) in response to sublethal concentrations of insecticides. The enzyme activities varied among the populations and treatments, with differences observed between resistant and susceptible populations.

Theme 4: Insect Physiology

Biochemical studies on hibernation in *Chilo partellus* (Swinhoe)

Chilo partellus (Swinhoe) is a major pest of cereal crops in Asia and Africa. In view of scanty information of biochemical alterations during hibernation, the current study mapped changes in total lipids, total proteins, total free sugars, amino acids, fatty acids, enzymes and cryoprotectant levels in hibernation (larvae: pre-hibernation,

hibernation; pupae: posthibernation) and corresponding non-hibernation stages, specifically in haemolymph, fat body, integument and the whole body of *C. partellus*. Total protein and lipid levels significantly increased in the whole bodyin pre-hibernation and decreased in hibernation, while total free sugars decreased in both pre-hibernation and hibernation as compared to non-hibernation stage of *C. partellus*. Across the larval stages, total protein and free sugar were highest in haemolymph, while lipid was highest in fat body. The results also revealed significant increase in palmitoleic acid, linoleic acid and cholesterol, while decrease in myristic acid, oleic acid, stearic acid, and squalene in different body parts of *C. partellus* larvae during hibernation as compared to nonhibernating larvae. Further, in the larval whole body the amino acids *viz.*, histidine, arginine, methionine, and proline increased while aspartic acid and alanine decreased during hibernation in comparison of its non-hibernating counterpart. Further the activity of enzymes ascorbic acid, lipid peroxidation and peroxidase increased, while amylase and protease decreased in all the larval tissues of hibernating compared to non-hibernating*C. partellus*. Highest activity of lipid peroxidation and protease was in haemolymph of hibernating, and fat body of non-hibernating*C. partellus* larvae, respectively. Across larval body tissues, total antioxidant, superoxide dismutase and catalase activity increased, while glutathione S-transferase and esterase activity decreased in hibernating compared to non-hibernating*C. partellus*. Furthermore, cryoprotectants *viz*., sorbitol and trehalose increased in all the body parts of hibernating over the non-hibernating, while glycogen decreased in hibernating over prehibernating larval stage of *C. partellus*. Glycogen content was significantly greater in larval fat bodies and pupal haemolymph. Overall, the findings highlight complexity of biochemical dynamics in different life stages and body tissues during hibernation, paving a way for deeper understanding on diapause related metabolic pathways, design novel pesticidal molecules, and devise alternate strategies for the management of *C. partellus.*

Studies on post mating transcriptional changes in female moths of fall armyworm, *Spodoptera frugiperda* (J.E. Smith)

Fall armyworm (FAW), *Spodoptera frugiperda*, is a highly destructive insect pest causing significant economic losses due to its wide host range, strong dispersal ability, and high reproductive fitness. Current control strategies for managing FAW are challenging due to its high fecundity, mobility and rapid development of insecticide resistance. Studying the mating induced gene expression changes enables us to understand the molecular responses that drive adaptations in female reproductive processes. In response to mating in *S. frugiperda*, a total of 13,207 transcripts exhibited differential expression. Among these, 846 (89 upregulated, 757 downregulated) transcripts showed significant expression at 24 hours post-mating. However, at 0 hours post-mating, only four transcripts were notably expressed, all of which were found to be upregulated. Gene Ontology analysis indicated that majority of the differentially expressed genes were involved in biological processes followed by cellular components and molecular function. Key upregulated genes like cathepsin B, cytochrome P450 6B1, ecdysone oxidase, and ribosome-binding protein 1 play crucial roles in egg development, detoxification, hormone synthesis, and protein production, all crucial for successful reproduction. Conversely, immune related genes such as serine protease inhibitor dipetalogastin-like, attacin, and lysozyme were downregulated, suggesting a strategic balance between resource allocation for reproductive success and immune defense. This phenomenon highlights the dynamic prioritization of energy resources to support reproduction while potentially compromising immune responsiveness. Targeting these key genes and pathways could hold promise for innovative approaches that disrupt reproductive success and population growth, potentially curbing the economic losses caused by this destructive pest.

Biochemical characterization of phosphine resistance in *Tribolium castaneum* (Herbst)

The development of resistance to the promising fumigant, phosphine by major insect pests of stored commodities worldwide has jeopardized phosphine's long-term sustainability and viability. However, the paucity of knowledge on phosphine resistance associated with metabolic enzymes is exacerbated in the timeline across the geographical territory. Further clarity of molecular introspection of phosphine resistance is limited. Henceforth, we studied seven selected Indian populations of the red flour beetle *Tribolium castaneum* (Herbst) at ICAR-IARI, New Delhi and assessed phosphine susceptibility, genotypic characterization, and nucleotide variations of the DLD protein (dihydrolipoamide dehydrogenase) responsible for phosphine resistance with its biochemical properties. Further, the magnitude of antioxidant and respiratory metabolic enzymes was determined. Dose response probit assays revealed that the LC50 values ranged from 0.040 to 1.515 mg/l showing 2.22 to 84.16-fold resistance to phosphine compared to the susceptible check. The CAPS-Mbo1 digestion resulted in resistant alleles ranging from 12.50 to 80.43 percent. A detailed study of the DNA sequences revealed that the single P to S amino acid substitution (P45S) in the DLD enzyme is implicated in developing strong resistance in *T. castaneum*. Polymorphism was detected in Faridkot, Saket, Hisar, Motihari, and Jagatsinghpur populations. DLD enzyme functioning as moonlight protein varied significantly among *T. castaneum* populations where DLD and diaphorase activity were elevated with reduced susceptibility. The kinetics parameters influenced variably across the populations. The pyruvate dehydrogenase and α-ketoglutarate dehydrogenase activities varied significantly and were associated positively with increased resistance. Likewise, peroxidase and superoxide dismutase were enhanced with increased phosphine toxicity, whereas catalase negates negatively. These findings would help to develop biochemical markers for phosphine resistance diagnosis in stored pests. Further studies on metabolomics and gene expression perspectives of phosphine toxicity may shed light on sustainable safeguarding of stored commodities.

Molecular characterization and dynamics of certain enzymes in DLD multi-enzyme complex in lesser grain borer, *Rhyzopertha dominica*

Molecular characterization and dynamics of certain enzymes in DLD multi-enzyme complex in lesser grain borer, *Rhyzopertha dominica.* The current research was on seven field populations of R. dominica showed a high level of phosphine resistance, with median lethal doses (LC50) ranging from 0.024 to 1.991 mg/l with a resistance ratio varying from 50.88 to 82.96% when compared to the susceptible check. PCR-RFLP using the CAPS marker examined the 'P49S' variant and had a lion's share of the 'R' allele in those populations exhibiting higher LC50 values. The molecular characterization of the rph2 fragment of the Dihydrolipoamide dehydrogenase gene was carried out and the P49S variant was found predominant. Differential levels of antioxidant enzyme activity were found, wherein the peroxidase activity and SOD inhibition increased with increased LC50. The PDH activity varied from 24.18 to 3.64 mg/ from Safidon to Laboratory population respectively. The α-keto glutarate dehydrogenase showed the same trend. The DLD activity varied between 0.5228 μ mol/ min in Sofidan to 0.2673 μ mol/ min in laboratory stock. The diaphorase varied similarly Sofidan showed the highest activity. The Vmax and Km for DLD varied from 42.38 μ mole/ min and 1.23 μ mol to 10.0 μ mol/ min and 1.0 μ mol respectively. The Vmax and Km for diaphorase varied from 45.40 μ mol/ min and 1.25 μ mol to 11.1 μ mol/ min and 1.1 μ mol/min respectively. The population with the highest activities of DLD and diaphorase has been shown to exhibit the highest Vmax to their respective enzymes. Safidon, Patiala, Hapur, Karnal, and Kota populations were found to exhibit serine protease.

Characterization of metabolic enzymes and energy transfer system in *Tribolium castaneum* (Herbst)

This study explored the roles of metabolic, mitochondrial, and detoxification enzymes in phosphine-resistant *Tribolium castaneum*. It delves into the activity and expression of metabolic enzymes linked to resistance and investigates the significance of mitochondrial enzymes in energy processes. Experimental results highlight complex metabolic adaptations in phosphine-resistant *T. castaneum*: GADPH decreased, 1.88-fold in Patiala; TPI consistently increased, over 2-fold; Carboxylesterase, Glutathione S-transferase, and Cytochrome P450 activities significantly increased, with over a 7.5-fold change. The mitochondrial enzyme activities significantly increased in resistant populations: DLD and COX by nearly 7-fold, and PDH by over 3.5-fold. The relative expression study revealed GADPH gene downregulation, TPI gene upregulation mirrored their enzymatic activity in resistance. Detoxification enzyme gene expression significantly increased in resistant populations. CE upregulated 95-fold in Moga, GSTD3 27-fold in Patiala, and among CYP346 genes CYP346B1 had a 686-fold change in Patiala, CYP346B3 a 362-fold change in Moga, signifying their key role in phosphine resistance and a coordinated molecular response. This highlights their role in phosphine adaptation. DLD and COX gene upregulation in the resistant population indicates their vital role in survival against phosphine. In resistant populations, increased detoxification enzyme activity enhances phosphine metabolism, supporting resistance mechanisms. Additionally, upregulated AChE gene expression compensates for enzyme activity effects. DLD and COX upregulation reflects metabolic adjustments, aiding energy production, and mitochondrial function under phosphine stress. CYP genes can serve as markers for resistance screening. Understanding regulatory pathways and gene functions is crucial for unravelling resistance mechanisms. It identifies key genes, aiding intervention. Validation ensures research reliability. Characterizing metabolic adaptations helps address evolving resistance. Molecular markers enable quick trait identification, supporting targeted management. This comprehensive approach enhances storage pest resistance control.

Colonization of Entomopathogenic bacteria in maize plant and their efficacy against fall armyworm, *Spodoptera frugiperda* (J.E. Smith), (Lepidoptera: Noctuidae)

Fall armyworm (FAW), *Spodoptera frugiperda*, an invasive polyphagous pest causes significant damage to several crops, including maize. *Bacillus thuringiensis* (*Bt*) is known as the most successful microbial insecticide worldwide, but its commercial application is limited due to its vulnerability to abiotic factors. To overcome these factors, the establishment of *Bacillus thuringiensis* (Bt) as an endophyte was attempted. Out of 49 native *Bacillus* isolates screened, five isolates were shortlisted, *viz*., BtVKK5, BtVKK1, S16C2, S25C1, and SOIL20, with >35% mortality in screening bioassays. Biochemical characterization of all these potential native *Bacillus* isolates, showed cellulase, chitinase and protease activity. While xylanase activity was observed in BtVKK1and *Bacillus paramycoides* (S16C2) three *Bacillus* isolates exhibited tyrosinase activity (S16C2, S25C1, and SOIL20). Moreover, BtVKK1, VKK5, and S25C1 showed plant growth promoting activity in terms of solubilization of phosphate and potassium as well as production of ammonia and indole-3-acetic acid. The present study reported successful colonization of BtVKK5 in five different maize cultivars, and their toxic effect against neonates of FAW was evident. Furthermore, green fluorescent protein (GFP)-tagged potential native *Bt* strains VKK1, VKK5, combination of VKK1+VKK5, and reference *Btkurstaki* HD1 were successfully inoculated in maize plants by different inoculation methods, *viz*., seed treatment (ST), seed treatment + foliar application (ST+FA), seed treatment + soil drenching (ST+SD), and combination of all (ST+SD+FA) as endophytes. The results indicated successful colonization by VKK1+VKK5, followed by VKK5, VKK1, and HD1. In accordance with inoculation methods, ST+FA+SD were found effective, followed by ST+FA for all *Bt* strains. Their translocation in the plant was visualized using a confocal laser scanning microscope. The bio efficacy of inoculated maize plants against FAW indicated highest mortality in VKK1+VKK5 (ST+FA+SD) (66.67%), followed by the ST+FA method for VKK1+VKK5 and ST+FA+SD method for VKK5 (50%) by detached leaf bioassay. Pot assay experiments indicated that damage by larvae was highest in the control plants and lowest in VKK1+VKK5-inoculated plants by the ST+FA and ST+FA+SD methods, followed by VKK5. The colonization of *Bt* as an endophyte inside the plant did not significantly affect its macronutrient and antioxidant activity. Establishment of Bt as an endophyte in maize plants, complemented with insecticidal, could possibly be an innovative approach for the management of *S. frugiperda* and other borers.

Development of cost-effective bio-insecticide based on potential native *Bacillus* spp. against fall armyworm *Spodoptera frugiperda* (J. E. Smith)

The fall armyworm (FAW), *Spodoptera frugiperda*, a polyphagous invasive pest causes significant damage to maize crop. FAW has developed resistance against many insecticides as well as against *Bt* crops. Thus, there is a need to look for novel *Bacillus* isolates effective against FAW for the development of formulations. Thus, a study on the biology of FAW was conducted using a semi-synthetic diet and four natural hosts, namely maize, cotton, castor, and cauliflower, under controlled conditions, a prerequisite for rearing and mass production of FAW for screening of *Bacillus* isolates. A semi-synthetic diet was found to be superior, with higher fecundity and growth attributes. Out of 64 *Bacillus* isolates, seven were shortlisted, *viz*., VKK-SL2, VKK1, VKK-AG1, VKK-MPW, VKK13, VKK-AC2, and VKK9, which showed >35% mortality in screening bioassays. Further, concentration-mortality bioassays indicated LC50 of VKK9 strain as 274.95 µg/g of diet and was found to be 7.2 fold less than the LC50 of Btk-HD1 (2002.35 µg/g of diet). Transmission electron microscopy of VKK9 revealed the presence of polymorphic crystals, confirming presence of *Bt*. PCR amplification using cry gene-specific primers showed that VKK9 possessed cry1A, cry1B, cry1C, cry1E, cry1I, cry2, and vip3A, while VKK1 had cry1A, cry1B, cry1C, and cry2 genes. Biochemical characterization of potential native *Bacillus* isolates showed its ability to produce the extracellular enzymes cellulase, xylanase, and chitinase. Besides, *Bt* strains VKK9, VKK-MPW, VKK-LE1, and Bt-HD2 showed antifungal activity against plant pathogenic fungi, *viz*., *Phomopsis vexans*, *Rhizoctonia solani* and *Fusarium solani*. The VKK9 showed antibacterial activity against *Ralstonia solanacearum*. Further, standardization of culture media was done with modifications in Peptone-Glucose-Salt- media, which resulted in maximum biomass (6.345 g/L) and viable spores (3.56x107 spores/mL). In fermentation kinetics, mass transfer coefficient (KLa) was 0.0367, Oxygen transfer rate (OTR) was 0.0204, and Oxygen Utilization Rate (OUR) was 0.10769 for VKK9. Two formulations of BtVKK9, BtVKK1, and a combination of VKK9 and VKK1 were developed. Dust formulation (10%) with maize stubble powder as carrier material and 1% encapsulated formulation with cyclodextrin as wall material. Approximately Rs 388/kg was required for development of a 10% *Bt* dust formulation. In the pot assay, the 1% encapsulated formulation of VKK9+VKK1 and the 10% dust formulation of VKK9+VKK1 were the best treatments, with a leaf damage rating of one and a percent damage of 20%. In field assays, a 10% dust formulation (VKK9+VKK1) showed good results with a mean leaf damage rating of 1.46 and a percent damage of 29.2%. The native *Bt* isolates were found to have novel cry genes with insecticidal activity and plant growth-promoting ability coupled with antifungal and antibacterial activity, which could be utilized in integrated pest and plant management systems.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Asmita Das (21631)	M.Sc.	Bio-efficacy of carvacrol and underlying enzymatic activity for the management of pulse beetle, *Callosobruchus maculatus*	Dr. S. M. Nebapure	ICAR-IARI, New Delhi
2.	Jessa Joseph (21632)	M.Sc.	Toxicity of phosphine and carbon dioxide against Drugstore beetle, *Stegobium paniceum* (L.)	Dr. S. M. Nebapure	ICAR-IARI, New Delhi
3.	Darshana Brahma (21633)	M.Sc.	Investigations on host plant resistance against brown planthopper, *Nilaparvata lugens* (Stal).	Dr. Subhash Chander	ICAR-IARI, New Delhi.
4.	Elika Pavan Venkata Kumar (21634)	M.Sc.	Quantification of the role of insect pollination on yield parameters of bottle gourd, *Lagenaria siceraria* (Molina) Standly.	Dr. Kumaranag	ICAR-IARI, New Delhi
5.	Eere Vidya Madhuri (21635)	M.Sc.	Assessing Brown planthopper damage by using hyperspectral remote sensing	Dr. Subhash Chander	ICAR-IARI, New Delhi
6.	Jagadam Sai Rupali (21636)	M.Sc.	Studies on postmating transcriptional changes in female moths of fall army worm, *Spodoptera frugiperda* (J.E. Smith)	Dr. Sagar D.	ICAR-IARI, New Delhi
7.	Aashique Poon V.S. (21637)	M.Sc.	Taxonomic studies of the family Tortricidae(Lepidoptera: Tortricoidea) of northern Kerala	Dr. P.R. Shashank	ICAR-IARI, New Delhi
8.	Arbud Lala (60100)	M.Sc.	Population dynamics and bio-intensive management of insect pest complex in high-density mango orchards	Dr. Jaipal Singh Choudhary	**ICAR-RCER, Plandu, Ranchi
9.	Kiran Kumar H. (60101)	M.Sc.	Allelochemical and antixenotic resistance traits of litchi fruits against *Conopomorpha* spp. complex	Dr. Jaipal Singh Choudhary	**ICAR-RCER, Plandu, Ranchi
10.	Gouranga Saw (80012)	M.Sc.	Studies on Silicon mediated management of insect pests of black gram (*Vigna mungo* L.)	Dr. R.K. Murali Baskaran	**ICAR-NBISM, Raipur
11.	Marella SaiManoj (80013)	M.Sc.	Studies on seasonal incidence and management of Fall armyworm, *Spodoptera frugiperda* (J. E. Smith) in Chhattisgarh plains	Dr. K.C. Sharma	**ICAR-NBISM, Raipur
12.	Archita Das (80014)	M.Sc.	Genotypic Characterization and population dynamics of *Bemisiatabaci* in vegetable crops in Chhattisgarh	Dr. K.C. Sharma	**ICAR-NBISM, Raipur
13.	Malawanthkar Rani (80015)	M.Sc.	Studies on exogenous application of chemical elicitors for management of Lepidoptera pests of wheat and chickpea	Dr. R.K. Murali Baskaran	**ICAR-NBISM, Raipur
14.	Rajgopal N.N. (10791)	Ph.D	Biosystematic studies of leafhopper tribe Scaphoideini (Hemiptera: Cicadellidae: Deltocephalinae)	Dr. Debjani Dey	ICAR-IARI, New Delhi
15.	Satyapriya Singh (10797)	Ph.D	Biochemical characterization of phosphine resistance in *Tribolium castaneum*(Herbst)	Dr. S. Subramanian	ICAR-IARI, New Delhi
16.	Venkatesh Y.N. (10921)	Ph.D	Quantification of wheat aphid (*Rhopalosiphum padi* L.) damage through simulation and spectral signatures	Dr. Subhash Chander	ICAR-IARI, New Delhi

17.	Nikhil Raj (11019)	Ph.D	Temperature-toxicity relationship studies of label claim insecticides against whitefly, *Bemisia tabaci* (Gennadius) in tomato (*Solanum lycopersicum* Mill)	Dr. G. K. Mahapatro	ICAR-IARI, New Delhi
18.	Ranjith H V (11235)	Ph.D	Molecular characterization and dynamics of certain enzymes in DLD multi-enzyme complex in lesser grain borer, *Rhyzopertha dominica*	Dr. S. Subramanian	ICAR-IARI, New Delhi
19.	Arya P S (11237)	Ph.D	Effect of crop phenology and climate change on rice leaf folder (*Cnaphalocrocis medinalis* G.) incidence	Dr. Subhash Chander	ICAR-IARI, New Delhi
20.	Gopalakrishnan R (11244)	Ph.D	Development of cost effective bio-insecticide based on potential native *Bacillus* spp. against fall armyworm *Spodoptera frugiperda* (J. E. Smith)	Dr. Vinay K. Kalia	ICAR-IARI, New Delhi
21.	Anand Harshana (11366)	Ph.D	Biosystematic studies on ants (Hymenoptera: Formicidae) of central India	Dr. Debjani Dey	ICAR-IARI, New Delhi
22.	Jadhav Mahesh Mahadev (11476)	Ph.D	Assessment of crop losses due to multiple pests and development of decision support tools in wheat	Dr. Subhash Chander	ICAR-IARI, New Delhi
23.	Santhosh Naik G. (11479)	Ph.D	Taxonomic studies on SuperfamilyTortricoidea (Lepidoptera)	Dr. P.R. Shashank	ICAR-IARI, New Delhi
24.	Ashok Kumar Sau (11482)	Ph.D	Biochemical studies on hibernation in *Chilo partellus* (Swinhoe)	Dr. M.K. Dhillon	ICAR-IARI, New Delhi
25.	Karshnal J. (11484)	Ph.D	Colonization of entomopathogenic bacteria in maize plant and their efficacy against fall armyworm, *Spodoptera frugiperda* (J.E. Smith), (Lepidoptera: Noctuidae)	Dr. Vinay K. Kalia	ICAR-IARI, New Delhi
26.	Anil Kumar S.T. (11486)	Ph.D	Host specific comparative toxicity studies in whitefly *Bemisiatabaci* (Gennadius) against selected safer insecticides	Dr. G. K. Mahapatro	ICAR-IARI, New Delhi
27.	K. Chandrakumara (11759)	Ph.D	Elucidating biological and biochemical interaction between popular cultivars of *Brassica juncea* (L.) Czern & Cross. and *Lipaphiserysimi*(Kaltenbach)	Dr. M.K. Dhillon	ICAR-IARI, New Delhi
28.	Hager Moustafa Mahmmoud Saleh (11925)	Ph.D	Biosystematic studies on hymenopterous parasitoids associated with insect pests of vegetables ecosystem	Dr. Debjani Dey	ICAR-IARI, New Delhi
29.	Laneesha (10788)	Ph.D	Toxicological investigation on effects of recommended pesticides on the brinjal shoot and fruit borer *Leucinodes orbonalis* Guenee	Dr. G.K. Mahapatro	ICAR-IARI, New Delhi
30.	Basavaraj N Hadimani (11488)	Ph.D	Biosystematic studies on Indian stingless bees (Hymenoptera: Apidae: Meliponini)	Dr. Debjani Dey	ICAR-IARI, New Delhi
31.	G R Hithesh (11483)	Ph.D	Studies on conservation of natural enemies in cabbage (*Brassica oleracea* L. var. *capitata*) ecosystem	Dr. Sachin S. Suroshe	ICAR-IARI, New Delhi
32.	Deeksha M G (11481)	Ph.D	Characterization of metabolic enzymes and energy transfer system in *Tribolium castaneum* (Herbst)	Dr. S. Subramanian	ICAR-IARI, New Delhi

**Outreach Institute

Nematology

6

Prof. Anil Sirohi

The Division of Nematology is mandated to work on nematodes which are the most numerous multi-cellular organisms inhabiting different habitats and belonging to diverse trophic groups. These nematodes inflict indirect damage to crop plants by pre-disposing them to other co-inhabiting pathogenic bacteria, fungi, pathogens, etc. They are considered a major biotic stress for the successful cultivation of various field and horticultural crops. Moreover, beneficial nematodes (entomopathogenic nematodes) have been successfully utilized as potential biocontrol agents, for the management of insect pests of crops. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Nematode Diversity and Biosystematics

Diversity and community structures of nematode species in the crops cultivated by drip irrigation system

The present study focused on the diversity and community structures of nematode species in crops cultivated using drip irrigation systems. The study aimed to collect, identify, and determine the densities of nematode species in the crop rhizosphere, analyze the ecological differences between drip and conventional irrigation systems, and profile nematodes using molecular and morphological methods. The study analyzed nematode populations in mandarin and pomegranate orchards using standard procedures. It identified 31 nematode genera in mandarin orchards and 29 in pomegranate orchards. They were classified into different feeding groups, including plant parasites, bacterial feeders, fungal feeders, omnivores, and predators. Drip-irrigated crops had more plant parasites, while surface-irrigated crops had more bacterivores. The Mandarin orchard had more predators, omnivores, and fungal feeders than the pomegranate orchard. During sampling from the pomegranate orchard, a new nematode species named *Ditylenchus Rafiq* n.sp. was identified based on morphological and molecular characterization. The species has distinct morphological features and molecular markers (ITS I & II and D2-D2 regions) sequences. Ecological analysis using diversity indices showed significant variations between the irrigation systems. Drip-irrigated crops had higher nematode diversity and community richness compared to surface-irrigated crops. Nematodes were more evenly dispersed in surface-irrigated crops. The study also investigated the impact of temperature and rainfall on plant parasitic nematodes (PPNs) in mandarin and pomegranate crops. Most PPNs (*Meloidogyne enterolobii*, *Pratylenchus coffeae*, *Rotylenchulus reniformis*, *Tylenchorhynchus brevilineatus*) had peak populations in May-August and low populations in November-February. The onset of monsoon led to an increase in nematode populations, which gradually decreased during winter. The study found that irrigation affected nematode abundance but not diversity. The study also analyzed nematode diversity in protected and open-field systems. Here drip-irrigated crops also had more PPNs, while surface-irrigated crops had more bacterivores. Irrigation significantly affected nematode abundance in the open field system, but not in the protected system. The protected system had the highest abundance of PPNs, while the open field system had more bacterivores. Surface-irrigated crops had more uniform nematode distribution compared to drip-irrigated crops. Crops and irrigation types significantly affected the functional diversity of soil nematodes. The study established correlations between nematode diversity indices and environmental factors such as moisture, temperature, rainfall, and organic carbon. Moisture positively correlated with PPNs and negatively correlated with bacterivorous nematodes. Organic carbon showed a positive relationship with bacterivorous nematodes. The analysis of nematode communities using principal component analysis showed that the protected system had a higher abundance of PPNs, while the open field system had more free-living nematodes. There was a negative correlation between plant parasites and free-living nematodes. The study also analyzed the soil food web dynamics and found that the open field system was stressed, had deteriorated soil with low nitrogen levels, and dominated fungal breakdown pathway while the protected and orchard systems were organized, contained undisturbed soil with moderate nutritional status, and dominated fungal breakdown pathway. The study also conducted taxonomic profiling of nematodes using molecular methods. High-throughput sequencing (HTS) of 18S rDNA identified a higher number of nematode genera (including animal parasites) compared to morphological analysis. However, morphological analysis identified a higher proportion of agriculturally important trophic groups, including omnivores and predators. The study revealed commonalities and differences between the two methods in identifying nematode genera, orders, and families.

Theme 2: Plant-Nematode Interaction

Comparative analysis of root-knot nematode species *Meloidogyne enterolobii* and *Meloidogyne incognita* to understand factors contributing to differences in plant pathogenesis

Nematodes are tiny aquatic roundworms that can either help or harm plants. Root-knot, cyst, and root lesion nematodes are particularly damaging to the plants. These nematodes puncture plant root cells and feed on nutrients, causing growth and yield reduction. The root-knot nematodes (*Meloidogyne* spp.) are among the most destructive plant-parasitic nematodes. They form galls on roots and hinder water and nutrient uptake by the plant, resulting in stunted growth and lower yields. *Meloidogyne enterolobii*, once considered a minor pathogen, has now evolved as a significant threat to global agriculture and can break nematode resistance in crops resistant to other *Meloidogyne* spp. This nematode, along with *Fusarium oxysporum* f. sp. *psidii*, causes guava decline or wilt, affecting guava orchards worldwide. The present study was conducted to understand the reasons for aggressive pathogenesis by *M. enterolobii* as compared to *M. incognita*. Comparative analyses of both species' life cycles and biology revealed that *M. enterolobii* was more invasive, and its J2 penetrated roots quicker and in more significant numbers, producing more numbers of and larger galls than *M. incognita*. *M. enterolobii* lays eggs in a staggered fashion throughout the growing season, whereas *M. incognita* lays eggs in a smaller time window. In addition, *M. enterolobii* had a larger genome with abundant effectors compared to M. incognita, such as more secretory-excretory and host-interacting proteins, suggesting a more extensive repertoire of genes to help with heightened aggression and host-immune evasion. Understanding why certain nematode species are more aggressive is crucial to knowing the disease mechanisms, outbreak prediction, and developing newer management solutions.

Theme 3: Molecular Nematology

Engineering resistance against root-knot nematode, *Meloidogyne incognita* in Arabidopsis by knocking out parasitism elicitor factors using CRISPR/Cas9 technology

Nematodes are microscopic, cylindrical in shape, unsegmented, bilaterally symmetrical, pseudocoelomatic invertebrates and are most copious metazoans on earth occurring as free-living or parasitic forms. Plant-parasitic nematodes (PPNs) result in substantial crop yield losses and economic damages thereby posing a significant threat to global food production. Among the PPNs, the root-knot nematode (*Meloidogyne* spp) is an economically highly significant obligate sedentary plant endoparasite because of its ability to parasitize a wide host range and to form disease complexes. Thus, there is an imperative need to devise effective strategies for its management to minimize crop losses and ensure global food security. Various approaches, including crop rotation, chemical treatments, biological control, and cultural practices, have been employed, but each has its limitations. Conventional breeding techniques, although effective, are time-consuming in improving crop yield. Alternatively, genome editing, particularly CRISPR-Cas9 technology, provides a faster and more precise method for modifying the DNA of organisms compared to conventional breeding techniques. CRISPR-Cas9 technology enables the enhancement of plant defense by targeting susceptibility genes and mutating those that promote nematode development, thus strengthening/enhancing resistance against pathogens. The versatility of CRISPR/Cas9 has been demonstrated in conferring genetic resistance to viruses by eliminating crucial host factors. Our study aimed to utilize CRISPR technology to modify plant genes involved in interactions with nematode glandular secretions during the formation of the feeding-site complex. The study intended to explore the potential of CRISPR/Cas9-mediated genome editing to enhance plant resistance against nematode infestation by targeting two host susceptibility genes, WRKY45 and KRP6, in Arabidopsis. The CRISPR/Cas9 constructs were developed using the Golden Gate Cloning method and transformed into Arabidopsis plants *via* the floral dip method. Molecular analysis confirmed the presence of mutations in the targeted genes in the transgenic plants. Nematode bioassays demonstrated a significant reduction in gall formation and the development of adult females in the edited lines compared to wild-type plants. The KRP6.1 and WRKY45.1 edited Arabidopsis lines exhibited a reduction in the number of galls by 62.14% and 46.16% respectively. The decrease in adult female development was 60.39% in the KRP6.1 and 53.33% in the WRKY45.1 transformed lines. These findings provide the proof of concept for the potential of CRISPR/Cas9-mediated gene editing as a management strategy for enhancing resistance to *M. incognita* in Arabidopsis.

Molecular and functional characterization of chemotaxis-related genes in *Meloidogyne graminicola*

Chemosensation is the major component of nematode host-finding behavior. *Meloidogyne graminicola* is the major phytonematode in rice-wheat cropping system that detects and transduces the chemical signals from the environment (rhizosphere) into neurological signals via chemosensory organs such as amphids and phasmids during host finding. When compared to free-living nematodes like *C. elegans*, the molecular information of *M. graminicola* (plant nematode) chemotaxis is yet to be explored. The current research focused on the molecular characterization of four potential chemosensory genes in *M. graminicola*, i.e., *Mg-odr-1*, *Mg-odr-3*, *Mg-tax-2*, and *Mg-tax-4*. The transcripts of *Mg-odr-1*, *Mg-odr-3*, *Mg-tax-2*, and *Mg-tax-4* exhibited significant expression during the early life stages of M. graminicola, indicating the potential involvement of these genes in host finding and recognition. By employing a reverse genetics approach, functional characterization of *Mg-odr-1*, *Mg-odr-3*, *Mg-tax-2*, and *Mg-tax-4* revealed behavioral abnormalities in *M. graminicola* and disrupted attraction and penetration towards host roots in the Pluronic gel medium. Knockdown of *Mg-odr-1*, *Mg-odr-3*, *Mg-tax-2*, and *Mg-tax-4* alters not only attraction and penetration but also the infection parameters like number of galls, egg masses, eggs per egg mass, and nematode multiplication factor. The silencing of *Mg-odr-1*, *Mg-odr-3*, *Mg-tax-2*, and *Mg-tax-4* led to impaired chemotaxis of *M. graminicola* towards a range of volatile compounds (including ketone, pyrazine, aromatic compound, thiazole, ester, alcohol), as well as non-volatile originating from plants (such as carbohydrate, organic acid, phenolic, phytohormone, amino acid) in an *in vitro* assay using the Pluronic gel. The results presented in the current thesis will help in understanding the early stage of rice-*M. graminicola* interactions and also lead to devising novel management strategies in rice, that can be targeted to disrupt the *M. graminicola* host-finding process.

Theme 4: Nematode Management

Effect of organic nutrient sources, botanicals, and biocontrol agents in the root-knot nematode (*Meloidogyne incognita*) infecting tomato

Tomato (*Solanum lycopersicum*), a solanaceous crop is mainly infected by root-knot nematode (Meloidogyne incognita) in India. In recent years, synthetic chemicals are easily available in the market but it has detrimental effects on the environment and human beings. Hence, it is a time to shift towards "Green pesticides" which include organic manures, botanicals extracted from plants, and biocontrol agents. Utilizing soil organic amendments is a time-honored agricultural method for enhancing the soil's physical and chemical properties. Botanicals and biocontrol agents have wide applications in medicine, pest and disease management. The bioefficacy of four botanicals and two biocontrol agents (plant growth-promoting rhizobacteria) were tested initially under *in vitro* conditions and followed by an experiment conducted to assess the effect of organic nutrient sources, botanicals, and biocontrol agents on root-knot nematode (*M. incognita*) infecting tomato grown in micro plots. All the botanicals and biocontrol isolates showed nematicidal activity, after 96h and 8 days on juveniles (J2s) mortality and egg-hatching inhibition respectively. Increase in the juvenile mortality and egg-hatching inhibition increased with an increase in concentration and time of exposure. *In vitro* toxicity (LC50) revealed that *Mentha spicata* oil and *Piper longum* oil were found to be more toxic to J2s compared with hexane extracts of both the botanicals at lower doses after 96h. All 18 treatments showed significant ($P<0.05$) differences among themselves compared with untreated control in the plot experiment. The results showed that soil NPK and organic C increased with the application of various treatments which followed the pattern of farmyard manure>vermi compost>paddy straw>biocontrol agents>botanicals. The plots treated with organic manures enhanced the plant growth even though they were heavily infested by nematodes. There was a significant ($P<0.05$) reduction of M. incognita incidence in the plots treated with the consortium (BS+BA+FYM) followed by the individual application of biocontrol agents and botanicals and their efficacy was comparable with synthetic nematicide, Velum Prime 400 SC (500g a.i./ha). The integrated use of organic manures, biocontrol agents, and botanicals would be an efficient approach for the management of M. incognita in tomatoes grown at the field level.

Theme 5: Entomopathogenic Nematodes

Isolation and identification of entomopathogenic nematodes from southern Rajasthan and their biocontrol potential against lepidopteran insect pests

A survey has been conducted and 115 soil samples were collected from different locations of Banswara, Dungarpur, Udaipur, Rajsamand, Bhilwara, and Chittorgarh districts of southern Rajasthan for isolation of EPNs. Out of 115 soil samples baited out, only five samples were found to be positive for entomopathogenic nematodes (EPNs). Among these EPNs, one EPN each was found from the Banswara, Dungarpur, Rajsamand, Bhilwara, and Chittorgarh districts. Among five isolated EPNs, two populations belong to the genus Steinernema, and three belong to the genus Oscheius. Our survey revealed that Oscheius spp. and Steinernema spp. were widely occurred. Entomopathogenicity of isolated EPNs was also tested against greater wax moth larvae, Galleria mellonella. Further, the efficacy of promising three EPNs viz., Steinernema sp. (EPN-RAJ- 07 CH), Steinernema sp. (EPN-RAJ-02 RD) and Oscheius sp. (EPN-RAJ-06 DR) were tested against lepidopteran insect pests Spodoptera frugiperda, S. litura, and H. armigera in Petri-plates. Among the tested EPNs, Steinernema sp. (EPN- RAJ- 07 CH) was found more pathogenic to all tested insects followed by Steinernema sp. (EPN-RAJ-02 RD) and Oscheius sp. (EPN-RAJ-06 DR). The information generated from the present study may form the base for developing novel formulations based on indigenous EPNs because these EPNs are adapted to the local environmental conditions and are natural regulators of insect populations.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Vimala, A.G. (21682)	M.Sc.	Effect of organic nutrient sources, botanicals, and biocontrol agents in the root-knot nematode (*Meloidogyne incognita*) infecting tomato	Dr. Pankaj	ICAR-IARI, New Delhi
2.	Adhuna KP (21683)	M.Sc.	Comparative analysis of root-knot nematode species *Meloidogyne enterolobii* and *Meloidogyne incognita* to understand factors contributing to differences in plant pathogenesis	Dr. Vishal Singh Somvanshi	ICAR-IARI, New Delhi
3.	Voodikala Sai Akhil (21684)	M.Sc.	Molecular and functional characterization of chemotaxis-related genes in *Meloidogyne graminicola*	Dr. Tushar Kanti Dutta	ICAR-IARI, New Delhi
4.	Kavita Jain (21740)	M.Sc.	Isolation and identification of entomopathogenic nematodes from southern Rajasthan and their biocontrol potential against lepidopteran insect pests	Dr. Rashid Pervez	ICAR-IARI, New Delhi
5.	Neeraj (11077)	Ph.D.	Engineering resistance against root-knot nematode, *Meloidogyne incognita* in Arabidopsis by knocking out parasitism elicitor factors using CRISPR/Cas9 technology	Dr. Anil Sirohi	ICAR-IARI, New Delhi
6.	G. Vyshali (11559)	Ph.D.	Diversity and community structures of nematode species in the crops cultivated by drip irrigation system	Dr. M.R. Khan	ICAR-IARI, New Delhi

Plant Pathology

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Prof. Robin Gogoi

The Division of Plant Pathology pioneers in disease diagnosis, detection of pathogens, pathogen population dynamics, pathogen characterization, pathogenomics, host-pathogen interaction with reference to mechanism of resistance, virulence/pathogenicity genes; microbiome/biological control, nanotechnology and dsRNA based disease management in crop plants, and human resource development. The research findings of post graduate students have been grouped under the following themes:

Theme 1: Disease Diagnosis and Pathogen Characterization

Identification, diversity analysis for races of Xanthomonas associated with bacterial leaf spot and development of multiplex PCR for seed borne bacterial pathogens of tomato and pepper

Tomato and pepper were important solanaceous crops grown across the world with production of 182 million metric tons and 2959 thousand tons, respectively. Among tomato and pepper bacterial diseases, bacterial leaf spot (BLS) caused by *Xanthomonas* species appears as the most devastating one, leading up to 23–44% crop losses. This study embarks on characterize and identify the species and races of BLS-*Xanthomonas* in India. BLS-infected tomato and pepper samples were collected from 9 different states of India *viz*., Haryana, Punjab, Andhra Pradesh, Telangana, Delhi, West Bengal, Uttarakhand and Himachal Pradesh. A total 79 isolates of BLS-xanthomonads were isolated, further characterized by employing polyphasic approaches. These isolates were categorized into tomato group (XCVT) and tomato-pepper group (XCVTP), Furthermore, the BLS isolates were identified by using species-specific primers, 16S rRNA and *hrp*B gene sequencing revealed that this isolates majorly belonging to *X. euvesicatoria*, *X. vesicatoria* and *X. perforans*. On race profiling based on HR response and effector-specific primers PCR, 83.54%, 7.5%, 6.3% and 1.2% strains belonged to race T1, T2, T3 and T4, respectively. It is the best of our knowledge report of *X. perforans* (race T3 and race T4) for were first time in India. Genetic diversity of 79 and 6 isolates of present and previous collected BLS *Xanthomonas* grouped into seven and six haplotypes were observed in BOX-PCR and ERIC-PCR fingerprinting, respectively. A significant high level of genetic diversity among Haryana and Punjab BLS xanthomonads exhibited variability in patterns compare to other state strains. Six virulent BLS strains genetic diversity explored by multilocus sequence analysis (MLSA) with five house-keeping genes (*dna*K, *atp*D, *gyr*B, *fus*A and *glt*A). The Multiplex- PCR protocol was developed to detect tomato seed-borne bacterial pathogens such as BLS- *Xanthomonas*, *Pseudomonas syringae* pv. *tomato* and *Clavibacter michiganensis* subsp. *michganensis* individually or simultaneously all of them. The highly robust recombinase polymerase amplification (RPA) protocols were developed followed by validation of specificity, sensitivity assays. The protocol of in-hand amplification by RPA protocols was achieved from artificially inoculated samples.

Virome analysis of grapevine (*Vitis vinifera* L.) cultivars and detection of important grapevine viruses using rapid and specific assays

Grapevine (*Vitis vinifera* L.) is a valuable fruit crop known to inhabit more than 100 viruses and viroidal pathogens globally. In order to develop indexing and certification system for grapevine in India, the current study included HTS-based virome analysis of sample pools and single plants from grafted nursery plants of two commonly grown grapevine cultivars *viz*., Super Sonaka and Anushka. RNA sequencing and analysis revealed the infection of 18 viruses and 5 viroids. Presence of grapevine virus D, grapevine virus H and GLRaV-7 have been recorded for the first time in Indian grapevine cultivars. Infection of the viruses obtained in HTS data was further confirmed through PCR/RT-PCR and Sanger sequencing. Using de novo assembly and reference-based mapping, 43 complete /near complete genomes of the above identified viruses and viroids were reconstructed from the ribosomal RNA depleted sequences of grapevine cultivars. Virome analysis of grapevine samples from vineyards of Anantapur region of Andhra Pradesh was also undertaken and it showed presence of 11 viruses and 4 viroids. Interestingly, all the viruses detected in Anantapur sample pools were also detected in the virome of nursery plants from the Solapur region suggesting the possible role of infected planting materials in introduction of these viruses in grapevine orchards. In this study, simple crude plant extract-based reverse transcription-recombinase polymerase amplification (RT-RPA) assay and RPA was developed for efficient detection of GLRaV-3 and GGVA respectively. In These assays tedious nucleic acid isolation is dispensed as grapevine leaf sap simply prepared in NaOH: EDTA (1:1) and 0.5M NaOH buffer was directly used as template for detection of GLRaV-3 and GGVA respectively. The simplicity and efficiency of the developed assays make them a promising tool for detecting these two viruses in grapevines samples, allowing for timely and accurate detection.

Virome analysis for identification and characterization of virus(es) associated with mosaic disease of mustard

Mustard is the 2nd most important commercial oilseed crop of India. Mustard mosaic disease, caused primarily by Turnip Mosaic Virus (TuMV) and occasionally in association with Cucumber Mosaic Virus (CMV), poses a substantial threat to global mustard cultivation, leading to severe economic losses. Despite its prevalence, there remains a dearth of comprehensive studies focusing on virus prevalence, genomic characterization, and transmission modes in Indian mustard crops. Our investigation employed electron microscopy and high-throughput RNA-sequencing techniques to analyze symptomatic mustard samples. Results unveiled mixed infections of CMV and TuMV during the 2020-21 season, and TuMV singular infection during the subsequent 2021-22 season, confirmed through Reverse Transcription-Polymerase Chain Reaction (RT-PCR). Notably, TuMV incidence reached 100% in mustard fields, with genomic analysis revealing the emergence of the world-B3 sub-pathotype in South Asia. Additionally, novel recombinant CMV isolates infecting previously unreported hosts were discovered in India. Our findings shed light on the seed transmission mode of TuMV dissemination, with aphids acting as carriers. We present compelling evidence suggesting true seed-borne transmission of TuMV, emphasizing its presence in immature seeds and subsequent association with TuMV in seedlings grown under aphid-free conditions. Furthermore, our research underscores the significant impact of mixed CMV and TuMV infections on mustard crop health including reduced yield by more than 50%, resulting in severe mosaic and puckering symptoms compared to the milder effects of TuMV single infections. This study marks the first natural observation of TuMV in black mustard and characterizes New Delhi TuMV strains as world-B3. Additionally, it identifies recombinant CMV subgroup IB isolates affecting diverse mustard seed varieties in India.

Diversity and infectivity of begomoviruses in major cucurbits in India

Cucurbits are an important summer vegetable crops and they are affected by several biotic and abiotic factors. Among the various biotic factors, begomoviruses are an emerging threat to the production of cucurbits in India. In the present study, in order to understand the diversity of begomoviruses, species-specific PCR diagnostics were utilized to detect begomoviruses in major cucurbit crops. During 2020 and 2021, a total of 551 leaf samples from eight different cucurbit species were collected from Haryana, Delhi, Uttar Pradesh, Chhattisgarh, Maharashtra, Telangana and Karnataka. The generic PCR results showed that out of 551 samples tested, 124 samples were positive for begomovirus and among them, 47 samples, 73 samples and 1 sample were positive for ToLCNDV, ToLCPalV and ChiLCV, respectively. Species-specific PCR unveiled the differential distribution pattern of two predominant begomoviruses, ToLCNDV and ToLCPalV in cucurbit crops in India. Further study on the complete genome characterization of begomovirus from the bottle gourd IC-0262269 genotype from Delhi identified the presence of ToLCPalV. PTR constructs were successfully developed and their infectivity was assessed through agro-inoculation to *N. benthamiana,* cucumber, bottle gourd and tomato plants by employing various delivery methods viz., syringe infiltration, vacuum infiltration and pin-pricking. Notably, the cloned genome components together exhibited characteristic disease symptoms in 100% *N. benthamiana*, 62.5% bottle gourd var. Pusa Naveen, and 100% tomato var. Pusa Ruby test plants at 6-20 dpi. Among the different delivery methods vacuum infiltration emerged as the most efficient method for delivering begomovirus DNA constructs. Cross-infectivity assay through whitefly inoculation of different begomovirus isolates showed that, ToLCNDV isolate originating from tomato could not be transmitted to cucurbits, however, the sponge gourd isolate of ToLCNDV was transmissible to tomato as well as bottle gourd and muskmelon. The bottle gourd and muskmelon isolates of ToLCPalV could be successfully transmitted between tomato and cucurbits. The cross-inoculation studies revealed that the tomato-infecting begomovirus isolates had differential transmission ability between Cucurbitaceous and Solanaceous host plants.

Morpho-molecular characterization of *Fusarium solani* species complex (FSSC) associated with root rot of tomato and development of Loop mediated isothermal amplification (LAMP) assay for rapid detection of major FSSC

Fusarium root rot affects various crops, leading to stunted growth, wilting and crop loss. This disease is caused by different *Fusarium* species like *F. falciforme*, *F. vanettenii*, *F. striatum*, *F. solani*, and *F. equiseti*. The root rot infected tomato plant samples and soil samples were collected from research fields of ICAR-Indian Agricultural Research Institute (IARI) New Delhi. A total of 44 *Fusarium* isolates were studied, primarily *Fusarium solani,* along with other species. Molecular (using *tef-1α* and *rpb2* genes) and morphological characterizations revealed that out of 44 isolates, the species of FSSC were predominant about 88.63% followed by *F. oxysporum* (4.54%), *F. fujikuroi* (2.27%), *F. equiseti* (2.27%) and *F. chlamysosporum* (2.27%). Under FSSC the predominant species was *F. falciforme* (64.10%). Further, the phylogenetic study with 1000 bootstrap replications five distinct polyphyletic lineages and eight distinct monophyletic lineages, and each of the monophyletic lineages was clearly connected with a particular FSSC haplotype species. Through artificial inoculation on susceptible tomato plants, 39 *Fusarium solani* isolates, encompassing eight identified species within the *F. solani* species complex (FSSC), were assessed for their ability to induce root rot and wilt disease. The pathogenic strains were classified into three categories based on severity and aggressiveness, ranging from weak pathogens (*F. striatum*, *F. petroliphilum* and *F. cyanescens*), pathogens that cause moderate damage (*F. solani FSSC5*, *F. metavorans* and *F. keratoplasticum*) pathogens that cause severe damage to tomato plants (*F. vanettenii* and *F. falciforme*). All eight identified species demonstrated pathogenic potential, prompting the development of species-specific markers. The *rpb2* gene was selected for designing species-specific primers for *F. falciforme* and FSSC (eight cryptic species) *viz*., F1/R1 and F3/B3 respectively. Further, a Loop-mediated isothermal amplification (LAMP) primer set was developed to detect the *F. solani* species complex (FSSC) with its specificity and sensitivity (10fg/µl).

Characterization of *Bipolaris sorokiniana*, transcriptome profiling and assessment of bioagents against spot blotch of barley

Spot blotch disease caused by *Bipolaris sorokiniana* is one of the major constraints in barley production. Forty-five isolates were established from diseased samples collected from different locations of Uttar Pradesh and Bihar, India. Characterization based on morphology revealed highest colony diameter of 80.33 mm in BS 36 (Varanasi, Uttar Pradesh) isolate and lowest colony diameter of 19.33 mm in BS 45 (Sultanpur, Uttar Pradesh) isolate. Conidia length ranged from 74.58 µm- 42.05µm and conidia width ranged from 22.94 µm- 12.18 µm across isoltes. Highest sporulation was observed in BS 32 isolate (Varanasi, Uttar Pradesh) and lowest sporulation was observed in BS 13 (Sultanpur, Uttar Pradesh). Analysis of pathogenicity revealed Pusa, Bihar isolates to be highly pathogenic amongst all other isolates. The cross infectivity assays found barley isolate to be less virulent on wheat and wheat isolate to be less virulent on barley. Out of all evaluated genotypes 3(EC0328964, IC0393134, IC0446132) were resistant and 5 were moderately resistant. Transcriptome analysis of resistant (EC0328964) and susceptible genotype (EC0578292) revealed a several defense related genes like resistant gene analogs (RGAs), disease resistance protein RPM1, pathogenesis-related protein PRB1-2-like, pathogenesis-related protein 1, thaumatin-like protein PWIR2 and defensin Tm-AMP-D1.2 to be upregulated and exclusively present in resistant genotype. *In vitro* inhibition studies using strains of *Trichoderma* and biocontrol bacteria against *B. sorokiniana* revealed *Trichoderma asperellum* 8686 and *Trichoderma asperellum* 8687 with highest percent inhibition of 71.73% and 71.37% respectively. *In planta* studies with selected biocontrol agents revealed *Bacillus amyloliquefaciens* to be most effective in seed treatment. Post inoculation with biocontrol agents showed *Bacillus amyloliquefaciens*, to be at par with *Trichoderma asperellum* and *Pseudomonas fluorescens*. In conclusion, *Bacillus amyloliquefaciens* showed better and consistent results.

Characterization, diversity analysis of *Clavibacter michiganensis* subsp. *michiganensis* and evaluation of resistance source against bacterial canker of tomato

Bacterial canker of tomato caused by *Clavibacter michiganensis* subsp. *michiganensis* which is one of the most devastating diseases and occurs in major tomato growing regions of the world including India. A survey was conducted during 2022-23, in three states *i. e.* Himachal Pradesh, New Delhi and Jharkhand of India where 5.69 to 34.67% disease incidence was recorded in the tomato fields. The bacteria were isolated on semi-selective media *i. e.* D2ANX and SCM. The pathogenicity assay was carried for all the six confirmed isolates on tomato cultivar Pusa Ruby on 4 weeks old plants. Various morphological and biochemical assays were carried out in order to confirm the isolates. Further the molecular characterization was carried out by PCR techniques using specific primers CMM-5 and CMM-6 targeting *pat-1* gene present in the plasmid of the bacteria. Multilocus sequence analysis was carried out for species level identification, using seven housekeeping genes (*gyrB*, *ppk*, *atpD*, *recA*, *rpoD*, *tufA* and *bipA*) along with 16SrRNA for four of the most virulent isolates (A4R-3, A1R-1, A2R-2 and A3R-4) out of six isolates. According to 16SrRNA analysis, all four isolates had nucleotide homology of 99.72–99.88% to the Egyptian strain of *Clavibacter michiganensis* subsp. *michiganensis* MS-1 [MF370397] isolated from tomato. Nucleotide homology of concatenated sequences of all the seven housekeeping gene revealed that among the four Indian isolates, A1R-1 and A3R-4, indicated that they were 100% comparable to one another. The Indian isolates A4R-3 and A2R-2, on the other hand, displayed 99% identity with other Indian isolates and these isolates belong to *Clavibacter michiganensis* subsp. *michiganensis*. 22 tomato genotypes were evaluated against bacterial canker under protected conditions and only one genotype MIDM was highly resistant, whereas Para Sanskrit found to be highly susceptible. Enzyme assays of about three defense related enzymes, Polyphenol oxidase (PPO), Superoxide dismutase (SOD) and Peroxidase (POD) revealed that the concentration of resistant (MIDM) increased and reached its maximum after 2 weeks of inoculation and then decreased gradually, whereas susceptible (Para Sanskrit) didn’t show considerable amount of fluctuations.

Theme 2. Host Plant Resistance

Isolation, characterization and molecular cloning of potential resistance gene analogues from lentil germplasm against Fusarium wilt

Fusarium wilt caused by *Fusarium oxysporum* f. sp. *lentis* (*Fol*) is the most destructive disease of lentil present worldwide and in India. Uncovering the genes associated with resistance aids in understanding the plant's defense mechanisms and provides valuable resources for breeding programs. In the present study, lentil germplasms belonging to seven species were screened against seven races of *Fol* in the years 2020 and 2021. Accessions showed degrees of resistance to *Fol* and three accessions namely, IC20156 (*Lens culinaris* subsp. *culinaris)*, EC714243 (*L. culinaris* subsp. *odemensis)* and EC718238 (*L. nigricans)* were highly resistant to *Fol*. Previously, cloning resistance gene analogues (RGA) have been a useful tool for isolating full-length functional R gene. Forty-five RGAs were cloned from the resistant accessions and were distinguished into two classes, Toll interleukin-1 receptor (TIR) and non-TIR. The phylogenetic analysis grouped RGA into six classes, LRGA1 to LRGA6 determining the diversity of RGA present in the host. The similarity index ranged from 27.85% to 86.98% among RGAs and 26.83% to 49.41% between known R genes. To elucidate the molecular mechanisms underlying resistance against Fusarium wilt, the expression of RGA at 24, 48, and 72 hours post-inoculation (hpi) was assessed by qRT-PCR in resistant and susceptible accessions against race 5 (CG-5). RGAs such as Lc2, Lc8, Ln1, and Lo6 exhibited cDNA signals during early infection (24hpi), suggesting their involvement in pathogen recognition. Notably, LoRGA6 displayed significant upregulation in resistant accessions indicating its role in resistance. The full-length of LoRGA6 loci was isolated by 5′ and 3′ RACE-PCR. *In-silico* characterization revealed that LoRGA6 codes for a 912-amino acid-long polypeptide with a TIR motif at the N-terminal and eight leucine-rich repeat (LRR) motifs at the C-terminal. The tertiary structure unveiled a concave pocket-like structure within the LRR domain, suggesting its potential involvement in interacting with pathogen effectors. This has further paved the path for functional analysis of the loci by VIGS to understand the molecular mechanism of resistance.

Characterisation of *Fusarium* spp. and vascular wilt resistance of brinjal (*Solanum melongena* L.)

Eggplant wilt, despite emerging as a severe disease in India, the aetiology must be better studied for its species' complexity and variability. The identity of fungal isolates was established morphologically followed by sequencing and phylogenetic analysis. Three species, *F. falciforme* of FSSC, *F. incarnatum* of FIESC and *F. proliferatum* of FFSC, were observed for the first time in India. In further studies, the genetic relatedness of the isolates for virulence was assessed with candidate avirulent (*SIX* effectors) and virulent (*Fow1* and *Fow2*) and could not delineate the virulent isolates. Hence, the *F. oxysporum* and *F. solani* isolates were genotyped with SSR markers. Though the clustering did not correlate with their virulence levels, the dendrogram grouping revealed variability among the *F. oxysporum* and *F. solani* isolates. This study concludes that although multiple species of *Fusarium* are associated with eggplant wilt, only *F. oxysporum* and *F. solani* are widespread. Only the SSR makers could identify the genetic variability and hence, would help screen eggplant germplasm for fusarium wilt resistance. A highly aggressive *F. oxysporum* isolate, BRFO-VRF-8 was used to screen the germplasm lines (17 nos), in pot culture and sick plot experiments. The cv. Swarna Mani was identified as resistant for displaying a reduced per cent disease index and high growth parameters. In pot experiments, the cultivar is also resistant to *F. solani* and *F. oxysporum* + *F. solani* infections. Q-PCR assays for candidate resistant and defence gene expressions identified 7 defence genes as highly expressing and were speculated for their roles in brinjal resistance. In further evaluating the resistant germplasm under endemic field conditions, the variety consistently displayed higher resistance with <PDI and higher fruit yield than the susceptible variety, Pusa Hara Baingan 1. The identified cultivar could be novel source of resistance to monitor the *Fusarium* population and for the improvement of other commercially cultivated brinjal varieties.

Identification and characterization of NLR candidate genes in pearl millet (*Cenchrus americanus* (L.) Morrone) for foliar blast resistance

Pearl millet (*Cenchrus americanus* (L.) Morrone), stands as the predominant staple crop for a vast number of small-scale landholders across Asia and Africa. Currently, one of the prominent concerns is blast disease caused by *Magnaporthe grisea*, which poses a significant risk to pearl millet cultivation. Plants have evolved multiple integral mechanisms to counteract the pathogens infection, among which plant immunity through NLR (Nucleotide-Binding site, Leucine-Rich Repeat) genes is at the forefront. Therefore, utilization of these *R* genes/ NLR genes is considered to be one of the most powerful strategies for managing blast disease. The genome-wide mining in Pearl millet (*Cenchrus americanus* (L.) Morrone) revealed 146 *CaNBLRRs*. The variation in the branch length of NLRs showed the dynamic nature of NLRs in response to evolving pathogen races. The orthology of NLRs showed the predominance of many-to-one orthologs, indicating the divergence of NLRs in the Pearl millet lineage mainly through gene loss events and gene gains through single-copy gene duplications. Further, the purifying selection ($Ka/Ks < 1$) shaped the expansion of NLRs with the lineage of Pearl millet and other members of Poaceae. Presence of *Cis*-acting elements, *viz*., *TCA element, G-box, MYB, SARE, ABRE* and conserved motifs annotated with P-loop, kinase 2, RNBS-A, RNBS-D, GLPL, MHD, Rx-CC and LRR suggesting their putative role in disease resistance and stress regulation. The qRT-PCR analysis in Pearl millet genotypes showing contrasting responses to *Magnaporthe grisea* infection identified *CaNBLRR20, CaNBLRR33, CaNBLRR46 CaNBLRR51*, *CaNBLRR78* and *CaNBLRR146* as putative candidates. Furthermore, molecular docking showed the involvement of His, Arg and Thr residues of the LRR domain of *CaNBLRRs* in the formation of H-bonds with effectors. The present investigation gives a comprehensive view of the *CaNBLRRs* and paves the foundation for their utility in understanding host-pathogen interactions and the Pearl millet breeding programme.

Screening finger millet germplasm and potential bacterial antagonists against sheathblight caused by *Rhizoctonia solani* Kühn

Finger millet (*Eleusine coracana*) is affected by one of the emerging fungal disease sheath blight caused by *Rhizoctonia solani*. In the current study, 53 finger millet germplasm accessions from a core collection were screened against sheath blight under artificial inoculation condition in field. None of the accessions was found highly resistant whereas 8 germplasm were found to be resistant, 29 germplasm were seen moderately resistant and remaining germplasm was susceptible or highly susceptible. The mean (RLH) values ranged from 14.72% to 67.68%, Mean PDI values ranged from 11.11% to 95.56%. The meanAUDPC values varied from 287.78 to 1454.44 among the germplasm screened. Germplasm GEC25, GEC67, GEC119, GEC123, GEC167, GEC224, GEC275, GEC296, GEC309, GEC448, and Indira Ragi-1 exhibited moderately resistant or resistant disease responses in both field and in pot studies. In detached leaf assay conducted in selected germplasm, only 2 accessions GEC119 and GEC448 recorded reduced lesion spread in leaves. 93 bacterial isolates obtained from finger millet rhizosphere and 10 isolates from the NIBSM collection were screened in vitro for their antagonistic activities. Two isolates F225T5 and RS-6 demonstrated the maximum inhibition of 51.11% and 50.74% in mycelium growth. 5 promising bacterial isolates were selected for morphological, biochemical characterization and assessment of their biocontrol attributes. A substantial enhancement in plant growth parameters was observed when treated with RS-6 and F225T5 isolates. In the *in-planta* efficacy assessment of two bacterial isolates in pots, isolate RS-6 application exhibiteddisease reduction ranging from 16.90% to 36.7%, while for F225T5, it ranged from 22.94%to 26.87%. The significant disease reduction (36.70%) was observed when isolate RS-6 was applied as a seed treatment and foliar spray. These isolates inhibited sclerotial germination of *R. solani* by 72% and 80%, respectively. RS-6 and F225T5 were identified as *Bacillus amyloliquefaciens* ssp. *plantarum* through MALDI-TOF mass spectrometry data. These two bacterial isolates hold promise to be potential biocontrol option for sheath blight in finger millet.

Genome characterization of cowpea mild mottle virus, its temperature dependent symptom expression and resistance mining in soybean

Cowpea mild mottle virus (CPMMV), a whitefly semi-persistently transmitted Carlavirus is emerging as an economically important virus affecting production and seed quality of soybean across the globe. In the present study, soybean leaves showing systemic mottling, and mosaic were subjected to electron microscopy which showed the association of flexuous filamentous virus particles. The transcriptome analysis showed the association of CPMMV which was confirmed through Reverse Transcription-Polymerase Chain Reaction using coat protein specific primers. The complete genome of 8201 nt was reconstructed which shared 96% sequence similarity with China isolate. Recombination analysis showed one event of recombination in triple gene block and coat protein regions of the genome. Viral symptom expressions are greatly influence by the temperatures. Threshold temperatures values for CPMMV induced mosaic disease was estimated at different temperature regimes. Typical CPMMV symptoms were observed with highest disease severity and minimum incubation period at 22ºC. Effect of temperature on mosaic disease development was fitted to a non-linear beta model. The model predicted the southern India and few pockets in northern India to be potential region for CPMMV infection during August to October. A set of 288 soybean genotypes was evaluated for CPMMV resistance through sap inoculation under controlled conditions. Among 288 genotypes, 43 (14.93%) showed resistant, 59 (20.48%) were moderately resistant while remaining 190 (64.58%) showed susceptible reaction. A set of 5 gene specific and 24 SSR polymorphic markers were used for the association study. The polymorphism information content of 29 markers varied from 0.14 to 0.37. Population structure and cluster analysis differentiated the genotypes into three and two distinct subpopulations, respectively. The association study explained 1.2% to 9.6% phenotypic variance. The outcome of the present study would help in improving CPMMV resistance through the identification of novel CPMMV R-genes and breeding new resistance varieties through marker-assisted selection in India and worldwide.

Theme 3: Disease Management

Determination of the synergistic effect of essential oil-grafted CuNPs against maize pathogens and its influence on defense gene induction in maize

A novel nanoformulation was developed based on essential-oil grafted copper nanoparticles (EGC). Characterization was carried out by UV-Vis spectroscopy, TEM, FTIR Spectroscopy, X-ray diffraction, DLS, and zeta potential. GC-MS confirmed no adverse effects on organic clove oil. EGC rendered significant growth inhibition at 20 µg ml^{-1} against *Bipolaris maydis, Rhizoctonia solani* f.sp. *sasakii, Fusarium verticillioides, Macrophomina solani,* and *Sclerotium rolfsii,* with complete inhibition at 100 µg ml^{-1}. Seed treatment and foliar spray at 250 mg L^{-1} significantly reduced PDI, showing prophylactic and curative effects. SEM disrupted fungal hyphae due to EGC at ED_{50}. Transcriptomic analysis revealed disruptions in metabolic processes, cellular components, and molecular functions in *B. maydis*. Detached leaf inoculation assay associated melanin loss with decreased virulence. EGC, CuNPs, and clove oil at 1000 mg L^{-1} exhibited phytotoxic effects. However, EGC at 250 and 500 mg L^{-1} improved physiological traits. ST (EGC) at 250 and 500 mg L^{-1} resulted in optimum Cu accumulation below 25 mg kg^{-1} DW. Higher EGC concentration (1000 mg L^{-1}) led to toxic Cu levels (>300 mg kg^{-1} DW), negatively affecting Zn and Mn homeostasis. Enzymatic antioxidants *viz., β*-1, 3-glucanase, phenylalanine ammonia-lyase (PAL), peroxidase (POX), and polyphenol oxidase (PPO) were significantly increased by 45.250%, 67.862%, 59.447%, and 22.939% at 250 mg L^{-1} of EGC. Total phenolic content also rose by 53.248% in maize leaves with EGC treatment. Gene expression analysis showed upregulation of defense-related genes *viz.,* β-1,3-glucanases, CAT, POX, SOD, PPO, APX, PR-1, and Chitinase2 at 250 mg L^{-1}, suggesting EGC can act as abiogenic elicitors. Our study highlights EGC's potential in plant disease management, showcasing antifungal activity, inducing plant defense mechanisms, and promoting benefits to sustainable agriculture. We also for the first time established the basis of the mode of action of copper-based nanoformulations using transcriptomic analysis.

Characterization of virulence-associated genes and evaluation of novel management options for *Burkholderia glumae* causing panicle blight of rice

Bacterial panicle blight, incited by *Burkholderia glumae,* has impacted rice production globally. This disease is a major challenge in the rice-growing belts of North-western India, resulting in yield reduction. We have characterized the twenty-one BG strains using the 16S rRNA and the *gyrB* gene-based sequence approach in the present study. Likewise, we sequenced the eight major virulence-associated genes *viz*., *toxA, toxB*, *lipA, lipB, pehA*, *pehB, flhC,* and *flhD* present across the genome of *B. glumae*, and identified their interacting proteins through STRING analysis. Virulence screening of twenty-one BG strains revealed the variation in the percentage of grains infected and the yield of rice plants. The most virulent BG1 strain resulted in the highest disease incidence (82.11%) and lowest yield (11.12 g/plant) and BG10 came out as the least virulent strain. The 23 rice varieties were screened by inoculating the most virulent BG1 at the booting stage of the rice plants. As a result of screening, we obtained 1 resistant variety (Valichuri) and 4 varieties (Pusa Sugandh-5, Pusa Basmati-1, Pusa Basmati 1692, and Pusa Basmati 1121) were found to be highly susceptible (>75%). Subsequently, the resistant variety showed a tremendous in total phenol, PAL, POX, and PPO activity compared to the susceptible variety. We observed a notable increase in transcript level upregulation of antioxidant genes *viz., OsPAL1, OsAPX1,* and *OsPPO1* in the resistant variety. Furthermore, *in vitro* evaluation of various biocontrol agents and nano copper at different concentrations revealed that nano copper at 1000mg/L inhibited the colony growth of *B. glumae.* The application of nano copper at 1000 mg/L reduced the disease severity to 21.23% and increased the grain yield to 31.76 g/plant. Remarkably, pre-inoculation with nano copper at 1000mg/L followed by challenge inoculation with *B. glumae* enhanced the activity of enzymatic and non-enzymatic antioxidant activity. Additionally, we observed a transcript level upregulation of defense-related genes to several folds *viz., OsPR2, OsPR5, OsWRKY71, OsPAL1, OsAPX1,* and *OsPPO1.*

Determination of efficacy of plant surface applied nanocarrier conjugated RNA against begomovirus infection

Begomoviruses (family *Geminiviridae*) are the most significant plant virus in food, fiber and ornamental crops in India. Chilli leaf curl virus is one of the typical monopartite begomoviruses that caused leaf curl disease and is one of the major constraints in chilli production in India. Effective management of leaf curl disease in chilli is a major challenge due to the unavailability of resistant sources, an abundance of whitefly vectors, and socio-political concerns involved in transgenic. In the present study, an alternative and novel approach was attempted to prevent ChiLCV infection transiently by triggering cellular defense through the external application of dsRNA. To implement this strategy, four viral suppressor genes (C2, V2, C4, and βC1) of ChiLCV were cloned into a dsRNA vector, L4440, and transformed into *E. coli* strain HT115. The dsRNAs were produced following an optimized method which was then externally applied to *Nicotiana benthamiana* and chilli hosts. While individual dsRNA treatments were not effective in *N. benthamiana*, a cocktail of dsRNA from C2, C4, and V2 provided significant protection, reducing disease incidence by 67.7%. In chilli plants, all four dsRNA treatments induced resistance, with dsC4 exhibiting a 75% disease incidence, dsC2 and dsV2 at 37.5%, and dsβC1 at 12.5%, compared to 87% in the positive control at 30 dpi. PCR and qPCR analyses confirmed a reduction in viral load across all dsRNA-treated plants. Furthermore, chitosan nanoparticles (CTNP) were used as carrier for dsRNA to enhance the stability of the applied dsRNA and to increase delivery efficiency. Topical application of CTNP-conjugated dsRNA in chilli plants demonstrated superior disease protection compared to direct application, with a sustained effect up to 48 dpi. This approach significantly reduced the viral load, providing a promising strategy for extending the disease protection window. In conclusion, this research will contribute to the development of sustainable and environmentally friendly strategies for managing begomovirus infections in crops.

Assessment of bioagents against *Fusarium graminearum* causing head blight of wheat and identification of resistance sources

Wheat, known as the "King of Cereals," holds significant importance worldwide. Fusarium head blight (FHB) is a critical disease affecting wheat in India, putting grain productivity and quality at risk. Eighteen isolates of *Trichoderma asperellum* and 15 isolates of *T. harzianum* and five bacterial strains, including *Bacillus amyloliquefaciens, B. subtilis, Pantoea* spp., *Pseudomonas chlororaphis* and *P. fluorescens* were evaluated *in vitro* for their biocontrol efficacy against two virulent isolates of *Fusarium graminearum.* The dual culture plate assay revealed that the bioagents exhibited significant inhibition of *Fusarium* growth *in vitro*. Certain isolates of *T. asperellum* (8686, 8687, 8619), *T. harzianum* (8681, 8621, 7349) and *Bacillus* species stood out for their strong antagonistic effects against *F.* graminearum. The volatile metabolites produced by the selected biocontrol agents were evaluated for their inhibition of Fusarium growth. Certain *T. asperellum* isolates *viz*., 8619 and 8686 and *Bacillus* species showed substantial mycelial inhibition, suggesting the potential role of these compounds in disease management. In controlled polyhouse conditions, the biocontrol agents were applied using different methods to assess disease control potential. Seed treatment with the *T. asperellum* 8619 and post inoculation and pre+post inoculation spray of *T. asperellum* isolates 8686 and 8687 were found to be most efficient in controlling FHB of wheat. A real-time gene expression study of *T. asperellum* during its interaction with *F. graminearum* provided insights into the molecular responses of the biocontrol agent. Genes associated with biocontrol activity namely *BGN*13*, TEX*1*, ACC, ECH* and *NAG*2 were upregulated, indicating potential mechanisms for controlling the pathogen. Among the genotypes evaluated, majority of the genotypes displayed susceptibility, with only five manifesting a moderate susceptibility (score 3). Thirty-one genotypes were categorized as susceptible (score 4), and 115 were highly susceptible (score 5). The AUDPC value revealed that, seven genotypes were identified with AUDPC values below 500, indicative of a slower disease advancement rate.

Functional characterization of the metabolome of a phyllobacterial consortium for the suppression of rice blast disease

Rice, the primary staple for more than half of the world's population, confronts significant challenges, with rice blast disease causing a decline in productivity and escalating cultivation costs due to extensive fungicide application. Traditional methods like fungicides and the development of disease-resistant rice strains have limitations, necessitating innovative approaches. The research focuses on EMPIRE™, a phyllospheric formulation containing diverse microorganisms, and evaluates its Co-metabolomes (Metabolomes of the Consortium of Phyllosphere Microorganisms) for their efficacy against *Magnaporthe oryzae*, the causative agent of rice blast disease. Through dual culture confrontation assays, the study verifies the antifungal properties of three metabolomes – secreted, cellular, and total – with an impressive 80% concentration displaying significant suppression of the pathogen. Further analysis using LC-MS identifies specific compounds in these metabolomes with antimicrobial activity. Noteworthy is the metabolomes' growth-promoting characteristics at lower concentrations (2% and 4%), enhancing overall plant growth and development. In in-planta studies, the application of secreted and total metabolomes at specified concentrations notably reduces disease incidence. Biochemical defense mechanisms in treated seedlings, including elevated levels of peroxidase and polyphenol oxidase, indicate a stimulated defense response. The study also reveals increased expression of potential defense genes, indicating a systemic defense activation against rice blast disease. In conclusion, this in-depth exploration of microbial metabolomes' potential in enhancing plant health and eliciting a defense response against rice blast disease presents promising prospects for effective agricultural management. These findings underscore the significance of this innovative strategy in addressing a critical agricultural challenge, offering sustainable and efficient solutions for rice production.

Identification and characterization of effective metabolite from biocontrol strain of yeast *Hanseniaspora uvarum* (LE 1) and their evaluation in the post-harvest disease management

Fruits play an essential part in human nutrition, being rich in vitamins, minerals, fibre and antioxidants. However, the quality of fruits is often compromised by post-harvest deterioration. To tackle this issue, instead of using artificial chemicals, biocontrol strategies are being explored and microbial antagonists have emerged as a promising alternative. This present study focussed on exploitation of antagonist yeast strain *Hanseniaspora uvarum* LE-1 for its potential to combat major post-harvest fruit pathogens like *Alternaria alternata*, *Colletotrichum musae*, and *Penicillium italicum*. The antagonistic yeast exhibited a strong ability to inhibit the growth of post-harvest pathogens, with notable inhibition percentages in dual plate assays, ranging from 45% in *P. italicum* to 67% in *C. musae*. Niche overlapping index indicated a potential for coexistence between the yeast and pathogens, suggesting a lower level of competition. While nutrient competition assay showed the competition for resources between the antagonist and pathogens influenced by glucose concentration. However, siderophore production seemed insignificant. The study also examined the volatile organic compounds (VOCs) emitted by *H. uvarum* LE-1, identifying various VOCs, particularly Trans-2-decenal and Undecanol, as prominent compounds. These VOCs displayed significant antifungal effects, inhibiting mycelial growth, spore germination, and inducing morphological deformities in the pathogens. Trans-2-decenal consistently exhibited stronger inhibitory effects compared to Undecanol, which is also reflected in EC_{50} calculated using statistical program IBM SPSS®. In vivo experiments too supported the efficacy of these pure VOCs in reducing disease severity in fruits such as apples, bananas, and oranges through fumigation. Trans-2-decenal showed better effectiveness, achieving maximum disease reduction (100%) against all pathogens in various fruits, particularly excelling against *C. musae*. Overall, the study highlights *H. uvarum* LE-1's potential as a biocontrol agent against postharvest fruit pathogens, primarily through the emission of Trans-2-decenal. This research provides insight into alternative approaches for preserving fruit quality and safety, with implications for sustainable disease management. Further research and field trials are needed to ascertain practical applications and optimize these biocontrol strategies for wider implementation.

Biocontrol potential of *Beauveria bassiana* (Balsamo) Vuillemin against soil borne pathogens of chickpea

The biocontrol potential of four isolates of *Beauveria bassiana* BbR1, BbR2, BbR3, and BbR4 was explored against chickpea pathogens, *Fusarium oxysporum* f. sp. *ciceris, Rhizoctonia bataticola, Rhizoctonia solani, Sclerotium rolfsii,* and *Sclerotinia sclerotiorum*. All four isolates were found antagonistic against *Sclerotinia sclerotiorum* and the isolate BbR2 displayed highest inhibition percentage against stem rot of chickpea caused by *Sclerotinia sclerotiorum*. The hydrolytic enzyme production capacity of all isolates were studied to understand the mechanism of antagonism. Lipase activity was found to be the highest in isolate BbR2 whereas amylase, protease, and cellulase activity were found to be the highest in the isolate BbR4. In-planta stem rot disease suppression data indicated that average lesion length on the stems of chickpea treated with BbR2 was consistently smaller than that on non-treated seedlings across time intervals. The effect of seed treatment with spores of BbR2 on physiological and biochemical changes was monitored. All the parameters such as peroxidase, polyphenol oxidase, total phenol, and chlorophyll content, displayed a pattern of initial increase until 3 days post-inoculation, followed by a subsequent decline with time. Chemical profiling of secondary metabolites indicated that the area under various beauverolide compounds as well as other compounds like bassiatin, beauvericin and tenellin was relatively higher in BbR2 and BbR3 isolates compared to other isolates. These findings suggest that these bioactive metabolites may be potentially involved in the antagonistic interactions. The Minimum inhibitory concentration of secondary metabolites from BbR2 was estimated to be 4000 ppm. From the present study it can be concluded that *Beauveria* isolates have properties similar to many other biocontrol agents in suppression of chickpea stem rot disease caused by *Sclerotinia sclerotiorum*. Therefore, BbR2 of *B. bassiana* could be included in the biocontrol of stem rot disease of chickpea and may be included in integrated disease management practices.

Theme 4: Host pathogen interaction

Analysing upregulated rice transcriptomes involved in T3SS-effector mediated pathogenesis by *Xanthomonas oryzae* pv. *oryzae* during bacterial blight development

Bacterial blight (BB), incited by *Xanthomonas oryzae* pv. *oryzae* (Xoo) limits the rice productivity globally. The study analyzed RNAseq based transcriptome profiles of rice infected with an Indian virulent Xoo strain Race 4 relative to its T3SS-defective mutant strain (Xoo ΔhrpX) at early and late hours of bacterial infection. The study carried out Gene Ontology & Pathway analysis and identified plant defence related 42 transcription factors (TFs) and 10 peroxidase genes. The novel defence related DEGs were validated through RT-qPCR. Our transcriptomic data reveals upregulation of genes involved in defence signalling pathways, including leucine-rich repeats (LRR), transposons, serine/threonine-protein kinase, PR proteins, cytochrome P450, secondary metabolites. We also evident T3SS-dependent induction of susceptibility genes, SWEET 6A and 15. Here the study exploits Rice Tungro Bacilliform Virus (RTBV) based VIGS silencing system to functionally validate upregulation of OsRPM1 in rice following Xoo Indian race 4 infection. VIGS vector containing the gene of interest (OsRPM1) was successfully constructed and confirmed with colony and plasmid PCR using OsRPM1 gene-specific primers and sequential digestion by PacI and MluI restriction enzymes. Agroinfiltration of pRTBV-MVIGS-OsRPM1, pRTBV-MVIGS-PDS1 and empty vector determined the efficiency of VIGS phenotype by producing typical white streaks solely in PDS1 inoculated plants. Quantitative real-time PCR confirmed silencing by showing decreased transcript levels of OsRPM1 and PDS1 compared to non-silenced plants. Upon challenge inoculation with Xoo, OsRPM1 silenced plants exhibited enhanced susceptibility in terms of maximum blight lesion length and bacterial population, reduction in generation of reactive oxygen species (ROS) viz., O2 and H2O2 and number of callose papillae relative to non-silenced plants. The study proved the robustness and amenability of the RTBV-based VIGS vector in deciphering the functional role of DEGs involved in rice-Xoo interaction. The potential role of OsRPM1 as a positive regulator in Xoo resistance highlights it as a prospective resort for rice breeding with broad-spectrum/multiple disease resistance and bestows novel prescience for tailoring durable resistance.

Histopathological-cum-biochemical changes and expression of defense genes in *Brassica juncea* infected with *Albugo candida*

Rapeseed-mustard is an edible oil grown in India. *Brassica juncea* is having a lion's share (about 36%) in edible oil. Several biotic and abiotic stresses attack the *B. juncea*, out of which *Albugo candida* is a serious one. The continuous identification of resistant sources across the Brassica germplasm is important due to the faster development of virulent races in *A. candida*. In the present study, 60 genotypes were evaluated and complete resistant genotypes- AJ-34, 252025, DRMR-2035, Heera, Donskaja-IV, Basanti, Pusa Jaikisan WRR, Pusa Bold WRR, DTM-34, GSL-1 were found at two locations. The morpho-pathogenic, and molecular variability were conducted for 10 isolates of *A. candida* collected from various locations in India. Morphological study was based on shape and size of sporangia (14.6 x 17.5 µm to 20.3 x 22.6 µm) and shape also ranging from ellipsoidal to spherical. The biggest sporangia were found in Morena isolate (20.3 x 22.6 µm), while the smallest in Baran (14.6 x 17.6 µm)**.** Based on the genetic study, 7 clusters are suggested for the COX2 gene and 4 clusters on ITS region-based phylogenetic analysis. Histopathological studies showed various pathogen structures such as haustoria and sporangia and callose deposition as a marker of defense was also observed. Two cultivars, Pusa Jaikisan (susceptible) and Pusa Jaikisan WRR (resistant) were taken to various biochemical parameters and PR genes evaluated for resistance. Total protein content, POX, CAT, SOD, PPO, PAL, total polyphenols, total proline, chlorophyll, and carotenoids showed higher activity in Pusa Jaikisan WRR as compared to Pusa Jaikisan. Salicylic acid SA-marker genes (*PR1* and *PR2*) and JA/ET-marker genes (*PR3* and *PR12*) were taken and was observed *PR1* and *PR2* had higher expression at nearly all the time intervals in Pusa Jaikisan WRR, thus establishing their role in defense. *PR3* gave relatively higher expression in initial stages (12 and 24 hpi) and *PR12* also had higher expression in Pusa Jaikisan WRR as compared to Pusa Jaikisan. The findings hint toward complementation of JA and SA pathways rather than antagonism.

Investigations on the morpho-biological and biochemical alterations as influenced by groundnut bud necrosis orthotospovirus (GBNV) in tomato plants

Groundnut bud necrosis orthotospovirus (GBNV) has been creating havoc on tomato production in the Asian sub-continent, including India. Virus infections are known to alter the morphological features as well as biochemical constituents in plants leading to yield loss. Therefore, understanding the extent of yield loss due to GBNV infection in tomato plants linked with changes in the biochemical constituents helps to know its economic impact. In the present study, bud necrosis disease (BND) in tomato plants was induced using GBNV-Tom-Del isolate. The chlorotic ringspots and veinal necrosis symptoms appeared at 10-15 days post-inoculation. Subsequently, the data obtained on growth and yield attributing characters revealed that there were significant reductions in the plant height (61.12%), the total number of leaves/plant (75.71%), the total number of branches/plant (68.50%), the total number of flowers/plant (66.67%), total number of fruits/plant (54.73%), total fruit weight/plant (73.36%), individual fruit weight (48.08%), the total number of seeds/plant (66.84%), germination percentage (38.25%), fresh and dry weight of plants (75.47% and 69.77%, respectively) in diseased plants over control. Besides, there was an insignificant reduction in the total number of seeds/fruit (27.78%), however, the reduction in 100 seed weight was significant (78.43%). This was attributed to the size of seeds in the diseased seeds being less over control (size not measured). Biochemical studies revealed that there was a peak significant increase in the activities of superoxide dismutase (SOD) (68.31%), catalase (CAT) (75.30%), and peroxidase (POX) (88.65%) enzymes in diseased plants at 4dpi, 8dpi, and 8dpi and reduced gradually in the later stages over control plants. Besides, there was a significant reduction in total chlorophyll (75.00%), total carbohydrate (87.33%), and total protein (66.21%) contents in diseased plants over control. The present study culminated with the findings that the BND infection in tomato plants had a severe negative impact on growth and yield attributing characters and different biochemical macromolecules like chlorophyll, carbohydrates, and soluble proteins, whereas, significant dynamics in the levels of antioxidant enzyme activities.

Whole genome sequencing and molecular analysis of phytoplasma associated with sesame phyllody

The study brought to light the existence of distinct phytoplasma subgroups, namely 16SrI-B in Punjab, Madhya Pradesh, Rajasthan and Tamil Nadu and 16SrII-D in Delhi, emphasizing regional variations in phytoplasma populations. This regional understanding is pivotal for devising targeted management strategies to combat phytoplasma infections in sesame crops effectively. A notable observation is the limited genetic resistance observed among the surveyed sesame accessions. Out of the 254 samples studied, only 31 accessions exhibited a high level of resistance or immunity to phytoplasma infection. The study extended its scope beyond sesame plants to detect phytoplasma infections in various weeds as well as alternate crop species. This revelation implies the transmission of phytoplasmas from these reservoir hosts to cultivated crops, posing a substantial risk to sesame production. Efficiency experiments highlighted leafhoppers (*Hishimonus phycitis* and *Orosius albicinctus*) and dodder as significant contributors to phytoplasma transmission, with high rates ranging from 60% to 95%, respectively. Wedge and leaf disc grafting methods exhibited transmission efficiency of >75% compared to plug and patch grafting (30%). Genome-level analysis and identification of effector molecules were also conducted. Whole genome sequencing of a prokaryotic-enriched sample revealed a genome with 98.76% similarity to the *Ca*. Phytoplasma aurantifolia strain WBDL reference genome. Identification of effector molecules contributes to understanding how these pathogens manipulate host cellular processes, aiding in disease development in sesame plants. In conclusion, this study significantly advances our comprehension of phytoplasma infections in sesame crops, providing a foundation for targeted management strategies. Ongoing research into insect incidence in different seasons and the role of effector molecules will further enhance our understanding, promoting sustainable disease management practices in sesame cultivation and ensuring agricultural sustainability in sesame-cultivating regions.

List of Contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Degree M.Sc/ Ph.D	Title of the thesis	Chairperson	Institute
1	Netra Kallegoudra (21689)	M.Sc.	Morpho-molecular characterization of *Fusarium solani* species complex (FSSC) associated with root rot of tomato and development of Loop mediated isothermal amplification (LAMP) assay for rapid detection of major FSSC	Dr. Deeba Kamil	ICAR-IARI, New Delhi
2	Manoj P N (1690)	M.Sc.	Assessment of bioagents against *Fusarium graminearum* causing head blight of wheat and identification of resistance sources	Dr. M. S. Saharan	ICAR-IARI, New Delhi
3	Elora Priyadarshini (21691)	M.Sc.	Functional characterization of the metabolome of a phyllobacterial consortium for the suppression of rice blast disease	Dr. A. Kumar	ICAR-IARI, New Delhi
4	Pratibha Murmu (21692)	M.Sc.	Identification and Characterization of effective metabolite from biocontrol strain of yeast *Hanseniaspora uvarum* (LE 1) and their evaluation in the post-harvest disease management	Dr. Amrita Das	ICAR-IARI, New Delhi
5	Ambalavanan. A (21693)	M.Sc.	Identification and characterization of NLR candidate genes in pearl millet (*Cenchrus americanus* (L.) Morrone) for foliar blast resistance	Dr. G. Prakash	ICAR-IARI, New Delhi
6	Poulami Basak (21694)	M.Sc.	Characterization of *B. sorokiniana*, transcriptome profiling and assessment of bioagents against spot blotch of barley	Dr. Malkhan Singh Gurjar	ICAR-IARI, New Delhi
7	Ayesha Siddiqa (0112)	M.Sc.	Characterization, diversity analysis of *Clavibacter michiganensis* subsp. *michiganensis* and evaluation of resistance source against bacterial canker of tomato	Dr. Dinesh Singh	#ICAR-IARI, Jharkhand
8	Cheruku Roshini (60113)	M.Sc.	Biocontrol potential of *Beauveria bassiana* (Balsamo) Vuillemin against soil borne pathogens of chickpea	Dr. Tusar Kanti Bag	#ICAR-IARI, Jharkhand
9	Lokesh G (60114)	M.Sc.	Investigations on the morpho-biological and biochemical alterations as influenced by groundnut bud necrosis orthotospovirus (GBNV) in tomato plants	Dr. Basawaraj	#ICAR-IARI, Jharkhand
10	Prajjwal Rai (80025)	M.Sc.	Histopathological-cum-biochemical changes and expression of defense genes in *Brassica juncea* infected with *Albugo candida*	Dr. Lakshman Prasad	**ICAR-NIBSM, Raipur
11	Manoj N S (80026)	M.Sc.	Screening finger millet germplasm and potential bacterial antagonists against sheath blight caused by *Rhizoctonia solani* Kühn	Dr. Sanjay Kr. Jain	**ICAR-NIBSM, Raipur
12	Gopi Kishan (10700)	Ph.D.	Virome analysis of grapevine (*Vitis vinifera* L.) cultivars and detection of important grapevine viruses using rapid and specific assays	Dr. V. K. Baranwal	ICAR-IARI, New Delhi

13	Oinam Washington Singh (11087)	Ph.D.	Determination of efficacy of plant surface applied nanocarrier conjugated RNA against begomovirus infection	Dr. Bikash Mandal	ICAR-IARI, New Delhi
14	Amrutha Lakshmi M (1090)	Ph.D.	Analysing upregulated rice transcriptomes involved in T3SS-effector mediated pathogenesis by *Xanthomonas oryzae* pv. oryzae during bacterial blight development	Dr. K. K. Mondal	ICAR-IARI, New Delhi
15	Naveen Nayaka S (11308)	Ph.D.	Diversity and infectivity of begomoviruses in major cucurbits in India	Dr. Bikash Mandal	ICAR-IARI, New Delhi
16	Manoj Kumar Yadav (11311)	Ph.D.	Genome characterization of cowpea mild mottle virus, its temperature dependent symptom expression and resistance mining in soybean	Dr. V. K. Baranwal	ICAR-IARI, New Delhi
17	Hemavati Ranebennur (11314)	Ph.D.	Whole genome sequencing and molecular analysis of phytoplasma associated with sesame phyllody	Dr. V. K. Baranwal	ICAR-IARI, New Delhi
18	Pankhuri Singhal (11567)	Ph.D.	Virome analysis for identification and characterization of virus(es) associated with mosaic disease of mustard	Dr. V. K. Baranwal	ICAR-IARI, New Delhi
19	Lham Dorjee (11572)	Ph.D.	Determination of the synergistic effect of essential oil-grafted CuNPs against maize pathogens and its influence on defense gene induction in maize	Dr. Robin Gogoi	ICAR-IARI, New Delhi
20	Nishmitha K (11573)	Ph.D.	Isolation, characterization and molecular cloning of potential resistance gene analogues from lentil germplasm against Fusarium wilt	Dr. Deeba Kamil	ICAR-IARI, New Delhi
21	Manikandan K (11575)	Ph.D.	Characterisation of *Fusarium* spp. and Vascular Wilt Resistance of Brinjal (*Solanum melongena* L.)	Dr. V. Shanmugam	ICAR-IARI, New Delhi
22	Pedapaudi Lokesh Babu (11578)	Ph.D.	Identification, diversity analysis for races of *Xanthomonas* associated with bacterial leaf spot and development of multiplex PCR for seed borne bacterial pathogens of tomato and pepper	Dr. Dinesh Singh	ICAR-IARI, New Delhi
23	Sreenayana B (11835)	Ph.D.	Characterization of virulence-associated genes and evaluation of novel management options for *Burkholderia glumae* causing panicle blight of rice	Dr. K. K. Mondal	ICAR-IARI, New Delhi

#IARI off campus

**Outreach Institute

Session III: School of Natural Resource Management

Thesis Summary

Discipline	Number of Thesis Submitted	
	M. Sc./M. Tech	Ph.D.
Agricultural Engineering	15	36
Agricultural Physics	04	08
Agronomy	19	20
Environmental Sciences	11	06
Microbiology	10	05
Soil Science and Agricultural Chemistry	11	15
Water Science and Technology	05	09
Total	**77**	**99**

SCHOOL OF NATURAL RESOURCE MANAGEMENT

Convenor: Dr. Monika A. Joshi, Professor, Division of Seed Science & Technology
Co-convenor: Dr. Shruti Sethi, Principal Scientist, Division of Food Science & Post harvest Technology

Chairperson: Dr. Gurbachan Singh, Former Chairperson, ASRB, New Delhi

Dr. Gurbachan Singh is currently the Chairman, Gurbachan Singh Foundation for Research, Education and Development (GSFRED) and Vice Chairman, TAAS, New Delhi and has earlier served as Chairman, ASRB, New Delhi; Agriculture Commissioner, Government of India; Director, CSSRI, Karnal; and ADG, ICAR, New Delhi. He has been an active researcher nearly for 20 years at CSSRI, Karnal where he developed a low cost, eco-friendly fuel wood and forage production technology for bio-amelioration of salt-affected soils through which more than 2 million hectare of salt land has been reclaimed. Dr. Singh's thought provoking exemplary work on development of integrated farming system model and ground water recharge research received Best Research Institute Award by ICAR and also the Ground Water Augmentation Award of Union Ministry of Water Resources. As Union Agriculture Commissioner, he coordinated agriculture development all over the country leading to 15% increased pulse production in one year. Dr. Singh has developed and implemented several national and international consultancies and projects. He is a recipient of Rafi Ahmed Kidwai Award, Hari Om Ashram Trust Awards of ICAR and Dr. M. S. Randhawa Memorial Award. Dr Singh has headed high level Indian delegations to meetings at FAO, BRICS and CG centres and is a distinguished fellow of National Academy of Agricultural Sciences (NAAS), Honorary Fellow of Indian Academy of Horticultural Sciences, Honorary Fellow of Arid Zone Association of India and Honorary Fellow of Indian Society of Soil Salinity and Water Quality plus fellowship of five other scientific societies. Dr. Singh also served as Chief Editor of Indian Journal of Agricultural Research; Honorary Member of Editorial Board of International Journal, Experimental Agriculture, UK and reviewer of more than 10 international journals.

Agricultural Engineering

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Prof. A.K. Mishra

The Division of Agricultural Engineering has the mandate to conduct advance research on development of precision machines/equipment and technologies in the area of farm power and machinery, precision agriculture, post-harvest engineering and structures, renewable energy and resources, protected cultivation, soil and water conservation engineering etc. It is instrumental in conducting graduate and post graduate teaching and research in three sub-disciplines viz.; Farm machinery and Power Engineering, Agricultural Structures and Process Engineering and Soil and Water Conservation Engineering. The Division is also engaged in commercial testing of farm tools/machines through a National Level Testing Centre, prototype production and supply of improved farm equipment under revolving fund scheme of the institute, skill development/ training to farmers, technicians and rural artisans, extension workers and subject matter specialist etc. in Agricultural Engineering. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Resource Conservation Technologies

Design and development of urea super granule (USG) application system integrated to paddy transplanter

An Integrated USG Applicator System for Paddy Transplanter was successfully designed and developed. In this study, a novel approach was explored, involving the coating of USGs with different materials as a vital nitrogenous fertilizer that significantly boosts paddy yields addressing challenges associated with urea application. The coated USGs application system integrated into the paddy transplanter, aimed to reduce the costs and enhance Nitrogen Use Efficiency (NUE). Optimized proportions for coating materials were determined to ensure efficient nutrient release. Using HYDRUS-2D software, nitrogen dynamics were simulated in various soil types, and optimal placement depths for the coated USGs were identified. The design of the USG applicator system integrated into the paddy transplanter considered soil types coated USG types, and machine parameters. The metering system parameters were optimized using EDEM-RSM techniques and validated through soil-bin laboratory studies, resulting in a well-performing system. The retrofitted system, based on the optimized design values, was evaluated in the field. Performance parameters, including theoretical field capacity, actual field capacity, field efficiency and field machine index, were observed. Energetic and ergonomic evaluations indicated a reduction in associated risks and an energy-saving of 7.58 kcal min^{-1}. The total cost of the USG applicator was estimated at ₹ 9420/-, with a break-even and payback period of 119 h year^{1} and 1.5 years, respectively. The optimized system demonstrated improved efficiency, reduced risks, and economic viability, making it a promising solution for enhancing paddy yield while minimizing costs and labour.

Development of a device for assessment of paddy lodging characteristics

A microcontroller-assisted portable device was developed for in-situ measurement of lodging of paddy. The challenge of crop lodging in field crops necessitates a scientific approach for quantifying lodging susceptibility in crop varieties. This issue is particularly critical in paddy and cereal crops, where lodging can result in substantial yield losses, reaching up to 50%. Stem strength is a vital indicator of crop health and lodging resistance, but field measurement is challenging. A survey and field observations on 20 paddy varieties were conducted, revealing significant effects of physical characteristics on stem strength and lodging susceptibility. The device comprises a plant stalk holder featuring a measuring system with a plant pushing unit. Additionally, it includes a data processing and storing system fortified with a micro-controller, and a rechargeable battery as a power source. This innovative system offers two visual display aids for monitoring real-time force and displacement changes on a graph, along with quantitative parameters. This device enables non-destructive strength measurement of individual plant tillers in paddy crop, ensuring minimal harm to the crop. Moreover, the device is designed to support IoT-enabled features, enhancing its adaptability and functionality. The device affords better-measuring intensity (less than 20 seconds per measurement) of about 180 to 240 measurements per hour. By making three significant observations per plant tiller, the device can measure around 60 to 80 plant tillers hourly, allowing for the evaluation of 480 to 640 plant tillers regarding their strength properties in a day. The developed device demonstrated comparable accuracy to a Texture analyser in measuring crop stem strength, showing a statistical correlation of 0.9 and a regression coefficient of 0.8 during field trials on 13 crop varieties. This technological device also opens avenues for further research and development in crop improvement, allowing breeders to incorporate necessary traits in existing varieties or develop new ones.

Studies on effect of tool geometry and operational parameters on soil failure in vertisols

Tillage, an energy-intensive agricultural operation, has led to various design enhancements aiming to reduce draft requirements and achieve optimal soil disturbance for different tillage tools in vertisols. The rupture width was measured using an image processing technique ($R^2 = 0.996$). Within the test range of tool width, CI, operating speed, and depth, the minimum and maximum draft requirements were found to be 196.5 and 1303.6 N; 132 and 875 N for the sweep and reversible shovel tool, respectively. Similarly, the minimum and maximum rupture widths were found to be 289 and 553 mm; 172.3 and 377.3 mm for sweep and reversible shovel tools, respectively, within the tested range of selected variables. The response surface methodology (RSM) and artificial neural network (ANN) models were developed and compared to be with other classical and numerical models to predict their draft and rupture width for tillage tools. A quadratic RSM model was found to be best suited for the draft ($R^2 = 0.96$) and rupture width ($R^2 = 0.98$) prediction of sweep tools among linear, interactive, quadratic, and cubic models. Similarly, a quadratic and two-factor interaction RSM model ($R^2 = 0.98$) was best suited to predict the draft and rupture width of reversible shovel tools, respectively. Overall, both ANN and RSM models predicted the draft and rupture width within an error of ± 5%. Field validation of the optimized solutions showed absolute percentage differences between optimized and field draft measurements for tillage tools, ranging from 4.81% to 10.68%. Likewise, rupture width measurements demonstrated values from 4.53% to 8.01%.

Studies on the development of retrofit seeding attachment for combine harvester

A retrofit seeding attachment for a combine harvester was designed and developed to achieve precision seeding in a no-till-residue condition during combine harvesting. Based on the range of the average physical and engineering properties of black gram and green gram seeds, a plate groove diameter of 4 to 6 mm was sufficient for dropping one seed per hill. The hopper volume and wall slope were calculated to be 0.0022 m^3 and 53.5^0, respectively, to meet the requirement of sowing one hectare of land in asingle operation while ensuring the smooth flow of seeds. The microcontroller-based seed metering mechanism was developedand tested for three forward speeds (1.5, 2, and 2.5 km h^{-1}), three groove diameters (Ø) (D1: 20%more seed Ø; D2: 10% more seed Ø; D3: average seed Ø), and two crop types (black gram and green gram). From the analysis of performance parameters, a mean seed spacing of 9.47 cm, minimum multiple indexes of 2.5%, highest quality feed index and lowest miss index of 90.1% and1.28, respectively, were observed at a forward speed of 1.5 km h^{-1} and plate groove diameter of D2. Three types of furrow openers (single disc, double disc and Inverted T-type with plain rollingcoulter) were developed. Soil bin studies were conducted to assess the impact of furrow openers, three forward speeds (1.5, 2, and 2.5 km h^{-1}), and three straw densities (1, 2, and 3 t ha^{-1}) on draftforce requirements and straw cutting efficiency. Inverted T-type furrow opener with a rolling coulter, operating at a forward speed of 1.5 km h^{-1}, demonstrates the highest straw-cutting efficiency of 85.64%, leading to its selection as the optimal tool and condition for no-till straw conditions. A prototype retrofit seeding attachment for a combine harvester was developed and evaluated in the field condition. The performance parameters were measured, including seed placement index (SPI), seed spacing, and germination percentage. The average seed spacing of 10.18 cm, along with the highest SPI and germination percentages of 85.29% and 94.2%, respectively, were observed at a forward speed of 1.5 km h^{-1}. Moreover, the prototype operation at this speed results in an average field capacity of 0.51 ha h^{-1}, a field efficiency of 78.95%, and fuel consumption of 18.2 liters. The estimated break-even point (BEP) and payback period (PBP) are 193 h yr^{-1} and 3.9 yrs, respectively. Based on the results, it was concluded that a retrofit seeding attachment for a combine harvester with an electronic metering mechanism leads to greater precision in seeding and enables the simultaneous execution of sowing and harvesting in a no-till residue condition.

Prediction of the soil properties using artificial intelligence

This study harnessed the power of the machine and deep learning techniques, aiming to predict soil properties from pre-processed soil images in Precision Soil Mapping. Agriculture is pivotal for India, serving as the backbone of its economy by employing over 50% of the workforce. Evolving over time, it has vastly improved resource efficiency and profitability. As the world eyes the "Agricultural Digital Revolution," precise soil mapping becomes crucial to meet global food demands. Precision farming relies on detailed soil insights for tailored practices, optimizing yields and promoting sustainability by aligning with soil needs. Soil testing in precision farming is pivotal, offering crucial insights into composition and health, optimizing nutrient application and irrigation. Traditional testing methods are slow and expensive. Digital soil testing, employing sensors and AI technologies like machine learning, promises rapid, scalable, and precise analyses. Soil pH and EC (Electrical Conductivity) testing are fundamental in precision farming. They provide critical insights into soil health and nutrient availability, enabling farmers to tailor agronomic practices for optimal crop growth, enhance nutrient utilization, and ensure sustainable soil management, ultimately leading to increased yields and cost-efficiency. Four AI models were explored: Support Vector Machine, K-Nearest Neighbours, Decision Tree, and Convolutional Neural Network. KNN outperformed SVM and DT in predicting soil pH and EC, achieving moderate accuracies of 61.9% and 65%, respectively, with fair efficiency in class differentiation. The CNN model exhibited 65% accuracy in predicting soil pH and an impressive 68.3% accuracy in predicting soil EC, showcasing its competence in classification. While all models provided valuable insights, the CNN model's precision underscores the increasing relevance of machine learning in agriculture and soil management. However, there is a discernible space for future improvements in optimizing these models for enhanced prediction accuracy.

Kinetic study on step pyrolysis of biomass

This study was conducted to analyze the benefits obtained in the products derived from step pyrolysis (SP), qualitatively, thermally, and kinetically. Step pyrolysis targets to the thermal degradation of individual bio-constituents based on their temperature ranges. Pigeon pea stalk (PPS) was selected as the experimental biomass for implementing the concept of step pyrolysis. To diagnose the thermal behaviour of PPS, thermogravimetric analysis was conducted at four different heating rates 10, 20, 30, and 40°C/min. A laboratory-scale reactor having capacity of 1 kg of chaffed PPS was developed. In the developed pyrolytic system, step pyrolysis as well as traditional pyrolysis (TP) was carried out by controlling the temperature, time, and heating rate. The adsorption indices elucidated a reduction in methylene blue values (15-25%) and an increase in iodine number (4-38%) due to processed by SP method. Based on the TGA data of a specific sample, kinetic parameters were calculated by using four iso-conversional methods (FWO, KAS, Starink, and Tang). A remarkable reduction was registered in average activation energy (from 11.5 to 33.7%) of SP method-based char (SP-char) over the product generated from TP method (TP-char). An increment in the estimated value of ΔG (3-5%) at comparatively higher heating rate (30 and 40 °C/min) and the decrement at lower heating rate (10 and 20 °C/min) was observed. Another hand, a decrement on estimated value of ΔH (from 11 to 33%) and ΔS (from 1 to 7%) were registered for SP-char over TP-char. The obtained results reflected that the SP-char had a better thermodynamic balance than the TP-char. Based on the findings of the study; it can be concluded that by using the step pyrolysis method a better-quality product can be generated.

Design and development of a battery-operated harvester for leafy vegetables

This study served as the foundation for determining the design parameters of a leafy vegetable harvester, including power requirements and cutting mechanisms. A cutting force measuring setup was created, incorporating a 1-inch angle iron, a double-acting cutter bar with multiple cutting knives, a digital LCD display, an S-type load cell, and a crop holding unit. The cutting force and cutting energy are observed at the lowest cutter bar speed with the highest number of petioles i.e., 15.68 N and 1354.7 N-mm respectively at 0.25m/s and 12 spinach petioles. Minimum cutting force and cutting energy are observed at the highest cutter bar speed with the lowest number of petioles i.e., 4.93 N and 141.9 N-mm respectively at 0.53 m/s and 8 spinach petioles. Cutting speed was inversely proportional to cutting force and cutting energy. After optimizing the parameters for cutting force in all three crops, the first two crops that demonstrated the highest cutting force were selected for further experimentation. The essential parts of the battery-operated leafy vegetable harvester are the reel, cutter bar, conveyor belt, drive wheel, front wheel, collecting box, baffle plate, handle, and electronic box. All these parts were fabricated and mounted on a chassis with provision for mounting batteries. The field evaluation showed a field capacity of 0.061 ha/h for spinach and 0.087 ha/h for fenugreek, with field efficiencies of 75.8% and 80.78%, respectively. The developed harvester demonstrated an efficiency of 86.6% in spinach and 91.15% in fenugreek, resulting in actual productivity rates of 215 kg/h and 414.8 kg/h, respectively. The drive wheel, reel, conveyor, and cutter bar had backup times of 1.542 hours, 1.05 hours, 0.84 hours, and 0.75 hours, respectively. In spinach, the power requirements for the drive wheel, reel, conveyor, and cutter bar were 187 W, 40.32 W, 134.4 W, and 61.56 W, resulting in a total power requirement of 423.28 W. In fenugreek, the power requirements were 235.6 W, 27.6 W, 134.4 W, and 42.14 W, resulting in a total power requirement of 439.7 W.

Development of paddy drum seeder-cum-fertilizer applicator

A four-row manual-operated paddy drum seeder-cum-fertilizer applicator was developed using 3-D printing technology for fabricating a complex drum seeder. The drum of the seeder comprises two truncated seed chambers and a central cylinder chamber for efficient seed and fertilizer application in two rows. The printing process involves printing of 14 components such as square guides for the drive shaft, truncated conical and cylindrical chambers, hoppers, lids, and orifice covers for each chamber and takes printing duration of 40 hours. Four-row paddy drum-seeder-cum-fertilizer applicator effectively addresses key challenges by integrating fertilizer application with the drum-seeding process using. The cost of fabrication of 3-D printed drums was Rs. 3290.4 which is 40% of the total cost of equipment. The cost of operation of a paddy drum seeder-cum-fertilizer applicator per hectare is 2.55 times less than the earlier reported cost of operation with a four-row paddy drum seeder. During performance evaluation the seed and fertilizer rate achieved was 43 kg ha^{-1} and 75 kg ha^{-1}, respectively and were close to theoretical recommendations. The area covered was 0.0945 ha h^{-1} at operating speed of 1.1 km h^{-1} with 85.9 % efficiency.

Study on optimization of geometrical and operational parameters of rotary tiller blades for efficient utilization of power in vertisols

The rotary tiller is the most widely used active tillage tool for seedbed preparation. In India, 'L'-shaped blade is the commonly used blade shape on rotary tillers. This experiment was performed with varying blade sweepback angles (0°, 6°, 12°, 18°), rotational speeds (200 rpm, 250 rpm, 300 rpm), depths (20 mm, 50 mm, 80 mm), and at a constant forward speed of 0.21 m s^{-1} (0.75 km h^{-1}). Optimization of the geometrical and operational parameters was performed for selected rotational speeds and depths with sweepback angle (0°, 6°, 12°, 18°) and forward speeds (0.3 km h^{-1}, 0.75 km h^{-1}, and 1.2 km h^{-1}) as independent parameters and i.e., power requirement, tangential cumulative contact energy, normal cumulative contact energy, disturbance intensity and mixing index. as dependent parameters. The performance of optimal and conventional L-shaped blade was compared in both soil bin and field. The calibrated values of yield strength (soil), coefficient of friction (soil-soil), coefficient of friction (soil-steel), energy density, and stiffness factor were found to be 1×10^6 Pa, 0.68, 0.35, 20 kJ, and 0.7, respectively. The average penetration torque experienced by the blades with sweepback angles of 6, 12 and 18° were 7.17, 14.71 and 20.94% lower than the blade with sweepback angle of 0°. The velocity vectors of soil particles for all blades showed a two-stream pattern of soil throwing. The outcomes of DEM single flange experiment revealed that all independent parameters had significant effect on all dependent parameters. The optimized values of rotational speed, sweepback angle, forward speed and depth were 236 rpm, 16°, 1 km h^{-1} and 39 mm, respectively. The comparative soil bin experiments revealed that the power required by the optimal 'L' blade was 17.35% lower than the conventional 'L' blade. In field tests, blade optimal 'L' blade outperformed the conventional 'L' blade in terms of power requirement, pulverization index and fuel consumption. The blade optimal 'L' blade had 16.48% less power requirement, 7.68% greater pulverization index and 14.16% less fuel consumption as compared to conventional 'L' blade, across all forward speeds and can be used to reduce the power requirement in Vertisols.

Design and development of mustard thresher for seed purpose

Mustard crops are typically harvested manually using sickles and then taken to a threshing yard. Existing commercial threshers were designed for threshing the crops for consumption purposes rather than for seed. To design an efficient thresher for seed purpose, engineering properties of mustard seed and pod, varying at 6% and 9% moisture content (wb) were studied. A thresher with a capacity of 20 kg h^{-1} was chosen, featuring two fabricated threshing units: shear and impact type, and shear type. The shear and impact type unit included a 130 mm diameter threshing cylinder rotating at 500 rpm, a 160 mm diameter concave, and a 260 mm long threshing cylinder. The shear-type unit had a 5 cm diameter and 250 mm long roller, with lower and upper roller assemblies, each comprising four rollers spaced 50 cm apart. Mounted on a 910×510×910 mm frame, the thresher's performance was evaluated using Box-Behnken experimental design for operational parameter optimization. For the shear and impact type unit, results showed threshing efficiency, cleaning efficiency, broken seed loss, sieve loss, and germination percentage at 99.89%, 98.94%, 0.83%, 0.36%, and 99.32%, respectively. The shear-type unit demonstrated 99.6%, 98.94%, 0.77%, 0.38%, and 99.45% for the same parameters. Optimization of the shear type involved a cylinder speed of 300 rpm and concave clearance of 12.09 mm, while the shear-type had a roller speed of 300 rpm, 13.35 mm belt clearance, and blower speed of 1499.99 rpm. The shear-type threshing unit showed high threshing efficiency (98.89%), cleaning efficiency (98.99%), germination percentage (99.38%), and low broken grain loss (0.61%) and sieve loss (0.39%) at the optimized parameters. The developed thresher's total cost was Rs. 44,194, with an operating cost of Rs. 138.16 per hour. For 100 kg of output, the cost was Rs. 690.8. The thresher's break-even point was 212.7 hours per year, and it had a payback period of 3.9 years.

Theme 2: Precision Farm Equipment

Development of sensor-based weed detection and herbicide application system

An image sensor-based herbicide system was developed for inter-row crop weed control, integrating a webcam-based weed detection system and variable-rate herbicide application using MATLAB and Arduino. The webcam and RGB algorithm calculate weed density as a percentage of green area in images, offering precise weed estimation. Under uncontrolled conditions, the weed detection algorithm achieved an average correct classification rate of 95.18% for weeds and 94.17% for soil, with a processing time of 0.5 s. Controlled conditions yielded correct classification rates exceeding 96.67%. The variable-rate herbicide application system, tested in the laboratory, exhibited an average error in the angle of rotation of the valve stem and discharge of 0.31 and 1.72%, respectively. Integration of both systems, calibrated for different rates against the percentage of green area, was achieved using MATLAB and Arduino. Field evaluations demonstrated the prototype's efficiency, chemical savings (up to 75.64%), and ergonomic feasibility. The prototype's design values included a 50 cm spray width, 63 cm webcam height, 30 cm nozzle height, 38.9 cm distance between camera and nozzles, 2 kg cm^{-2} spray pressure, and 2 km h^{-1} forward speeds. Under field conditions, the prototype exhibited a weeding efficiency of 91.26%, an application rate of 301.64 l ha^{-1} in variable mode compared to 91.57% and 507.6 l ha^{-1} in constant rate mode, with chemical savings of 40%. The entire system demonstrated a field efficiency of 63.4% and field capacity of 0.063 ha h^{-1}. Moreover, ergonomic analysis indicated a significant reduction in heart rate, energy expenditure, and workload compared to manual operation at 2.0 km/h. The prototype has potential for use in crops such as maize, pigeon pea, and soybean, aiming to reduce environmental risks and ease farmers' workload. This technology aims to improve yields and lower cultivation expenses by tackling herbicide overuse effects.

Investigations on microcontroller-based precise fertilizer dispensing system for spot application in widely spaced crops

Fertilizer application is vital for crop production. The current scenario demands precise use of chemical inputs in crop cultivation. However, manual methods used for applying fertilizer in widely spaced crops require more labors. Furthermore, the available machinery for fertilizer application by broadcasting/banding results in wastage of fertilizer, contributing to environmental pollution. Therefore, this study was undertaken to minimize fertilizer wastage and drudgery through sustainable production, achieved by precisely applying fertilizer near plants. The physical and mechanical properties of granular DAP and SSP were determined. A new metering mechanism with grooved belt was developed. A sensor selection study was conducted and ultrasonic sensor (3.4% detection error and 0.203 s response time) was selected for automatic plant detection system. The developed spot fertilizer applicator was evaluated in laboratory for optimization of operational and machine control parameters i.e., groove volume (50, 100 and 150 cm^3), plant spacing (450, 600, 750 and 900 mm), metering belt speed (8, 9 and 10 m.min^{-1}) and forward speed (2.0, 2.5 and 3.0 km.h^{-1}). The values of band length, band width, fertilizer placement inside and outside were 203.43, 110.98, 101.05 and 212.71 mm, respectively at the optimized groove volume (50 cm^3), plant spacing (450 mm), belt speed (10 m.min^{-1}) and forward speed (3 km h^{-1}). There was no significant difference between actual and measured fertilizer application amount (variation <4.15%). The developed spot fertilizer applicator was evaluated in guava (2×2 m) and mango (3×3 m) orchards with optimized groove volume and metering belt speed at three different forward speeds (2.0, 2.5 and 3.0 km.h^{-1}). Average field capacity and field efficiency were 0.59 ha.h^{-1} and 79%, respectively for mango field. The operation cost of the developed machine was 536 ₹. ha^{-1}. The machine reduced operating cost and time by 97 and 50%, respectively as compared to manual ring basin method.

Design and development of automatic control system for agricultural tractor

In India, where small and marginal land holdings constitute 86% of total operational land, the reliance on small tractors is pivotal for agriculture, covering 47% of the cropped area. These compact tractors, adept at navigating narrow and uneven farm pathways, cater to the prevalent small and fragmented landholdings. However, frequent gear changes, clutch and brake pedal operations, and steering adjustments in the limited workspace of small tractors impose significant physical and mental strain on operators, affecting productivity. To address these challenges, an automatic remote-controlled system for tractors was developed. Actuating force requirements for various transmission controls were measured during field operations, revealing maximum forces for the clutch, brake, accelerator, driving shift gear, and range shift gear levers. Finite element modeling assessed vibration characteristics transmitted through different body segments of the operator during tractor operations. The study informed the design and development of automatic actuating mechanisms for the remote-controlled system, encompassing brake, clutch, gear, accelerator, and steering control. Electronic control units and PID-based control algorithms were implemented for each mechanism, with optimization through response surface methodology. An integrated artificial neural network (MLPNN) and PID-based algorithm were devised for brake control, exhibiting high accuracy in predicting sensor digital output and deceleration. The developed automatic remote-controlled system demonstrated successful laboratory evaluation, with each control system following desired positions. Field evaluation on asphalt roads at various speeds exhibited increased response times with higher tractor speeds. The system's overall cost was estimated at ₹54,000, with an operating cost of ₹104 per hour. The break-even point and payback period were determined at 182.23 hours per year and 1.85 years, respectively, showcasing the potential for revenue generation and return on investment.

Studies on systems for harvesting of cabbage

Cabbage is an important leafy vegetable and cultivated worldwide. The farm operations in cabbage cultivation such as raising seedlings and seedbed preparation are almost mechanized. However, transplanting, weeding and harvesting are still carried out manually. This study has been undertaken to mechanize the cabbage harvesting operation to minimize associated labour, drudgery and ensure timeliness of operation. The physical and mechanical properties of cabbage variety *Syngenta BC-79* were measured at maturity stage. Laboratory set-ups were developed to investigate the effect of constructional and operational parameters on cutting and conveying of cabbage crop. The different cutting disc blades (smooth, serrated and teethed) were evaluated individually in terms of cutting torque and power requirement at blade speeds (3.93, 5.52, 7.85, 10.18 and 11.78 m.s^{-1}), forward speeds (1.5, 2.0, 2.5, 3.0 and 3.5 km.h^{-1}) and stem diameters (20, 24, 30, 36 and 40 mm). The conveyor belts such as flat, flat belt with cleated lug and flat belt with rounded head lug were evaluated individually in terms of conveying efficiency and power requirement at inclination angles (15, 25 and 35º) and belt speed ratios (1:1.1, 1:1.2 and 1:1.3). The serrated blade was selected for cutting mechanism based on minimum cutting torque (9.4 Nm) and power requirement (0.87 kW). The flat belt with rounded head lug was selected based on maximum conveying efficiency (96.5%) and minimum power requirement (138 W). The average cutting, conveying and harvesting efficiency of developed harvester were 97%, 95% and 92%, respectively, with total harvesting loss of 10.6 per cent. The average effective field capacity and field efficiency of the harvester were 0.08 $ha.h^{-1}$ and 67%, respectively. The cabbage harvester reduced the operating cost and time by 51% and 95%, respectively as compared to manual method of harvesting.

Design and development of sensor-based multiple-input application system for seeder

Precision agriculture, involving the meticulous application of different inputs like seeds, fertilizers, water, and pre-emergence herbicides, is integral to modern farming. The rate of application of selected inputs were varied as per forward speeds of operation for simultaneous application of seed, fertilizer, water and pre-emergence herbicide using electronically controlled metering system. The present study on design parameters of individual metering systems of a seeder was undertaken to design sensor based multiple input application system for seeder. The seed cum fertilizer metering system for wheat was designed with a 6.0 kg hopper capacity. A stepper motor, regulated by a motor driver, controlled the fluted roller speed. In the water metering setup, the 3-way bypass valve's opening was accurately adjusted by the servo motor, aligning it with the forward speed and precisely controlling the water amount. The maximum discharge rate of 6.42 lpm was observed at a 90° rotation angle and 0 kg cm^{-2} operating pressure. Only one solenoid valve operated within the speed range of 0-2.0 km h^{-1}, while both operated at speeds of 2.0 km h^{-1} and above. In the case of pre-emergence herbicides metering, an experimental setup and spray patternator were used to observe the effect of operational parameters like forward speed (1.5, 2.0, and 2.5 km h^{-1}) and operating pressure (1.5, 2.5, and 3.5 kg cm^{-2}) on selected nozzle types. The discharge rate of the air-injector flat spray nozzle ranged from 1.03 lpm to 2.42 lpm, the air-injector flat spray compact nozzle ranged from 0.8 lpm to 1.4 lpm, and the pre-emergence flat spray nozzle ranged from 1.02 lpm to 1.73 lpm with an increase in pressure. With an increase in forward speed, VMD, droplet density and the homogeneity factor decreased. The sensor-based multiple-input application system able to apply all selected inputs i.e., seeds, fertilizers, water, and pre-emergence herbicides simultaneously as per forward speed of the Seeder.

Design and development of precise intelligent cauliflower harvester

India, the second-largest global cauliflower producer, faces challenges with manual harvesting, which constitutes up to 50% of total production costs. The manual method is labour-intensive, time-consuming, and physically demanding, requiring around 100 man-h per ha. This becomes economically unfavourable due to increased labour costs and scarcity. To overcome these challenges, efforts focused on developing a precise intelligent cauliflower harvester. Two cauliflower cultivars, Pusa Meghna and Pusa Sharad, were studied for physical properties, and design values for various harvester components were determined based on these measurements. The developed harvester integrates a maturity detection unit, actuating arm unit, cutting unit, and cutting height adjustment unit. The maturity detection unit, employing an RGB camera, achieved a segmentation performance of 70.83% recall, 99.37% precision, and 99.08% accuracy. It detects cauliflower head maturity based on size using the chromatic aberration method. The cutting unit, equipped with a 30 cm cutting chain and guide bar, demonstrated optimal cutting force, splitting failure, and cutting time when cutting the stem at a distance of 15 mm from the curd bottom with specific parameters. The actuating arm unit rotates the cutting unit for selective harvesting. The development of a precise intelligent cauliflower harvester represents a significant step towards enhancing the efficiency and sustainability of cauliflower production in India.

Design and development of sensor-based monitoring and control system for safe and effective operation of tractor implement system

Tractors serve as the primary power source in diverse agricultural activities, encompassing various tasks on Indian farms. Ensuring the effective operation of tractor-implement systems is crucial for both work efficiency and fuel conservation. Accidents, particularly rollovers involving these systems, pose a significant threat, leading to severe injuries or fatalities. To address these challenges, a sensor-based monitoring and control system was innovated. This system provides real-time feedback to operators, empowering them to make informed decisions, thus promoting the safe and efficient functioning of tractor-implement systems. The development included a slip monitoring system based on hall sensors and a draft monitoring system utilizing load cells which showed high accuracy in draft measurement ($R^2 = 0.99$) and 99.64% precision in slip monitoring. Additionally, a safety feature alerts operators to potential hazards like rollovers or excessive wheel slip, enhancing overall performance. The field evaluation of the developed system was conducted to study the effect of three levels of each operational parameter, namely, engine speed (1000, 1500 and 2000 RPM), gear selection (L_3, L_4 and H_1) and depth of operation (7, 10 and 13 cm) on performance parameters, namely, draft force (kg), wheel slip (%), roll angle (°) and pitch angle (°) for three implements, namely, cultivator, disc harrow and bund former. The draft force and wheel slip increased significantly for each level of engine speed, gear, and depth of operation for all selected implements. The developed performance monitoring system enabled operator to track safety and performance parameters and was capable to alert the operator when wheel slip exceeded the threshold limit (8 to 15%) or roll angle exceeded beyond the recommended range. The system's data collection and analysis capabilities provided valuable insights into the optimum draft and slip values. This has resulted in increased work performance and a more efficient use of resources.

Theme 3: Ergonomics and Safety in Agriculture

Occupational health hazards of tobacco cultivation and development of safety interventions

Tobacco (*Nicotiana tabacum*) is a major commercial crop in India. A study, conducted among 120 tobacco farmworkers in Andhra Pradesh, India, focused on two soil regions, Northern light and Southern light soils, designated by the Tobacco Board of India (2019-20). Postural stresses during cultivation were evaluated using the "Rapid Entire Body Assessment" (REBA), "Body Part Discomfort Score" (BPDS), and "Overall Discomfort Score" (ODS) techniques. Survey results and postural analysis prompted the creation of a two-row battery-operated tobacco transplanter. Survey revealed prevalent GTS symptoms among tobacco farmworkers, with headaches (14.17%) and nausea (11.67%) being the most frequent. Skin conditions, including allergies (4.17%) and itching (3.33%), were occasional. Standard Nordic Questionnaires highlighted MSDs, predominantly in one or both knees (47%), followed by ankles/feet (43%), shoulders/neck (37%), wrist/hands (27%), lower back (24%), hips/thighs/buttocks (19%), and upper back (10%). Postural stress assessments using REBA scores for transplanting, weeding, and harvesting tobacco leaves were categorized as "High risk, investigation, and implement change" with scores of 8.0, 8.16, and 8.2, respectively. The BPDS and ODS were highest during tobacco leaf harvesting (50.25 and 3.90), followed by transplanting seedlings (39.5 and 3.82) and weeding (40.20 and 2.87). There is necessity for ergonomic interventions to address health risks of tobacco farm workers. The "Petit Havana" crop displayed seedling characteristics ranging from 71.61 mm to 222.62 mm in height, 13.32 to 25.12 g in weight, and 4 to 7 leaves. The two-row planter achieved an average plant-to-plant spacing, row-to-row spacing, and seedling depth of 521.8 mm, 1015.3 mm, and 45.71 mm, respectively. Performance indicators included a miss index of 3.52%, multiple indexes of 4.81%, and quality feed index of 91.67%. Plant stands, plant mortality, field capacity, and transplanting efficiency averaged 61.66%, 45.83%, 0.13 ha h^{-1}, and 66.66%, respectively. Physiological parameters (HR) ranged from 84.99 to 120.17 beats min^{-1}, with a mean HR of 105.39 beats/min, indicating a medium workload. The O_2 consumption and energy expenditure ranged from 0.5 - 1.0 to 1.0 - 1.5 lit min^{-1} and 10-20 to 20 – 30 kJ min^{-1} respectively. The average REBA score was 7.12 (Medium risk, further investigation, change soon) and the risk index score was 1.70 (RI >1). The developed two-row battery-operated tobacco improves the posture during transplanting operation. It increases productivity and decreases the labour requirement for transplanting.

Study of sugarcane mechanization and health hazards in erode district

Sugarcane holds significant economic importance in India, contributing about 6% to the agricultural GDP. This study focuses on the mechanization of sugarcane cultivation in Tamil Nadu, analyzing the prevalent farming practices and identifying potential interventions to mitigate injuries associated with the process. Seventy-two farmers from three villages in Erode district participated, providing insights into mechanization levels, equipment adoption, injuries, and cultural practices. The farmers allocated 36.26% to 48.09% of their available land for sugarcane cultivation. A notable increase in the use of 30 to 35 kW tractors was observed among 76.3% of the farmers. Out of 18-unit operations, five were fully mechanized, and partial mechanization occurred in drip irrigation. Despite a power source of 4.13 kW ha^{-1}, the overall mechanization indicator was 0.162, highlighting the need for promoting advanced technologies in villages. Injuries were predominantly associated with sugarcane leaves, constituting 88% of total injuries, while tools accounted for the remaining 12%. Factors contributing to injuries included cuts from leaf blades during field entry, deep cuts from pulling and plucking leaves, and tool slippage (spade) when encountering obstacles. These injuries adversely affected worker productivity and efficiency. Preventive measures such as wearing foot-wear face shields, and cotton hand gloves were identified to address tangible injuries. Acknowledging farmers' preference for small, manually portable tools, a foot-operated sett cutter was developed. The cutter's dimensions were 600 × 500 × 940 mm (l × w × h), demonstrating capacities of 830 and 673 setts per hour in standing and sitting postures for male and female workers, respectively. Compared to traditional methods, the developed sett cutter increased sett cutting productivity by 10.84% and 9.80% for male and female workers, respectively. This innovation presents a practical solution to enhance efficiency and reduce injuries in sugarcane cultivation.

Development of vibration reduction intervention in single axle tractor-trailer system

The utilization of tractor-trailer combinations for both on and off-road transportation exposes tractor drivers to significant occupational health issues due to vibrations. To address this concern, it is imperative to quantify the vibrations at the driver-seat interface and implement interventions for minimizing health risks. This study introduced two interventions between a 2WD tractor and a single-axle trailer, measuring vibrations with and without interventions at various payload levels on two terrains – asphalt roads and farm terrain. Measurements were conducted at different speeds, aligning with normal working conditions, both on asphalt roads and farm terrain. A tri-axial seat pad accelerometer recorded whole body vibrations (WBV) in x, y, and z-axis directions. The results indicated that interventions effectively reduced vibrations in all three directions and total vibration values across speeds and loads. On asphalt terrain, total vibration values ranged from 0.441 to 0.860 m s^{-2}, 0.516 to 1.103 m s^{-2}, and 0.656 to 1.329 m s^{-2} for no, half, and full payload trailers, respectively. On farm terrain, corresponding values varied from 0.334 to 0.996 m s^{-2}, 0.398 to 1.279 m s^{-2}, and 0.544 to 1.545 m s^{-2}. The percentage reduction in vibration was highest in the x-axis, followed by the z-axis and y-axis directions. Maximum total vibration reduction on asphalt roads occurred at 22 km h^{-1} with intervention (I2), reaching 16.86%, 21.12%, and 25.51% for no, half, and full payload trailers, respectively. On farm terrain at 12 km/h, reductions were 17.07%, 23.77%, and 28.67%.

Health guidance caution zone (HGCZ) limits were determined for all operating conditions, with interventions resulting in increased lower and upper HGCZ limits, thus contributing to enhanced driver well-being.

Theme 4: Climate Change Impacts and Integrated Water Resources Management

Investigations on straw incorporation system with chopping unit using discrete element modelling

A straw chopper cum mixture machine was developed for straw incorporation system with chopping unit. The physical and mechanical properties of paddy straw were determined for calibration of DEM parameters. Soil and straw were modelled by Hertz-Mindlin linear cohesion and Hertz-Mindlin with parallel contact model, respectively. Single straw and straw bunch were calibrated with relative error <10%. SMS serrated, cutter bar and SMS plain blades were evaluated using DEM. SMS serrated blade (cutting torque 5.06 N.m) was selected for chopping unit. Mixing index (MI), mean weight diameter (MWD), effective field capacity, straw length and fuel consumption were 96%, 8 mm, 0.15 ha.h^{-1}, 5 mm and 3.06 l.h^{-1}, respectively at 1.8 km.h^{-1} forward speed and 25% straw moisture during field evaluation. The experiments were performed in DEM and field for three-forward speeds at 25% moisture content (5 DAH). The straw retained at four different vertical soil sections (depths 0-3, 3-6, 6-9 and 9-12 cm) varied from 16.4 to 26.1, 37.2 to 44.1, 32.5 to 15.7 and 6.3 to 1.8 %, respectively. A seven-row straw chopper cum mixer with seeder (SCMS) was developed and compared with prevailing practices. SCMS performed better having 14.45 cm depth, 5 cm straw length, 6.75 l.h^{-1} fuel consumption, 9.2 mm MWD, 90.42% MI and 18.5% BDI. The germination count and yield of wheat were 4.72% and 7.33% higher, respectively compared to traditional practice. Operating cost of machine was ₹. 2560 ha^{-1} (54.12% saving compared to super seeder). The BEP and PBP were 174 h. year^{-1} and 3.4 years, respectively. SCMS can be a better solution for integrating straw management, tillage and sowing operations in single pass of tractor thereby saving the fuel, time and energy.

Study on extent and severity of waterlogging and soil salinity of the Bhal region of Gujarat, India

The study focuses on assessing agro-land suitability in the Bhal region, which spans parts of Ahmedabad, Bhavnagar, and Anand districts in Gujarat, India. The main objective is to identify the causes of waterlogging and drainage issues impacting agriculture, particularly in the cultivation of GI tagged Bhaliya Wheat. Various criteria, including land use/land cover (LULC), slope, texture, moisture, water holding capacity (WHC), pH, and electrical conductivity (EC), were considered in the analysis. Remote sensing-based indices such as NDVI, NDWI, and NDSI were employed, and the SALTCALC model, chosen among various drainage models, was used for assessing drainage and salinity. Different management combinations were explored, considering input data availability, climate data, and drainage types. The study revealed that the Bhal region exhibited high to very high soil salinity levels and pH ranging from 0.101 to 48.134 dS m^{-1} and 7.31 to 8.82, respectively, during the post-monsoon season of 2023. Water electrical conductivity (EC) and pH in the post-monsoon season ranged from 1.01 to 5 dS m^{-1} and 8.02 to 9.44, indicating medium to high saline water. Indices during Kharif and Rabi seasons highlighted areas affected by waterlogging and salinity. Using the SALTCALC model, predictions were made for different drainage scenarios. The findings suggested that maintaining current agricultural and drainage conditions until 2033 could result in an average annual water table increase of 0.231 m and a rise in groundwater salinity to 6.71 dS m^{-1}. However, increasing drain depth to 0.3 m showed consistent drops in salinity in the root zone and lowering of the water table. To address the salt-affected waterlogged soil, the study recommends an elaborate on-farm subsurface drainage network supported by a network of drainage channels/canals as the most effective technological solution for the Bhal region in Gujarat, India. This approach aims to ameliorate soil conditions and promote sustainable agriculture in the region.

Development of irrigation water release schedule information system for a minor canal command

Recently, water and land scarcity intensified due to population growth, urbanization, pollution, and climate change. Agriculture, consuming 70% of water, faces challenges exacerbated by diminishing water resources. India anticipates 22% absolute water scarcity by 2050. Groundwater and canals, major irrigation sources, cover 50% and 25% of net irrigated areas. Urgently addressing this, a study in Haryana developed an information system for a canal command area, integrating geospatial data for soil, crops, land use, canals, and water productivity. Employing METRIC-EF Flux for actual evapotranspiration estimation, the study conducted water supply-demand analysis, establishing a comprehensive water budgeting assessment for effective irrigation scheduling in the Jhajjar district. It was observed that the total crop evapotranspiration for rice was 683.4 mm, with an effective rainfall of 361.88 mm and an irrigation requirement of 555.5 mm. Despite over-irrigation during a few months (July and August), a scarcity (23.82%) was observed during the *kharif* season. During the *rabi* season, the actual evapotranspiration was 373.6 mm and the effective rainfall received was only 77.4 mm, leading to an irrigation requirement of 319 mm to meet the crop water requirement. Subsequently, a mobile application (MA) CAMS (Command Area Management System) was developed in the Flutter platform using DART Language. The CAMS app consisted of irrigation scheduling, crop advisory and water release information and was evaluated in the canal command. It was observed that by using CAMS mobile app-based decisions, there was an increase in the water productivity of rice by 0.22 kg m^{-3} to 0.29 kg m^{-3} and in wheat by 1.52 kg m^{-3} to 1.95 kg m^{-3}. Overall water productivity by 31.81% and 28.28% for rice and wheat, respectively as compared to conventional irrigation rostering. Nonetheless, the developed CAMS would assist the stakeholder to improve irrigation scheduling and for better water management practices in the canal command.

Theme 5: Precision Irrigation

Study on water productivity of greenhouse capsicum with and without IoT-based automation

Water and nutrients are two important factors affecting the growth and quality of greenhouse vegetables. The pH and EC can be used as effective indicators for scheduling fertigation and managing water and nutrients for the greenhouse crops. The experiment was conducted inside climate-controlled greenhouse of CPCT, ICAR- IARI, New Delhi to study the water productivity of greenhouse capsicum with and without IoT based automatic system. Treatment considered under the study were T1- 80% recommended dose of fertilizer (RDF) & 60% ET_C, T2- 80% RDF & 80% ET_C, T3- 80% RDF & 100% ET_C, T4- 100% RDF& 60% ET_C, T5- 100% RDF & 80% ET_C, T6- 100% RDF & 100% ET_C and T7- fertigation based on soil moisture sensor and soil EC & pH sensors. Soil EC & pH based automated fertigation system was developed, calibrated, and installed in the greenhouse capsicum field with three capacitive soil moisture sensors at depths of 15, 30, and 45 cm, Soil EC sensor and pH sensor and installed in the root zone of greenhouse capsicum to measure the real-time soil moisture and nutrient levels. The sensors were connected to the microcontroller, then to the IoT platform, and the data was stored in MySQL database. For automatic fertigation system, Node MCU was connected to the relay to turn ON and OFF the motor and the solenoid valve. Manual irrigation was based on the pan evaporation inside the greenhouse. Regular monitoring of the mineral nitrogen, available potassium and phosphorus in the soil were done using NPK sensor. Water productivity and nutrient use efficiency were highest in automatic fertigation system which was followed by T5. The automatic fertigation system saved 4.83% water and 5.43% nutrients compared to the best manual fertigation system, still producing better quality fruits.

Comparative study on irrigation and mulching effects in two wheat varieties

Optimizing wheat production amidst increasing population and climate change necessitates strategic selection of varieties and water-efficient practices. This study aimed to evaluate the performance of two wheat varieties, one tall and drought-tolerant, and the other high-yielding but drought-susceptible, under varying irrigation levels with and without mulch. The treatments provided to the wheat varieties are T1 (Irrigation at 14% soil moisture and mulch with plastic beads), T2 (Irrigation at 14% soil moisture and no mulch), T3 (Irrigation at 12% soil moisture and mulch with plastic beads) and T4 (Irrigation at 12% soil moisture and no mulch). Results revealed that T1, characterized by irrigation at 14% soil moisture with mulch, provided optimal conditions for both varieties. In this treatment, growth parameters, photosynthetic activities, and yield attributes exhibited superior performance compared to other treatments. Conversely, T4, with delayed irrigation at 12% soil moisture, induced drought stress and resulted in lower values across measured parameters. Irrigating at 70% field capacity (T1) proved more favourable than 60% (T4), emphasizing the importance of adequate water supply. Additionally, mulched plants in T3 showed improved performance even under reduced irrigation, highlighting the positive impact of mulching on wheat cultivation in water-scarce regions. Water use efficiency (WUE) and transpiration efficiency (TE) were critical indicators. Under T1, WUE was 3.8 for the drought-tolerant variety (HD-3271) and 3.2 for the high-yielding but drought-susceptible variety (C-306). However, under T4, WUE reduced significantly, particularly for HD-3271, indicating its vulnerability to drought stress. Notably, the drought-tolerant variety demonstrated resilience, showcasing its ability to thrive under stress conditions. Transpiration losses were higher in this variety, suggesting effective water utilization. Consequently, the study recommends selecting a high-yielding variety in water-abundant regions and a drought-tolerant variety in water-scarce regions for optimal wheat production. These findings underscore the importance of variety selection and efficient water management practices in achieving sustainable productivity amid changing environmental conditions.

Studies on the microclimate variations in different mulching conditions under drip irrigated sweet corn using internet of things

Smart irrigation is one form of precision irrigation that can help farmers maximize crop production while preserving water and energy. A two-year (2020-22) field experiment on sweet corn crop (var. KPCH) was conducted with two irrigation scheduling approaches i.e., ETc-based drip irrigation and IoT-based smart drip irrigation scheduling under three mulches: black plastic mulch, silver plastic mulch, and control (bare soil) in three replications. Irrigation scheduling was programmed using upper (field capacity) and lower thresholds (50% plant available water). The information captured by the sensors is wirelessly uploaded to the cloud server using IoT technology (Thing Speak) using ESP8266 Wi-Fi module, which can be accessed from anywhere. Results indicated that the smart drip irrigation system based on IoT with 100% field capacity yields significantly higher than an ETc-based 100% drip irrigation system. It was consistently found that black plastic mulch increased the soil temperature by 2.65°C at 15 cm depth more than other mulches, followed by silver mulch (2°C). The IoT with 100% field capacity smart drip irrigation system had the highest plant height with black mulch followed by silver mulch and bare soil. The maximum stover, cob, and grain yields were observed in IoT-based smart drip irrigation system with 100% field capacity with black mulch treatment (25.93 t ha^{-1}), (17.6 t ha^{-1}), and (7.51 t ha^{-1}). From the study, it was observed that IoT-based smart drip irrigation at 100% field capacity resulted in the highest cob water productivity (4.41 kg m^{-3}) compared to 100% ETc-based drip irrigation (3.3 kg m^{-3}) and IoT-based smart drip irrigation at 80% field capacity (3.82 kg m^{-3}). It was found that IoT-based smart drip irrigation with 100% field capacity and 80% field capacity consumed 12.7% and 24.5% less irrigation water, respectively, and produced

12.8% more marketable yields than 100% ETc-based drip irrigation. The developed system was rugged, and a water-resistant enclosure allowed its use in outdoor agriculture fields.

IoT-enabled irrigation water management system for enhancing water productivity

The present study was aimed to develop an IoT-enabled Irrigation Water Management System (IoT-IWMS) for real-time scheduling of irrigation besides a digital water allocation system to supply required amount to improve water productivity. Climate data of the study area in the ICAR-IARI farm was subjected to trend analysis using Mann-Kendall (ZMK) and Sen's slope approach indicated intra variability in monthly and seasonal rainfall trend. Significant increasing trend were found for March, April, July, pre-monsoon and rabi crop season with ZMK of 0.22, 0.23, 0.34 and 0.30, respectively. The prediction of weather parameters using soft computing techniques viz. ANN and LSTM for different scenarios indicated that the ANN outperformed ($0.75<NSE\leq1$; PBias<±10; KGE ≥0.75) over LSTM except for the peak values of pan evaporation and sunshine hour. Moreover, the use of static time series variables viz. date and month, and days of the year as input improved the LSTM performance, while degrade the performance of ANNs. Waterproof capacitive soil moisture sensor was evaluated and observed to perform better with prediction error statistics viz. RMSE (0.23-0.31) and MARE (0.01-0.02) were minimum and NSE>0.95, KGE>0.95, PBias~0, R2>0.95 as compared to capacitive v1.2 and capacitive v2.0 sensors. Similarly, the pipe flow sensors were calibrated and the IoT enabled soil moisture sensing system and portable water allocation system were fabricated. Further, the mobile application to retrieve and analyze the data measured through the soil moisture sensor was developed. Performance of developed IoT-IWMS for irrigation scheduling of two wheat cultivars (viz. HD:2967 and HD:3086) under three irrigation regimes (i.e. Field capacity, 20% and 40% deficit irrigation) indicated that soil moisture sensing system measured the soil moisture content in close agreement with the observed values for all irrigation regimes. Grain yield was observed to be 5.66 and 5.21, for HD:2967 and 5.45, and 4.89 t/ha for HD:3086 under field capacity for rabi season 2021-22 and 2022-23, respectively. The developed IoT enabled IWMS can be used for irrigation water management in field crops to improve agricultural water productivity for other regions with location specific calibration of sensors.

Application of IoT technique for irrigation scheduling based on environmental conditions in a naturally ventilated greenhouse

This study focussed on creating an IoT system for cucumber cultivation in a naturally ventilated greenhouse. Environmental parameters like temperature, humidity, light intensity, and soil temperature are monitored. Collected data is utilized for soil moisture prediction using various machine learning techniques (Decision Tree, Random Forest, Multiple Linear Regression, Extreme Gradient Boosting, K-Nearest Neighbour, and Artificial Neural Network) with different input combinations, aiming to enhance irrigation precision and resource efficiency. The input combination using four parameters (T, RH, LI, ST) gave better results than those using three (T, RH, LI) and two parameters (T, RH). RF showed better accuracy ($R^2 = 0.951$), followed by XGB ($R^2 = 0.941$). This prediction of SM based on environmental parameters would aid in maintaining the required amount of water per plant in real-time, preventing the plant from experiencing stress. An IoT system was developed to irrigate the cucumber crop automatically based on SM depletion. Three treatments were considered to evaluate the performance of IoT system (Evapotranspiration (ET)-based (T1), Field capacity (FC)-based (T2) and model-based (T3). In T1, the irrigation was provided based on the calculated crop ET and in T2, it was by programming the IoT system with an upper limit as FC and a lower limit as 50% available water. However, in T3, the predicted SM from MLR ($R^2 = 0.909$) equation was used to provide the irrigation so that the IoT system's development cost will be less. These three treatments were evaluated by comparing the yield and vegetative parameters of the cucumber crop in rainy and summer seasons inside a naturally ventilated greenhouse. Vegetative parameters like vine length and leaf dimensions exhibit no significant differences among treatments. However, yield-related factors such as fruits per vine, yield per plant, total yield, and water use efficiency vary significantly. T3 treatment outperforms others, particularly T2, showing the highest yield and water use efficiency 68.6 t ha^{-1}, 30.6 kg m^{-3}, and 68 t ha^{-1}, 28 kg m^{-3} in rainy and summer seasons, respectively. Fruit characteristics like length, diameter, and weight remain unaffected by the treatments. T3 saved the most water, 22 mm (rainy) and 32 mm (summer) over T1, and 10 mm (rainy) and 23 mm (summer) over T2. The IoT irrigation system efficiently predicted soil moisture one day ahead, outperforming FC-based and ET-based irrigation methods.

Investigations on magnetically treated irrigation water and system performance

Water resources are crucial for food supply and environmental health. The study explores optimal configurations for a 7000-gauss magnetic treatment device on water, known as magnetized water (MW). Laboratory tests, including untreated and magnetically treated water samples (bore, hard, saline, and wastewater), assess parameters like pH and EC. A field experiment gauges magnetized water's impact on tomato and French bean biometrics, yield, and quality. Soil properties post-magnetic treatment and drip hydraulics are also analyzed, offering insights into the potential benefits of Magnetic Field (MF) treatment in agriculture. Maximum chemical changes in parameters of poor-quality water (hard, waste and saline) were observed at a velocity (F1) of 0.8 m s^{-1} (Discharge= 3.0 lps) as compared to flow rate of (F2) 1.0 m s^{-1} (Discharge= 4.0 lps) and to flow rate (F3) of 1.2 m s^{-1} (Discharge = 5.0 lps). The increase in pH and reduction in electrical conductivity was more conspicuous at the higher level of water hardness and salinity. On magnetic treatment of irrigation water, the pH has increased from 7.10 to 7.46 in bore water, 7.54 to 7.95 in hard water, 7.21 to 7.60 in saline water and 7.69 to 8.09 in wastewater treatments. At a velocity of 0.8 m s^{-1}, the recorded values of EC were observed significantly lower in magnetic treated hard water (1.29 Ds m^{-1}) and saline water (2.57 dS m^{-1}) compared to untreated hard water (1.48 dS m^{-1}) and saline water (2.98 dS m^{-1}). On magnetic treatment of irrigation water total hardness of water decreased from 11.60 to 9.80 meq l^{-1} in bore water, 20 to 18.76 meq l^{-1} in hard water, 12.83 to 12.01 meq l^{-1} in saline water and 11.79 to 8.26 meq l^{-1} in wastewater treatments. ii in tomato crop, among the different type of irrigation water tried, magnetically treated wastewater recorded the maximum plant height (92.44 cm), number of branches per plant (19.81) and LAI (3.04). The magnetised wastewater treatment (88.64 gm^{-2} soil week^{-1}) resulted in the highest values of crop growth rate followed by treatments of magnetised bore water (80.59 gm^{-2} soil week^{-1}). The magnetic treatment of bore water, wastewater and saline water enhanced the yield of tomato by 7.74, 12.89 and 10.38 % over their respective non-magnetic treated plots. The maximum firmness was recorded in magnetised bore water (9.72 kg cm^{-2}) followed by treatments of non-magnetised bore water (9.01 kg cm^{-2}) and magnetised wastewater (8.84 kg cm^{-2}). In French bean crop, magnetically treated wastewater recorded the maximum plant height (48.77 cm) and LAI (3.24). The magnetic treatment of bore water, wastewater and saline water enhanced the yield of French bean by 9.17, 13.11 and 8.66% over their respective non-magnetic treated plots. Irrigating crops with magnetically treated water positively influenced crop quality parameters, enhancing vitamin A, potassium, calcium, and seed protein. The magnetic treatment of wastewater and saline water significantly reduced soil electrical conductivity post-harvest of tomato and French bean crops. Nitrogen, phosphorous, and potassium concentrations in crop straw increased with magnetically treated water irrigation. Reductions in dripper discharge variations (qvar) were observed, with a 17.70% decrease in non-magnetically treated wastewater and a 10.55% decrease in magnetized wastewater treatment. Similarly, for non-magnetized saline water, qvar decreased by 15.65%, while it was 8.00% for magnetized saline water treatment. This preliminary study suggests potential benefits of magnetic treatment on water properties, crop yield, quality, soil, and reduced dripper clogging.

Development of sensor-based automated fertigation system for vertical farming

The Indoor cultivation of lettuce in a vertical hydroponic system (VHS) under artificial lighting was done inside climate-controlled greenhouse. Two separate experiments were conducted to standardize the light parameters namely daily light integral (DLI) and red/blue (R/B) ratio. The effect of DLI and R/B ratio on the physiological, morphological, and nutritional parameters, as well as the resource use efficiency of iceberg lettuce (cv. Glendana) grown in an indoor VHS was studied. In the DLI related experiments, seedlings were grown in a photoperiod of 12 h, 16 h, and 20 h with a photosynthetic photon flux density (PPFD) of 200 µmol m^{-2} s^{-1} using white LED lights. The results obtained were compared with plants grown in VHS under sunlight condition inside the greenhouse. The DLI values for 12 h, 16 h, and 20 h were 8.64, 11.5, and 14.4 mol m^{-2} d^{-1}, respectively. The shoot fresh weight (FW) at harvest increased from 275.5 g to 393 g as the DLI increased from 8.64 to 11.5 mol m^{-2} d^{-1}. DLI of 14.4 mol m^{-2} d^{-1} had a negative impact on FW, dry weight (DW), and leaf area. The transition from VHS without artificial lights to VHS with artificial lights resulted in a 60% increase in fresh weight. Significantly higher water use efficiency (WUE) of 71 g FW/L and energy use efficiency (EUE) of 206.31 g FW/kWh were observed under a DLI of 11.5 mol m^{-2} d^{-1}. The study recommends an optimal DLI of 11.5 mol m^{-2} d^{-1} for iceberg lettuce grown in an indoor vertical hydroponic system. In the R/B ratio related experiments, seedlings were grown in under red and blue LEDs in an indoor VHS under three R/B ratios namely, R/B=2, R/B=3, and R/B=4. The PPFD of 200 µmol m^{-2} s^{-1} was maintained in an indoor VHS. The results obtained were compared with VHS without artificial lights inside thegreenhouse. Shoot FW increased significantly by 43% as the R/B ratio increased from 2:1 to 3:1. However, further increasing R/B ratio to 4:1 resulted in a nonsignificant decrease in shoot FW by10%. Chlorophyll content and antioxidant activity was optimized at R/B ratio of 3:1, whereas total phenols were highest under R/B ratio of 2:1. Significantly higher WUE (134.38 g FW L^{-1} H2O) and EUE of 373.81 g FW/kWh were observed in R/B ratio of 3:1 compared to all other treatments. Plants grown under R/B ratio of 3:1 had 81 % more FW and 1.5 times more WUE than the plants grown under sunlight. The study recommended R/B ratio of 3:1 for iceberg lettuce grown under red and blue LEDs for optimal growth, nutritional quality and resource use efficiency. Automated fertigation system maintained the nutrient solution parameters within desired range. Automated system had significantly higher (24% more) WUE than the manually operated system.

Data-driven techniques for evapotranspiration modelling in different agro-ecological regions of India

This study focussed on developing Machine Learning (ML) and Deep Learning (DL) algorithms for accurate estimation of crop water requirement using reference evapotranspiration (ET_0). ML algorithms—Random Forest (RF), Light Gradient Boosting (LGB), and Extreme Gradient Boosting (XGB)—optimized with Grey Wolf Optimizer (GWO), along with DL models—Artificial Neural Network (ANN), Recurrent Neural Network (RNN), and Long Short-Term Memory (LSTM)—were compared with empirical ET_0 equations. Daily meteorological data from 2001 to 2020 across diverse climatic regions informed the models. The study contributes to improved water management in agriculture by enhancing the understanding and efficiency of estimating ET_0, crucial for hydrological studies and irrigation scheduling in arid, semi-arid, humid, and sub-humid regions. A web-application named Data-driven interface for Crop Evapotranspiration (DiCE) was developed based on the best performed data-driven models. GWOLGB and GWOXGB demonstrated superior accuracy, outperforming XGB and RF in most locations and input combinations. The Light Gradient Boosting (LGB) model exhibited better prediction efficiency than other conventional Machine Learning models. Hybrid ML models consistently surpassed conventional and empirical models in accurate predictions across all stations. The Valiantzas 2 equation excelled in estimating ET_0

at arid and semi-arid stations, while the Turc model performed well in humid and sub-humid locations. Among Deep Learning models, LSTM and ANN6 (2 hidden layers, 10 neurons each) outperformed RNN and ANN1 (1 hidden layer, 5 neurons). Utilizing all inputs yielded the most accurate results, contrasting with models using only air temperature data. Wind speed proved crucial in arid and semi-arid regions, while solar radiation enhanced ET_0 estimation in humid and sub-humid areas. The DiCE web application demonstrated reliable accuracy in predicting crop evapotranspiration (ETc) and ET_0, validated with lysimetric data in semi-arid (Delhi) and sub-humid (Bhopal) regions. Such user-friendly tools empower on-farm water management for technicians, farmers, and academicians, facilitating improved irrigation scheduling.

Lysimeter based crop evapotranspiration and crop coefficient for irrigated maize and brinjal in hot and sub-humid zone

Water supplies to agriculture sector are declining on account of global climate change, diminishing groundwater levels and a rising occurrence of extreme weather events. Keeping in view the sensitivity to these stresses and huge requirements, precise quantification of irrigation water needs is critical to ensure efficient water application. FAO's climate-based approach involving reference crop evapotranspiration (ETO) and crop coefficient (KC) is one of the most widely used approaches to estimate crop water requirement. This approach requires crop and site specific valued of KC for accurate assessments of crop water requirements. This study applied the concept of lysimeter based root zone water balance approach to assess the 'crop evapotranspiration' of brinjal and maize crop under four distinct fertilizer management practices in Eastern Plateau and Hill Region (EPHR) of India. In estimation growth stage wise KC values, this approach used reference evapotranspiration estimated using classical Penman-Montieth method. In order to address the limited data availability situations, this study also evaluated the empirical ETO estimation approaches such as Hargreaves-Samani, Blaney-Criddle and Romenenko as an alternative to Penman-Montieth method. The results indicated that the seasonal ETC values for brinjal under control, inorganic, organic and Integrated Nutrient Management (INM) fertilizer treatments were 346.7, 349.8, 341.9 & 321.0 mm while the respective values for maize were 398.1, 440.3, 450.0 and 428.4 mm. The recommended values of KC for Brinjal during initial, development, mid and late stages were 0.44, 0.88, 0.64 and 0.69, respectively whereas in case of maize the respective values of KC were 0.43, 0.92, 1.13 and 0.67. Among the alternative methods, the Hargreaves-Samani method was adjudged the best alternative method to estimates ETO. The KC values estimated in this study will be useful to the researchers, farmers and other stakeholders involved in planning and management of irrigation water resource.

Conjunctive use for enhancing water productivity in Rarh region of West Bengal, India

In the pursuit of sustainable agriculture, food security, and ecological well-being, the focus of this study is on enhancing water productivity in the Rarh region. This area, located between the Chotanagpur Plateau in the west and the main Ganges River flow in the east, spans parts of West Bengal, including Bankura, Bardhaman, Birbhum, Murshidabad, Paschim Medinipur, and Purba Medinipur districts. The region faces a hydrological challenge, with water levels dropping 1-2 meters pre-monsoon due to poor infiltration from hard rocks. The study suggests water management strategies, including rainwater harvesting, aquifer recharge, efficient irrigation, and precise scheduling, aiming to shift from water deficiency to self-sufficiency. Utilizing secondary data, the study assesses surface and groundwater potential, examining temporal and spatial variations in the districts. The calculated water demand for agriculture in the Rarh region, using the CROPWAT model, is approximately 16,537.2 million cubic meters (Mm^3). The estimated direct surface runoff, computed using the SCS CN method, is around 39,586.8 Mm^3. By allocating 50% of this total surface direct runoff for agriculture, the available water supply is estimated to be approximately 19,794 Mm^3. Utilizing Analytic Hierarchy Process (AHP) analysis with GIS, the study reveals that roughly 36.24% of the region falls into zones with very low to low groundwater potential. Consequently, the net groundwater availability, based on data from the Central Ground Water Board (CGWB), is approximately 13,430 Mm^3. In total, the cumulative water supply for both surface and groundwater in the Rarh region of West Bengal amounts to 33,224 Mm^3. Given the ongoing decline in groundwater availability, it is crucial for the residents of the Rarh region to increasingly depend on surface water to meet agricultural water demands.

Effect of deficit irrigation on garlic (*Allium sativum* L.) cultivars in Deccan Plateau of India

Adverse effect of water deficit stress on crop productivity is major concern world-wide. Particularly, in Deccan plateau of India, it is critical to quantify the impact of water stress on shallow rooted crop like garlic, which is grown under diversified crop and water management practices on shallow basaltic soils. A study was conducted during year 2022–23 to evaluate the interactive effect of garlic cultivars (Cv. Godavari, Cv. Phule Baswant, Cv. Local–1, Cv. Bhima Purple, Cv. GG–4, and Cv. Local–2) and deficit irrigation levels (100, 75, 50 and 25% ET) applied based on crop evapotranspiration using line source sprinkler (LSS) system. The maximum total bulb yield (TBY) of 12.68 Mg ha^{-1} was obtained at full irrigation (100% ET) and declined to 10.68, 7.13 and 3.21 Mg ha^{-1} at low (75% ET), medium (50% ET) and severe (25% ET) water deficit conditions, respectively. The maximum values of water productivity (WP) were ranged between 2.71–4.38 kg m^{-3} for different garlic cultivars. Further use of stress tolerance cultivars can substantially reduce water use by 7.8– 47.5%. A lower value of yield response factors $KG \leq 1$ of Cv. Godavari also shows its higher tolerance to alleviate water deficit stress owing to its better growth, canopy and physiological traits. The physiological and functional quality traits (mean bulb weight, bulb diameter and firmness, DM, RR, TPC, TFC) and biochemical and functional (DM, RR, TPC and TFC) properties were improved with water deficits. Whereas, TSS considerably decreased under medium to sever water deficit. It is concluded that shifting towards stress tolerant cultivars such as Cv. Godavari and Cv. Phule Baswant under medium deficits could help to substantial water saving, rational utilization of water resources, and thus enhanced bulb yield and quality of garlic under water scarce regions of Deccan Plateau, India.

Theme 6: Quality Storage of Agricultural Produce

Development of vacuum impregnation technology for shelf-life enhancement of vegetable

This research delves into enhancing the quality and shelf-life of select vegetables through a vacuum impregnation (VI) system, aiming to address issues like spoilage, diminished nutritional quality, and texture loss. VI involves transferring a suitable solution into the internal porous matrices of fruits and vegetables, resulting in compositional alterations and quality improvement. The VI system developed for the study includes a 25 mm thick acrylic sheet vacuum chamber, a high-performance single-stage vacuum pump, and an automation setup. Cost economic analysis estimates an operating cost of Rs. 12.64 Kg^{-1}. Broccoli florets, coriander leaves, and iceberg lettuce were impregnated with a solution mixture of ascorbic acid and calcium chloride. The process variables for the VI system were optimized using response surface methodology (RSM) with a 4-factor Box-Behnken design. Variables considered were vacuum pressure, vacuum time, solution concentration, and restoration time. Quality parameters such as total phenolic content (TPC), total flavonoid content (TFC), ascorbic acid content (AAC), free radical scavenging activity (FRSA), total chlorophyll content (TCC), and carotenoid content (CC) were optimized using both RSM and artificial neural network (ANN) modelling. For broccoli florets, optimized conditions included 0.2 bar vacuum pressure, 11 min vacuum time, 12 min restoration time, and a 1.5% concentration. Corresponding values for TPC, TFC, AAC, TCC, FRSA, and CC were 297.58 mg/100g, 11.22 mg/100g, 359.92

mg/100g, 1.21 mg/g, 79.77%, and 8.58 mg/g, respectively, with an overall desirability of 0.896. Coriander leaves and iceberg lettuce exhibited their respective optimized conditions and quality parameter values. The vegetables impregnated under optimized conditions underwent storage studies at different temperatures and with various packaging materials, with comparative analysis against fresh untreated samples under identical conditions.

Machine learning based non-destructive system for pesticide residue detection in apple

Apples are popular worldwide for their nutritional value. However, they face challenges from fungal diseases like apple scab and powdery mildew. Carbendazim, a potent fungicide, is commonly used by farmers to counteract these diseases. However, concerns arise due to its residues in harvested fruits, prompting the need for rapid and accurate measurement methods to address consumer apprehensions about food safety, health, and environmental impact. Traditional techniques for measuring pesticide residues in fruits are time-consuming, require expensive equipment, and are environmentally unfriendly. This study employs advanced technologies including Vis-NIR spectroradiometry (350-2500 nm), hyperspectral imaging (HSI) (398-1003 nm), and digital imaging, to detect pesticide residues, particularly Carbendazim, in apples. After acquisition of the reflectance data using spectroradiometer, pre-processed was carried out using Standard Normal Variate (SNV). Various sensitive band selection methods are employed, including Wrapper Forward Selection, Wrapper Backward Elimination, and Random Forest feature selection. The residue content of Carbendazim was predicted using regression models such as CART, ANN, and SVM, concluding that combining Random Forest features with SVM yields superior results. In HSI technique, acquisized hyperspectral images were pre-processed with multiple scattering correction (MSC), SNV and Savitsky-Golay (SG) smoothing. The potential wavelength (613nm) was selected based on PCA loadings to distinguish between pesticide treated and untreated apples. The hyperspectral imaging technique achieves high accuracy, with a maximum of 93.4% using Partial Least Squares-Discriminant Analysis. The study also incorporates digital image processing techniques where, statistical and textural features were extracted in spatial domain using Gray- Level Co-occurrence Matrix (GLCM) from the selected region of interest. The ANN classifier demonstrated superior performance in identifying Carbendazim residue in red delicious apples, achieving an accuracy of 92% along with high average precision, recall, and F1-score. The results demonstrate that hyperspectral imaging and digital imaging, coupled with appropriate classification techniques, effectively distinguish pesticide-contaminated apples and also confirming the potential of spectroscopy techniques for predicting Carbendazim residue in apples.

Studies on storage and packaging of marigold (*Tagetes erec*ta) loose flowers in Pusa Farm Sun Fridge (PFSF)

Marigold is one of the popular loose flowers that earns high domestic as well as export value. Postharvest management of these loose flowers is crucial to get reasonable remuneration. It is important to enhance the shelf life of the marigold loose flowers and keep them attractive for longer times after consumers purchase them. The selection of appropriate packaging material and availability of solar-based cold storage may be game changers in maintaining the quality of loose flowers during storage. Keeping these points in view, the present investigation was conducted to study storage and packaging (uncovered, shrink wrap, bamboo basket covered with jute cloth) of marigold loose flowers in Pusa Farm Sun Fridge (PFSF) and compared with cold storage and ambient. Temperature variation within PFSF during loaded condition ranged between 6.5°C to 14°C with relative humidity ranging from 88% to about 100%. A total of 11 days storage was achieved in cold store {with 30% rotting and 10.61% shrivelling} (5±1°C, 90% RH) under shrink wrap, compared to 9 days in Pusa farm sun fridge (with 50% rotting and 3.61% shrivelling), and 4 days in ambient (with 53.33% rotting and 6.36% shrivelling). However, maximum shelf-life was recorded as 7 days in PFSF and cold store under uncovered packaging, compared to 3 days in ambient. The shrivelling percentage was observed maximum of 20.38% in ambient uncovered condition on 3rd day, 16.11% in cold store uncovered packaging on 7th day and 10.41% in PFSF uncovered packaging on 7th day. Flower colour changed (faded) more in ambient as compared to PFSF and cold store. Flowers packaged in shrink-wrap showed the maximum carotenoids (lower reduction in carotenoids) when compared to the uncovered and bamboo basket packaging under all storage conditions.

Infrared thermography for modelling of refractance window drying of aonla (*Emblica officinalis*) slices

The study involved the development of a batch-type Refractance Window (RW) dryer, aiming to preserve the sensitive constituents of Aonla that are prone to heat degradation. The central composite experimental design incorporated operational variables like water temperature (75, 82.5, and 90 °C) and slice thickness (2, 4, and 6 mm) to assess their impact on response variables. Under the optimized conditions of 83°C water temperature and 4 mm slice thickness, Aonla slices exhibited enhanced characteristics, including 269.03 mg/100 g ascorbic acid content, 242.33 mg GAE/100 g total phenolic content, 87.11% free radical scavenging activity, 3.62% titratable acidity, and 4% moisture content. The efficacy of the RW dryer and the potential of RW drying (RWD) for Aonla preservation were evaluated by comparing it with conventional drying methods—hot air drying (HAD) and osmotic drying (OSD). RW-dried Aonla slices demonstrated approximately 5% higher levels of ascorbic acid and total phenolic content compared to OSD and HAD samples, showcasing a smoother and more uniform microstructure. Additionally, the study delved into advanced techniques, incorporating artificial neural network (ANN) modeling alongside infrared thermography. Analysis of thermal images using MATLAB software and the GLCM approach for textural properties provided insights into the drying process dynamics. The selected ANN model, employing a transfer function of tansig, Levenberg-Marquardt back propagation as the training algorithm, and featuring four neurons in the second hidden layer, exhibited high accuracy in predicting surface temperatures. Mass transfer parameters, including Biot number, effective moisture diffusivity, and mass transfer coefficient, were estimated using the Dincer and Dost diffusion model. Effective moisture diffusivity exhibited variability across different drying conditions, ranging from 4.27×10^{-10} to 1.09×10^{-9} $m^2\ s^{-1}$, while the Biot number reflected a range of 0.268 to 8.666. To scrutinize microstructural alterations during RW drying, instrumental analyses like scanning electron microscopy (SEM), Fourier transform infrared spectroscopy (FTIR), and X-ray diffraction (XRD) were employed. XRD patterns indicated semicrystalline structures in RW-dried Aonla slices, with pronounced changes to amorphous structures at higher water temperatures. SEM images revealed the disintegration of cell wall/membrane, resulting in smooth, flaky microstructures with sharp edges. The study emphasized the suitability of RW drying for preserving heat-sensitive compounds in Aonla, highlighting better quality retention and morphological characteristics. Furthermore, it underscored the potential of ANN and IR thermography for precise surface temperature prediction during the RW drying process.

Design and development of IoT based monitoring system for storage of mangoes in Pusa Farm Sun Fridge

The environmental factors like temperature and relative humidity play key role that affect storage of vegetables and fruits. The study aimed to design and develop IoT based temperature and RH monitoring system and to evaluate the quality change in stored mangoes and cost economics. Hence, an IoT based remote monitoring system has been designed and developed and uses a microcontroller – an Arduino UNO which uses C++ programming language. It was installed in PUSA Farm Sun Fridge (FSF) which is a 100 % solar-powered, battery-less cold store that has capacity of around 2 tonnes of freshly harvested produce. In mango loaded condition Pusa Farm Sun Fridge maintained low temperature of 4-18 °C whereas outside ambient temperature was recorded up to 46°C. Pusa Farm Sun Fridge maintained high relative humidity as in between 70 to 90%. The physical properties of mango such as weight loss, colour change, firmness and the bio-chemical changes such as respiration rate, titratable acidity and total soluble solids (TSS) were studied during the storage period of mango cultivars (Safeda and Kesar). The results revealed that physiological loss in weight (PLW%), TSS and colour values of mango of both varieties showed increasing trend with increase in temperature and decrease in relative humidity for both selected storage conditions as PFSF and ambient storage condition. Respiration rate of mangoes at first decreases slowly, then it increases up to its peak and after that decreases during storage period in PFSF but after putting mangoes in ambient condition respiration rate increases rapidly up to its peak, then it decreases with time. Respiration rate increases with increase in temperature and decrease in relative humidity. Maximum respiration rate was observed in Safeda (ambient) and minimum in Kesar (PFSF). Firmness and titratable acidity (TA) of mango of both varieties showed decreasing trend with increase in temperature and decrease in relative humidity. The effect of abiotic parameter i.e., temperature and relative humidity of selected storage structures (PFSF and ambient storage condition) on storability parameters was found significantly different at 5% level of significance ($P<0.05$).

Design and development of an integrated earth air heat exchanger cum evaporative cool (EAHE-EC) storage structure for fresh produce

In the present research work, an integrated earth air heat exchanger cum evaporative cool (EAHE-EC) storage structure was designed and developed to store fresh produce at the farm level. The integrated EAHE-EC storage structure works based on the combined principle of geothermal energy and adiabatic cooling. It comprises a storage room, earth air heat exchanger, and evaporative cooling systems. The cooling performance of the developed EAHE-EC system was evaluated at three different air velocities (4 to 6 m/s), water flow rates (0.032 to 0.096 kg/s), and thickness of the cooling pad (50 to 150 mm). These independent parameters were optimized using Box-Behnken Design (BBD) under Response Surface Methodology (RSM) in Design-Expert Software. The corresponding optimum values for maximum temperature drop (16.80°C) and humidity rise (70.85%) within a range of input variables were found to be 4 m/s air velocity, 0.065 kg/s water flow rate, and 150 mm thickness of the cooling pad. The effectiveness of the developed EAHE-EC system for its capability to extend the shelf life of fresh commodities was studied by assessing the effect of storage conditions on each postharvest quality parameter of tomato and mango fruit. Based on the retention of the overall quality and microbial load till the end of the storage period, the shelf life of tomato and mango fruit stored inside the EAHE-EC system was recorded as 21 and 12 days, respectively, which was 2.5-3 times higher than ambient storage (9 and 4 days). The extra shelf-life gained by tomatoes and mangoes inside the EAHE-EC system can provide a sufficient buffer period for farmers for retailing and marketing.

Development and evaluation of non-destructive technique for precise detection of internal quality of mango fruit

The Indian mango sector grapples with challenges, including postharvest losses, limited infrastructure, and quality standards awareness. The Alphonso mango faces global market setbacks due to inaccessible postharvest solutions, affecting storage potential. Spongy tissue and fruit fly infestations hinder exports, impacting internal quality. To tackle this, a study in Konkan, Maharashtra, assessed mango supply chains and challenges. Three non-destructive techniques X-ray imaging, VNIR spectroscopy were evaluated. Machine learning models were developed for automatic classification of spongy tissue-affected and healthy mangoes, aiming to enhance quality and address export concerns. The survey identified two primary mango supply chains domestic and export-oriented in the study area. The export chain, predominantly run by young, educated farmers, yielded higher returns. Substantial losses, ranging from 30-40 % in pre-harvest stages to 15-20% in post-harvest handling, were observed. Cold storage mitigated spongy tissue disorder, curbing heat accumulation and seed germination during ripening. The evaluation of the X-ray imaging technique involved capturing 260 mango images, augmented to 1430, utilizing various augmentation methods. K-means clustering and edge detection effectively segmented healthy and spongy tissue-affected parts, with k-means showing superior differentiation. Machine learning algorithms—CNN, VGGNet, AlexNet, ResNet, and SVM—achieved high overall accuracy (98.60%, 98.95%, 98.85%, 99.30%, and 95.35%, respectively), with ResNet outperforming others. In Vis-NIR spectroscopy, spectral signatures were acquired, and principal component analysis identified key wavelength regions (670-770, 900-970, 1100-1170 nm) for clear classification. SIMCA modelling in these regions achieved accuracies of 94.5%, 96.6%, and 87.7%, confirming the discrimination power of the 670-1170 nm wavelength range for identifying internally damaged mangoes. Minimizing pre- and post-harvest losses with proper handling, packaging, and non-destructive techniques like X-ray imaging and VNIR spectroscopy can reduce losses, improve quality, boost exports, and increase returns in the mango supply chain.

Design and development of IoT based smart grain storage structure

Grain storage structures play a vital role in the economies of developing countries by providing a secure environment to prevent grain losses caused by adverse weather, moisture, pests, and microorganisms. In particular, pulses, considered a nutritious vegetarian staple, face post-harvest losses of 10-30% in subtropical regions due to inadequate storage practices. Addressing this challenge, an integration of conventional methods with modern technologies like the Internet of Things (IoT) and Wireless Sensor Networks has been attempted to modernize agriculture. The study focused on determining the physical and mechanical properties of pulses (lentil, pigeonpea, and chickpea) at varying moisture content. Key dimensions, such as geometric mean diameter and 1000 seeds mass, increased with moisture content. Sphericity, porosity, and angle of repose exhibited linear growth, while bulk density and true density decreased. The coefficient of static friction increased with moisture, with stainless steel surface showing the minimum. Pulse hardness decreased linearly with increasing moisture content. Respiration rates, crucial for establishing proper management, were measured at different moisture and temperature combinations over a 42-day storage period. Pigeon pea showed higher respiration rates compared to chickpea and lentil. The rates correlated positively with final moisture content and free fatty acid value, while negatively with seed germination. Crude protein and ash content remained relatively stable, while total phenolics and carbohydrate exhibited a decreasing trend after 42 days. IoT-based smart grain storage structure was developed with real-time monitoring capabilities for temperature, humidity, and CO_2 concentration. The system, comprising a 500 kg capacity grain storage structure, an embedded system with sensors and relays, and integration with an IoT system and air-blowing system, was evaluated by storing chickpea grains for ten months. Results demonstrated effective monitoring and control of storage conditions, leading to better retention of quality parameters compared to conventional silos. The IoT-based smart grain storage silo holds significant potential for facilitating long-term, quality pulse storage in rural households, minimizing spoilage losses with real-time information.

Improved process technology for rancidity alleviation in pearl millet

Pearl millet flour faces storage challenges due to rancidity, resulting in undesirable odour and flavour. Physiochemical factors like lipase enzyme and fat content impact its storage life. To address this, a three-stage study optimized pre-milling treatments, milling methods, and packaging operations to enhance the storage life of pearl millet flour and mitigate chemical deterioration. Initially, the investigation aimed to select a suitable pearl millet variety based on energy consumption during grinding. Seven cultivars (Pusa1201, Pusa1801, Pusa1601, PC701, PC443, PC343, and PC612) underwent assessment for geometric, gravitational, mechanical, and frictional properties at varying moisture contents (10%, 15%, 20%, and 25%, wb). Pusa1801, Pusa1601, and Pusa1201 exhibited higher thousand grain weight, resulting in increased flour yield compared to composite varieties (PC701, PC383, PC612, and PC434). Pusa1201, with its maximum sphericity, showed a negative correlation between porosity and hardness, indicating lower energy consumption during grinding. Consequently, Pusa1201 was chosen for subsequent treatments. For both hammer and plate mills, minimum energy consumption, kicks constant, and bond work index were identified at 8.63% moisture content and 6.5 kg h^{-1} feed rate. Moisture content and feed rate significantly influenced average particle size, fineness modulus, and water absorption capacity of pearl millet flour. Three pre-milling treatments, namely decortication (3%, 6%, and 9%), infrared (1min, 3min, and 5min), and combined treatments (various combinations), were applied. These treatments, along with storage duration, significantly affected rancidity parameters. The combined treatment of 9% decortication and 3-minute infrared exposure yielded maximum reductions in comprehensive acid value (37.34%), comprehensive peroxidase value (38.46%), and lipase enzyme (37.77%). Flour rancidity increased for all treatments up to 30 days, with the minimum increments observed for the combine treatment (1.642% in moisture content, 41.28% in comprehensive acid value, 39.66% in comprehensive peroxidase value, and 31.89% in lipase). Selected pre-treated and untreated samples were packed with polypropylene (PP) and Aluminium (Al) using vacuum and non-vacuum methods, significantly affecting moisture content, comprehensive acid value, and comprehensive peroxidase value. While packaging materials did not significantly impact colour value, the vacuum method with Al material proved superior, enhancing the shelf life of selected pearl millet flour for 60 days.

Design and development of an IR based hybrid dryer for horticultural produce

Apple is one of the most consumed foods in India both in raw and processed form (chips). Not only it satisfies the food cravings but also it has numerous potential health benefits against chronic disorders. But being seasonal in nature, it needs to be preserved to avail year-round. Drying is one of the convenient techniques of preservation in large scale. Mostly sun drying is followed but both the physical and chemical quality of the apple slices gets hampered with longer drying time. So, in this study a time efficient, energy efficient, technically advanced dryer was developed for drying of apple slices by combining the infrared and convective mode of drying. Drying unit, recirculatory unit, power control unit were the integral parts of the developed dryer. The dryer could be used in infrared mode, convective mode or in combine mode. The terms of performance evaluation, the drying process parameters were optimised using the desirability function of Response Surface Methodology. Twenty sets of experiments were formulated with CCRD. The Drying time, effective moisture diffusivity, drying efficiency, SPC along with physical (Colour, hardness and rehydration ratio) and chemical parameters like (TPC, TFC, AA and Antioxidant content) was studied with variation of independent responses like infrared intensity (0.15 - 0.25 W/cm^2), air velocity (0.5-1.5 m/s) and radiation distance between source and sample (10-18 cm). Cost economic evaluation was done for the developed hybrid dryer in considering the ownership cost and operating cost. Breakeven point and payback period was also analysed. It is concluded that, the infrared assisted hybrid dryer is not only time and cost efficient but also good quality of final dried product was obtained with high throughput capacity.

Pretreatment and process optimization for infrared dehydration of carrot shreds

Carrots (*Daucus car*ota) are nutrient-rich root vegetables, known for β-carotene, vitamin A, and potassium. Moisture retention challenges affect freshness and shelf life. Infrared (IR) drying is explored for preservation, offering extended storage and economic viability. The study optimizes IR dehydration for carrot shreds, considering pre-treatment methods, sugar concentration, time, and temperature. Ultrasonic-osmotic pre-treatment reduces final moisture content compared to osmotic dehydration. Osmotic dehydration at 30%, 15 min, 40°C yields the shortest drying time (75 min). Ultrasonic-osmotic pre-treatment enhances moisture removal and effective diffusivity. Higher sugar concentrations reduce L* values in dried shreds. Biochemical changes include increased phenolic and flavonoid content, reduced carotenoids. Optimal pre-treatment for IR dehydration is osmotic dehydration at 15%, 15 min, 40°C, balancing nutritional preservation and drying characteristics. IR conditions impact drying behaviour, with distance affecting moisture content and drying time positively, while wattage has a negative influence. Far-infrared bulbs outperform, retaining bioactive compounds and achieving higher rehydration ratios. Response Surface Methodology optimization suggests Mid Infrared bulbs at 15 cm, 3.5 W g^{-1} intensity, provide the most favourable results across various parameters.

Theme-7: Value Addition of Agricultural Produce

Extraction of cellulose nano crystals (CNCS) from legume husk and process design for its use in polymer as reinforcement

This study set out to extract nanocellulose from chickpea husk and assess its influence on Poly Lactic Acid (PLA)-based composite materials and an alkali treatment method was employed for extraction. The optimization of this process, utilizing Box-Behnken design and response surface methodology (RSM), resulted in a 73.08% yield of crude cellulose under optimized conditions: 0.84 M NaOH concentration, 70°C process temperature, and 2 hours extraction time. Validation through paired t-tests indicated non-significant differences ($p>0.05$). Characterization of the crude cellulose unveiled an 89.5% crystallinity index via X-ray diffraction, confirming lignin removal as evidenced by FTIR and TGA. Cellulose nanocrystals (CNC) were synthesized from the crude cellulose through acid hydrolysis, with Box-Behnken optimization yielding an optimal condition of 43% H_2SO_4 concentration, 40°C process temperature, and 87.08 minutes extraction time. Predicted CNC properties encompassed a size of 424.83 nm, zeta potential of -17.96 mV, 98.46% crystallinity index, 1.63 mPa s^{-1} viscosity, and an 84.35% yield. Validation results demonstrated non-significant differences ($p>0.05$). CNC was further characterized for size, zeta potential, and crystallinity index. In the development of biodegradable nanocomposites (PLA/CNC), PLA was chosen as the foundational matrix; with CNC concentrations ranging from 0 to 10% incorporated using the solvent casting method. Evaluation parameters included barrier properties (water vapor permeability and oxygen transmission rate), mechanical properties (tensile strength and elongation at break), thermal properties (melting temperature, glass transition temperature, weight loss onset temperature, and weight loss peak temperature), and morphological study via SEM. Optimal outcomes revealed a notable 52.74% reduction in water vapor permeability at 4% CNC loading and a prominent 56.58% reduction in oxygen transmission rate at the maximum 10% CNC loading, in comparison to the pristine PLA film. Tensile strength exhibited improvement with escalating CNC loading, albeit at the expense of elongation at break. Consequently, the incorporation of CNC into PLA is recommended as a viable alternative for the formulation of biodegradable composite packaging materials.

Effect of IR treatment on pigeon pea dehulling and its quality characteristics

Pulses have been an integral part of the human diet for centuries, known for their nutritional value. Traditionally, legumes undergo pre-milling treatments, including both dry and wet processes, involving repeated pitting, moistening, and drying during milling. The current investigation delves into the impact of infrared radiation under various voltage (V) settings (203, 210, 220, 230, and 237 V) and exposure times (T) ranging from 1.3 to 4.7 minutes. Different grain moisture content levels (MC; 8.6%, 10%, 12%, 14%, and 15.4% wet basis) were considered, assessing forces related to dehulling, such as hull adhesion strength, cotyledon integrity (cotyledon adhesion and shear strength), and dehulling characteristics (dehulling index, degree of dehulling, dehulling efficiency, dehulling losses, and husk removal). Central composite rotatable design and response surface methodology were employed for experimental design and analysis, respectively. A strong correlation between infrared heating parameters and grain moisture was observed. Voltage (V) exhibited a significant negative effect on hull adhesion strength (Hs) and dehulling losses (DL), while it positively influenced dehulling efficiency (DE), dehulling index (DI), and degree of dehulling (DD). Optimized conditions were determined at 228 V, 12.4% moisture content, and 2.9 minutes exposure time, resulting in a desirability of 1.0. Two-tailed paired t-tests affirmed the model's accuracy in predicting values. Infrared treatment significantly reduced hull adhesion strength (from 8.80 to 2.37 N mm^{-2}). Furthermore, the study investigated the variation in infrared intensity across different voltage levels and its impact on thermal properties, specifically specific heat (Cp), thermal conductivity (kp), and thermal diffusivity, of pigeon pea grains at various moisture levels. The research confirmed improved milling properties and altered thermal characteristics of pigeon pea grains under infrared treatment, with observed changes in biochemical, functional, cooking, and microstructural properties.

Development of microwave-assisted enzymatic oil extraction technology for oilseeds

India, a vast agrarian nation, hosts 26% of the world's farming population on 12% arable land, importing 60% of its edible oils despite significant oilseed production. To address this, A laboratory prototype of a Microwave-assisted enzymatic extraction system was developed to enhance oil yield from the sesame seed. This eco-friendly approach reduces solvent usage, energy consumption, and processing time, offering a potential solution to India's edible oil import dependency while minimizing environmental impact. The system's efficiency was gauged by assessing the impact of various solvents (Ethanol, Iso-propanol, Methanol, Ethyl acetate, Acetone, and Hexane) on sesame oil extraction yield and slurry temperature. Preliminary experiments determined influential parameters, established procedures, and ensured repeatability. To maximize sesame seed oil yield, experiments optimized green solvents, enzymes, particle size, soaking time, and solvent-to-seed ratio. Variables included solvents (Ethanol, Iso-propanol, Methanol, Ethyl acetate, and Acetone), enzymes, particle size (<0.4mm, 0.6mm, and 0.8mm), soaking time (20, 40, 60, and 80 min), and solvent-to-seed ratio (2:1, 3:1, 4:1, 5:1, and 6:1). Optimum values for maximum oil yield were determined, and these variables remained constant in final experiments. The study optimized Microwave-assisted enzymatic extraction (MAEE) for sesame seed oil, using a central composite rotatable design with MW power (90-700 W), Treatment time (60-300 min), enzyme: seed ratio (0.2-1 g : 100g), and pH (2-6). Isopropanol was the most effective solvent, emphasizing enzyme importance, with xylanase as the best and hemicellulase the least effective. Optimal conditions (160 W, 187.8 s, 0.28:100 enzyme: seed ratio, pH 5) yielded 45.20% oil with maximum retention of oil quality like 1.33±0.08 mg KOH/g of FFA, 192.20±1.48 mg KOH/g of saponification value, 1.792±0.015 meq O_2/kg of peroxide value, 111.19±1.02 meq I/g and light yellow in colour (61.46±2.25). The crude oil yield obtained with the optimum condition of MAEE (45.20%) was higher than the conventional mechanical extraction (35.40%) and Aqeous enzymatic extraction (27.89%). The properties of the oil extracted from sesame seeds at the optimized condition of MAEE highly resembled the properties of yellow Sesame seeds oil also met the standards suggested by "FSSAI standards, 2009".

Characterization and processing of mango kernel for its use in food products

The perishable nature of fruits necessitates processing for prolonged shelf life. Mango processing generates by-products—peel and stone. Mango stone, constituting 35% of the fruit, yields approximately 68% kernel, 29% shell, and 3% testa. Global mango kernel production from processing industries is around 123,000 metric tons annually. Being a potential source of bioactive compounds and nutrients mango seed kernels (MSK) contain antinutritional factors (ANFs) like tannin and phytate, limiting their direct use in food products. Present study is aimed to characterize mango stone and kernel of select verities, explore hurdle technology for effective reduction of ANFs and to utilize processed mango kernel flour (MKF) in the development of food product. Linier dimension of mango fruit, stone, fresh and dry kernel varied significantly among varieties. For dried kernel, maximum coefficient of friction was observed on test surface galvanized iron followed by mild steel, aluminium and glass. The force required to break the kernel was higher in dried kernel (95.2 to 359.3 N) as compared to the fresh kernel (69.2 to 124.7 N). Biochemical properties viz. total phenol content (TPC), DPPH, tannin and phytic acid content varies from 39.43 to 60.78 mg GAE/g, 94.5% to 95.7%, 48.8 to 107.7 mg tannic acid/g and 17.4 to 23.4 mg /g respectively for selected varieties. Combination processing – boiling for 3 h followed by 15 min infrared treatment – was observed to effectively reduce ANFs and save approximately 23% energy and 20% time to process the kernel as against 4 h continuous boiling. This process technique could able to reduce 60% phenol, 1% DPPH, 61% tannin and 37% phytic content in the mango kernel. Processing significantly altered functional, rheological and biochemical properties of mango kernel. Processed mango kernel flour addition, sonication and their interaction effect were observed to be significant on textural, biochemical and sensory characteristics of multi-millet eggless muffins. Sonication had a negative influence on muffin desirable characters; addition of processed mango kernel flour up to 10% in multi-millet eggless muffins is feasible with better nutritional, physical and sensory qualities.

Pre-treatment strategies for improved oil recovery from mustard seeds

Mustard (*Brassica juncea*) faces challenges due to limited production and low oil recovery rates. This study explores effect of microwave (MW), infrared (IR) and ohmic heating (OH) pre-treatment methods on millable oil recovery from mustard seeds, assessing availability, compositional quality and fatty acid profile. Hyperspectral imaging (HSI) using visible near-infrared (Vis-NIR) and short-wave infrared (SWIR) spectra analyses oil content, fatty acids, and spatial distribution. Chemometric techniques, including principal components analysis (PCA), partial least square discriminant analysis (PLS-DA) and regression (PLSR), process spectral data for improved recovery techniques in meeting the rising demand for high-quality mustard oil. Results indicated significant influences of pre-treatment methods on millable oil recovery. MW pre-treatment achieved the highest oil recovery (33.71%), while IR treatment (32.13%) and OH treatment (33.18%) also showed notable results. Pre-treatments affected peroxide value, acid value, FFA content, and colour of milled mustard oil, with refractive index, density, and viscosity remaining unaffected. The fatty acid analysis showed variations in the levels of different fatty acids based on the pre-treatment method employed. Hyperspectral data analysis using PCA indicated differences between treated and untreated mustard seeds, with SWIR spectra providing better discrimination. PLS-DA models successfully classified the pre-treated mustard seeds using spectral pre-processing methods, achieving high sensitivity, specificity, precision and accuracy above 95%, with SWIR spectra outperforming Vis-NIR spectra. PLSR models accurately predicted millable oil and fatty acid content, with SWIR spectra ($R^2>0.80$) achieving superior performance compared to Vis-NIR spectra ($R^2>0.65$). The study also identified optimal wavelengths for oil content and fatty acid component predictions using the iPLS model. Prediction maps were generated to visualize the spatial distribution of oil and fatty acid content within the pre-treated mustard seeds. The findings enhance understanding of effective pre-treatment strategies for mustard seed oil recovery, guiding operating protocols and employing hyperspectral imaging for rapid predictions.

Development of hybrid ultrasonic-microwave assisted essential oil extraction technology and its kinetics for tuberose flowers (*Polianthes tuberosa* L.)

The tuberose (*Polianthes tuberosa* L.) is a perennial plant known for its aromatic white flowers, utilized in perfumery for essential oil extraction. Traditional methods, requiring substantial solvents and extended durations, are being replaced by modern techniques like ultrasonic-microwave assisted extraction (UMAE). UMAE, employing ultrasound and microwave energy, enhances extraction efficiency, and statistical models like RSM and ANN optimize the process parameters. The sequential ultrasound-microwave assisted extraction (UMAE) method was employed to assess the impact of varying factors on the extraction yield of concrete from tuberose flowers. Parameters investigated included solvent type (n-hexane, methanol, and petroleum ether), size (cut flower and whole flower), and soaking durations (0, 30, and 60 min). The optimized conditions resulting in the highest extraction yield (95.04%) were found to be n-hexane as the solvent, cut samples, and a 30-minute soaking duration. The tuberose concrete obtained through all three extraction methods using n-hexane as the solvent revealed the presence of aroma compounds, including 1,8-cineole, methyl benzoate, indole, α-terpineol, trans-methyl isoeugenol, trans-farnesol, and benzyl benzoate. Attenuated total reflectance-Fourier transform infrared spectroscopy (ATR-FTIR) spectra of concretes extracted with n-hexane were notably similar. Principal component analysis (PCA) and sparse Partial Least-Squares Discriminant Analysis (sPLS-DA) effectively distinguished volatile organic compounds, with sPLS-DA outperforming PCA. The concrete yield from UMAE samples ranged from 82.2% to 97.1%, with the highest yield (97.1%) observed under specific conditions: 640 W microwave power, 300 W ultrasonic power, 240 s microwave exposure time, and 720 s sonication time. Artificial neural network (ANN) models exhibited superior performance compared to response surface methodology (RSM) in predicting concrete yield, with R2 values of 0.980 for ANN and 0.904 for RSM. Additionally, ANN models had lower RMSE (1.177) and mean absolute error (1.385) compared to the RSM model (RMSE: 1.284, mean absolute error: 1.65). For the optimization of extraction parameters using response surface methodology, a quadratic model predicted an optimum phenolic content of 247.26 mg/g. The developed ANN models for total phenols exhibited slightly lower R2 values (0.816) than RSM models (0.829), while RSM models had lower RMSE (3.5) and mean absolute error (12.25) compared to ANN models (RMSE: 12.689, mean absolute error: 161.0). The study highlights UMAE as a rapid method for extracting total phenols from tuberose flowers, with the developed models proving significant and well-fitted, as indicated by low P-values ($P<0.05$) for antioxidant capacity. The antioxidant capacity of ANN models had lower RMSE (1.44) and mean absolute error (2.10) compared to RSM models (RMSE: 2.255, mean absolute error: 5.086). The first-order kinetic model was found to be more suitable for describing and fitting the experimental data.

List of contributing students and Chairpersons of their advisory committees

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Mukesh Pattaiya (21575)	M.Tech.	Characterization and processing of mango kernel for its use in food products	Dr. Arun Kumar T V	ICAR-IARI, New Delhi
2.	Matondkar Piyusha Mahendra (21576)	M.Tech.	Pretreatment and process optimization for infrared dehydration of carrot shreds	Dr. Arun Kumar T V	ICAR-IARI, New Delhi
3.	Saurabh Kumar Gupta (21577)	M.Tech.	Studies on storage and packaging of marigold (*Tagetes erecta*) loose flowers in Pusa Farm Sun Fridge (PFSF)	Dr. Pramod Kumar Sharma	ICAR-IARI, New Delhi
4.	Subrata Mandal (21578)	M.Tech.	Design and development of IoT-based monitoring system for storage of mangoes in Pusa farm sun fridge	Dr. Pramod Kumar Sharma	ICAR-IARI, New Delhi

5.	Mohanaselvan. T (21579)	M.Tech.	Study of sugarcane mechanization and health hazards in Erode district	Dr. Shiv Pratap Singh	ICAR-IARI, New Delhi
6.	Radha Krishnan (21580)	M.Tech.	Development of paddy drum seeder-cum-fertilizer applicator	Dr. Shiv Pratap Singh	ICAR-IARI, New Delhi
7.	Rachamalla Naveen (21581)	M.Tech.	Development of vibration reduction intervention in single axle tractor-trailer system	Dr. Adarsh Kumar	ICAR-IARI, New Delhi
8.	Soubhagya Sekhar Nayak (21582)	M.Tech.	Design and development of sensor-based multiple-input application system for seeder	Dr. Satish Devram Lande	ICAR-IARI, New Delhi
9.	Sathish Kumar B N (21583)	M.Tech.	Design and development of mustard thresher for seed purpose	Dr. Tapan Kumar Khura	ICAR-IARI, New Delhi
10.	Jadav Kaushik Amrishbhai (21584)	M.Tech.	Study on extent and severity of waterlogging and soil salinity of the Bhal region of Gujarat, India	Dr. Anil Kumar Mishra	ICAR-IARI, New Delhi
11.	Sridhanabharathi B (21585)	M.Tech.	Comparative study on irrigation and mulching effects in two wheat varieties	Dr. Dhirendra Kumar Singh	ICAR-IARI, New Delhi
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13.	Barnali Saha (21588)	M.Tech.	Conjunctive use for enhancing water productivity in Rarh region of West Bengal, India	Dr. Anil Kumar Mishra	ICAR-IARI, New Delhi
14.	Rauminsh Kumar (60093)	M.Tech.	Lysimeter-based crop evapotranspiration and crop coefficient for irrigated maize and brinjal in hot and sub-humid zone	Dr. Santosh Sambhaji Mali	#ICAR-IARI Jharkhand
15.	Bhavani (70008)	M.Tech.	Effect of deficit irrigation on garlic (*Allium sativum* L.) cultivars in Deccan Plateau of India	Dr. Goraksha Chimaji Wakchaure	**ICAR-IARI Baramati
16.	Puneet Kumar (10738)	Ph.D.	Effect of IR treatment on pigeon pea dehulling and its quality characteristics	Dr. Subir Kumar Chakraborty	**ICAR-CIAE, Bhopal
17.	Changchuk Lamo (10743)	Ph.D.	Extraction of cellulose nano crystals (CNCs) from legume husk and process design for its use in polymer as reinforcement	Dr. Praveen Chandra Bargale	**ICAR-CIAE, Bhopal
18.	Prem Veer Goutam (10953)	Ph.D.	Studies on effect of tool geometry and operational parameters on soil failure in vertisols	Dr. Prem Shanker Tiwari	**ICAR-CIAE, Bhopal
19.	Monika Satankar (11170)	Ph.D.	Improved process technology for rancidity alleviation in pearl millet	Dr. Pramod Kumar Sahoo	ICAR-IARI, New Delhi
20.	Rahul Shubhash Yadav (11173)	Ph.D.	Development of hybrid ultrasonic-microwave assisted essential oil extraction technology and its kinetics for tuberose flowers (*Polianthes tuberosa* L.)	Dr. Debabandya Mohapatra	**ICAR-CIAE, Bhopal
21.	Lalita (11175)	Ph.D.	Infrared thermography for modelling of refractance window drying of aonla (*Emblica officinalis*) slices	Dr. Nachiket Kotwaliwale	**ICAR-CIAE, Bhopal

22.	Pankaj Malkani (11176)	Ph.D.	Development of sensor- based weed detection and herbicide application system	Dr. Indra Mani	ICAR-IARI, New Delhi
23.	Aman Mahore (11178)	Ph.D.	Investigations on microcontroller-based precise fertilizer dispensing system for spot application in widely spaced crops	Dr. Krishna Pratap Singh	**ICAR-CIAE, Bhopal
24.	Rohit D. Nalwade (11180)	Ph.D.	Study on optimization of geometrical and operational parameters of rotary tiller blades for efficient utilization of power in vertisols	Dr. Krishna Pratap Singh	**ICAR-CIAE, Bhopal
25.	Bhagwan S. Narwariya (11183)	Ph.D.	Studies on systems for harvesting of cabbage	Dr. Kamal Nayan Agrawal	**ICAR-CIAE, Bhopal
26.	Asha K. R. (11186)	Ph.D.	Development of a device for assessment of paddy lodging characteristics	Dr. H. L. Kushwaha	ICAR-IARI, New Delhi
27.	Venkatesh (11187)	Ph.D.	Development of irrigation water release schedule information system for a minor canal command	Dr. Arjamadutta Sarangi	ICAR-IARI, New Delhi
28.	Abhishek Patel (11189)	Ph.D.	Investigations on straw incorporation system with chopping unit using discrete element modelling	Dr. K V Ramana Rao	**ICAR-CIAE, Bhopal
29.	Dharmender (11389)	Ph.D.	Development of microwave-assisted enzymatic oil extraction technology for oilseed	Dr. Indra Mani	ICAR-IARI, New Delhi
30.	Silpa Mandal (11392)	Ph.D.	Machine learning based non-destructive system for pesticide residue detection in apple	Dr. Pramod Kumar Sharma	ICAR-IARI, New Delhi
31.	Khushboo Gupta (11393)	Ph.D.	Design and development of IoT based smart grain storage structure	Dr. Tapan Kumar Khura	ICAR-IARI, New Delhi
32.	Rajendra Hamad (11394)	Ph.D.	Pre-treatment strategies for improved oil recovery from mustard seeds	Dr. Subir Kumar Chakraborty	**ICAR-CIAE, Bhopal
33.	Chinmayee Parida (11395)	Ph.D.	Design and development of IR based hybrid dryer for horticultural produce	Dr. Pramod Kumar Sahoo	ICAR-IARI, New Delhi
34.	Aseeya Wahid (11398)	Ph.D.	Development of vacuum impregnation technology for shelf-life enhancement of vegetables	Dr. Saroj Kumar Giri	**ICAR-CIAE, Bhopal
35.	Nrusingh Charan Pradhan (11399)	Ph.D.	Design and development of automatic control system for agricultural tractor	Dr. Pramod Kumar Sahoo	ICAR-IARI, New Delhi
36.	Omkar Gupta (11401)	Ph.D.	Design and development of sensor-based monitoring and control system for safe and effective operation of tractor implement system	Dr. Indra Mani	ICAR-IARI, New Delhi
37.	Vijay Kumar (11403)	Ph.D.	Prediction of the soil properties using artificial intelligence	Dr. Krishna Pratap Singh	**ICAR-CIAE, Bhopal
38.	Parmananad Sahu (11404)	Ph.D.	Kinetic study on step pyrolysis of biomass	Dr. Sandip Gangil	**ICAR-CIAE, Bhopal
39.	Ajay Kushwah (11406)	Ph.D.	Design and development of precise intelligent cauliflower harvester	Dr. Pramod Kumar Sharma	ICAR-IARI, New Delhi

40.	Ramineni Harsha Nag (11408)	Ph.D.	Design and development of a battery-operated harvester for leafy vegetables	Dr. Pramod Kumar Sharma	ICAR-IARI, New Delhi
41.	Sidhartha Sekhar Swain (11411)	Ph.D.	Design and development of urea super granule (USG) application system integrated to paddy transplanter	Dr. Tapan Kumar Khura	ICAR-IARI, New Delhi
42.	Achugatla Kesav Kumar (11412)	Ph.D.	Occupational health hazards of tobacco cultivation and development of safety interventions	Dr. Adarsh Kumar	ICAR-IARI, New Delhi
43.	Amit Kumar (11417)	Ph.D.	IoT-enabled irrigation water management system for enhancing water productivity	Dr. Arjamadutta Sarangi	ICAR-IARI, New Delhi
44.	Gottam Kishore (11422)	Ph.D.	Investigations on magnetically treated irrigation water and system performance	Dr. Ranjay Kumar Singh	**ICAR-CIAE, Bhopal
45.	Vinod Kumar (11423)	Ph.D.	Studies on the Microclimate Variations in Different Mulching Conditions under Drip Irrigated Sweet Corn Using Internet of Things	Dr. Chandra Deep Singh	**ICAR-CIAE, Bhopal
46.	Kishor Pandurang Gavhane (11648)	Ph.D.	Development of sensor-based automated fertigation system for vertical farming	Dr. Murtaza Hasan	ICAR-IARI, New Delhi
47.	Madhusudan B S (11657)	Ph.D.	Studies on development of retrofit seeding attachment for combine harvester	Dr. H L Kushwaha	ICAR-IARI, New Delhi
48.	Laxmi Pojitha Chhalla (11658)	Ph.D.	Application of IoT technique for irrigation scheduling based on environmental conditions in a naturally ventilated greenhouse	Dr. Chandra Deep Singh	**ICAR-CIAE, Bhopal
49.	Patil Rajvardhan Kiran (11675)	Ph.D.	Development and evaluation of non-destructive technique for precise detection of internal quality of mango fruit	Dr. Roaf Ahmad Parray	ICAR-IARI, New Delhi
50.	Praween Kumar Nishad (11678)	Ph.D.	Design and development of an integrated earth air heat exchanger cum evaporative cool (EAHE-EC) storage structure for fresh produce	Dr. Shukadev Mangaraj	**ICAR-CIAE, Bhopal
51.	Pangam Heramb (11693)	Ph.D.	Data-driven techniques for evapotranspiration modelling in different agro-ecological regions of India	Dr. K V Ramana Rao	**ICAR-CIAE, Bhopal

#IARI off campus

**Outreach Institute

Agricultural Physics

9

Prof. P. Krishnan

Endowed with a mission to study Soil-Water-Plant-Environment Energetics for eco-friendly and sustainable exploitation of agricultural resources, the division of Agricultural Physics focuses its research in four major research areas: Plant-Biophysics, Soil Physics, Environmental Physics and Agricultural Meteorology. Regular PG courses, summer/winter schools and specific training programmes in Remote Sensing and its applications in agricultural resources management became part of the activities since 1970. Ever since its inception, the Division has collaborated in Inter-Divisional, Inter-Institutional and International research activities. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Remote Sensing in Agriculture

Hyperspectral remote sensing of wheat yellow rust (*Puccinia striiformis f. sp. tritici.*)

Wheat serves as the primary food source for approximately 35% of the global population. Yellow rust or stripe rust causes annual average losses of up to 50 per cent in wheat yield and higher losses is possible if the infection commences early. Unfortunately, there is a lack of fundamental information on the spectral signature of wheat yellow rust disease, hindering its real-time detection and management. The current study aims to characterize the spectral reflectance of wheat affected by yellow rust to detect the sensitive spectral range. Field experiment at IARI New Farm area was conducted for the winter wheat crop with different level of yellow rust infection. Spectral observations were taken at canopy level in field condition in the spectral range of 350-2500 nm. Yellow rust severity level was graded from 0-9 score as per standard procedure. The 1st derivative spectral analysis of disease severity levels was conducted to distinguish the sensitive bands. Two newly proposed indices were formulated and evaluated as Normalized Yellow Rust Index 1 (NYRI1), Normalized Yellow Rust Index 2 (NYRI2) with identified wavebands at 675 nm and 1100 nm for NYRI1 and 1750 nm and 2000 nm for NYRI2. Utilizing the spectral data and the sensor response function of the Sentinel-2 sensor, broadband indices were calculated for the Sentinel-2 MSI band information. Among the existing indices, EVI yielded superior results with an R2 of 0.89 in predicting disease levels. Different multivariate and machine learning algorithms such as partial least square regression (PLSR), multiple linear regression (MLR) and random forest (RF) were also evaluated to predict disease severity levels. All the models were found to be good predictors. However, PLSR yielded the highest R2 of 0.977, RPD of 0.08 and least RMSE of 0.439. The research affirms the capacity of hyperspectral remote sensing to evaluate and differentiate the various degrees of severity in wheat yellow rust disease.

Agricultural drought monitoring and early warning using meteorological and remote sensing datasets for India

Agricultural drought is a complex natural hazard which has serious adverse impacts on crop growth and yield, livelihoods of farmers and socio-economic conditions of India. The adverse impacts of agricultural drought can be avoided and mitigated by accurate and timely monitoring as well as early warning of the spatial extent, severity and progression of the agricultural drought. In this study drought indices were developed for India at 1 km spatial resolution and 16 days' temporal resolution from 2001 to 2021 using the long-term datasets. It was found that the drought indices developed from same inputs were highly correlated with each other, but less correlated with other input-based indices. Composite Drought Index (CDI) was developed to integrate their multidimensional effects into a single index. CDI was developed by assigning the weightages to the selected drought indices using Principal Component Analysis (CDI_{PCA}) and Analytical Hierarchical Process (CDI_{AHP}) methods. The input drought indices used for CDI_{PCA} were SPI-6, SESR, VCI_{Tadj}, SNDWI and SSWDI, while for CDI_{AHP} were SPI-1, SPI-2, SPI-6, SESR, SNDVI, SNDWI and SSWDI. CDI_{PCA} was selected for the generation of agricultural drought outlook for the next 16 days for Karnataka state using different machine learning algorithms i.e., Artificial Neural Network (ANN), Classification and Regression Tree (CART) and Random Forest (RF). The input data used for generation of CDI outlook were CDI of the current and two previous time periods, forecasted weather data on precipitation flux, vapour pressure, cloud cover, maximum and minimum temperature of the next 16 days, and percentage irrigated area. The study is an advancement in developing a high resolution near-real time drought monitoring and forecast system for India. Adoption of such system by state and central agencies may help in risk management of drought for agricultural sector by prioritizing mitigation plans and timely initiating contingency measures.

Assessment of wheat stripe rust and chickpea wilt through thermal and optical remote sensing

Reliable and quick assessment of plant disease is essential for minimizing losses and for ensuring food security. Field experiments on wheat yellow rust and chickpea wilt were conducted for 2 and 3 years, respectively, for disease assessment using thermal and optical remote sensing. Biophysical parameters were also measured at regular intervals along with NDVI and visual scorings of disease severity in both crops. Supervised image classification was performed to estimate yellow rust severity. AI based Machine learning models were employed to predict disease severity and predict crop yield based on biophysical parameters and image derived indices at different growth stages in both crops. Results revealed that the LAI, RWC, MSI, photosynthesis, stomatal conductance, transpiration, NDVI, and crop yield in both crops showed a consistent and similar trend of decreasing values with increasing levels of disease severity at all growth stages. The thermal image derived canopy temperature of both crop increased with crop diseases severity. Our results demonstrated the potential of thermal and visible imaging techniques to estimate stripe rust severity with good accuracy. For both visible and thermal images used in this study, support vector machine gave the best estimates of the rust severity with R2 above 0.85 and accuracies above 98% for both thermal and visible images. Cubist was the best model to predict wheat yellow rust severity. Our results indicated that the model combination techniques improved the prediction accuracy of wilt severity over individual ML models. Least Absolute Deviation combination technique was the best predictor of wilt severity. ML models used in our study were also able to make good predictions of yield under diseased conditions. The present study will be useful to farmers and policy planners for guidance on effective resource allocation. For researchers, it offers valuable insights into using thermal and optical imaging for plant disease assessment.

Theme 2: Nanotechnology

Effect of zinc oxide nanoparticles on biophysical parameters and biofortification in rice

This research investigates the effect of various size of zinc oxide nanoparticles (ZnO-NPs) on the physiological, biochemical, yield quality attributes of two rice crop varieties, PB-1121 and PB-1509. The study aimed to explore the potential of ZnO-NPs as a novel agricultural input to enhance crop performance and nutrient content in rice plants. The physiological attributes showed significant variations in plant height, photosynthetic rate, stomatal conductance, chlorophyll and carotenoid contents, and root morphological attributesacross the treatments of ZnO-NPs. The 30 nm ZnO-NPs showed the most positive effects on photosynthetic rate and stomatal conductance. Among the treatments the soil+ foliar application of ZnO-NPs performed better than other size NPs. It was found that ZnO-NPs application led to significant increases in protein content, proline, SOD, and CAT activities. Moreover, the 30nm ZnO-NPs treatment exhibited the highest biochemical response, indicating its superior performance over larger-sized ZnO-NPs. The application of ZnO-NPs positively affected the number of tillers, productive tillers, length of panicle, grain weight, filled grain, unfilled grain (spik^{-1}), grain yield, biomass (hill^{-1}) and harvest index, with the 30nm ZnO-NPs treatment displaying the most significant improvement in grain yield and filled grain percentage. The results revealed a notable decrease in phytic acid content in the grains treated with ZnO-NPs, particularly in the 30nm ZnO-NPs. This finding implies that ZnO-NPs can potentially mitigate the anti-nutritional effects of phytic acid in rice grains. The ZnO application increases the Zn content in leaves, roots and crop grains. The enhances the biofortification of Zn in rice grains.Between the mode of application of ZnO-NPs, the soil +foliar application is better than only soil application. This research provides valuable insights into the potential use of ZnO-NPs as an effective agricultural input to improve rice crop productivity and nutritional quality. However, further investigations are required to explore the long-term effects and environmental implications of ZnO-NPs application in agriculture.

Theme 3: Soil Physics

Efficacy of nano- vis-à-vis prilled urea on plant biophysical attributes and nitrogen uptake in rice

The present study was conducted to monitor plant biophysical processes, N uptake, and apparent N balance in basmati rice (var. Pusa Basmati-1692) at IARI farm during kharif season (2022) [both field and pot grown rice]. The experiment consisted of three treatments viz., T1 [recommended dose of N, P and K-soil application], T2 [75% of N-soil application + foliar sprays at active tillering and flowering stage of 2% prilled urea solution] and T3 [75% of N + foliar spray at active tillering and flowering stage of nano-formulation @ 4ml L^{-1}]. Nitrogen fertilizers, whether applied to soil or through soil + foliar methods, had little impact on plant growth except for the foliar spray (25% of N) as nano urea, which resulted in more effective and higher leaf area. The type and application method had no appreciable effect on root growth either. Chlorophyll a and b, carotenoid and chlorophyll-carotenoid ratio were higher in nano urea foliar spray, which also exhibited higher stomatal conductance, internal CO_2 concentration, transpiration rate and photosynthetic capacity in rice. Several yield attributes viz., panicle and flag leaf length, number of total and filled grains were higher with nano urea; however, the yield was comparable to soil application of urea-N. Soil application of urea resulted in higher total N-uptake, although grain N in rice was similar among treatments. Total residue N in soil and apparent N balance was comparable among the treatments; however, NH_4-N of residue N was higher, and NO_3-N was lower in the soil under the foliar application of 25% N. Thus, 25% savings of N can be achieved through nano urea foliar spray without reduction in yields, but with lower total N uptake, indicating more research is necessary to recommend on the effective substitution of conventional soil application of N by nano urea foliar spray to the rice crop to achieve environmental sustainability.

Assessment of fly ash application on soil quality and input use efficiency in maize -wheat cropping system

Field experiment was conducted during the year 2022-23 in the second year of an ongoing long-term field experiment in maize-wheat cropping system in a sandy loam soil at the research farm of the Indian Agricultural Research Institute, New Delhi. Treatmenst comprised of T1 -Control (only recommended NPK to every crop); T2-FYM @5t/ha (every *kharif* season) + Recommended dose of NPK; T3- Fly Ash @10 t/ha (every year) + T2;

T4- Fly Ash @ 20 t/ha (every year) + T2; T5-Fly Ash @ 40 t/ha (every year) + T2; T6- Fly Ash @20 t/ha (every alternate year) + T2; T7- Fly Ash@ 40 t/ha (every alternate year) + T2; T8-Fly Ash @80 t/ha (every alternate year) + T2; T9- Fly Ash @100 t/ha (once) + T2; T10-Fly Ash @ 200 t/ha (once) + T2;T11- Fly Ash @ 400t/ha (once)+T2 and T12-Fly Ash @ 20 t/ha (once) + T1. Results showed an increase in the sand content and decrease in the clay content with the increase in the fly ash application dose. Application of fly ash along with FYM and recommended dose of NPK was found to decrease bulk density, increase porosity, water holding capacity, water stable aggregates and hydraulic conductivity of soil. There was decrease in SOC, available N and S content, SMBC of soil with the increase in fly ash application. Soil Quality Index was maximum for the recommended dose of NPK and FYM application and showed a decreasing trend with increase in Fly ash application. Effect of fly ash application on Water use efficiency of maize and wheat was not statistically significant. Fly ash @10t/ha every year along with recommended dose of NPK and FYM @ 5t/ha is recommended for obtaining higher yield and nutrient use efficiency without any adverse effect on soil health in maize-wheat cropping system in Inceptisol.

Theme 4: Biophysics and Image Processing

Thermal and visible image-based analysis of tomato genotypes to characterize the fruit growth stage

The present study was aimed to characterize the fruit growth stages in ten different genotypes of tomatoes using nine biophysical and biochemical parameters coupled with multivariate analysis, 31 image-derived indices using seven different machine learning techniques. Experiments were conducted with ten distinct genotypes of tomato at the Centre for Protected Cultivation Technology (CPCT), ICAR-Indian agricultural research institute, New Delhi. Fourteen different fruit growth stages of tomato were characterized by Biophysical, biochemical parameters, CIElab-based indices, Visible and thermal image indices. It was observed that all the biophysical and biochemical parameters were well correlated (r >0.55) with fruit growth stages except for Titratable Acid (TA) and Ascorbic acid. Among the different CIELab Indices considered in this study, indices like a^*, b^*, Chroma, Colour Index, $(a^*/b^*)^2$ and a^*/b^* showed increasing trend whereas indices like L^*, Hue and Colour Differences showed decreasing trend during the Ripening stages of the tomato fruit. A new index, called Tomato Fruit Stage Index (TFSI) was developed with the biophysical and biochemical parameter to identify the tomato fruit growth stages using multivariate techniques like Principal Component Analysis (PCA), Hierarchical Cluster Analysis (HCA), and Discriminant Analysis (DA). TFSI, demonstrated a higher accuracy ($R^2 = 0.959$) in identifying the tomato fruits in different developmental stages like Immature Green, Mature Green, and Ripening fruit stages. Ultimately, the study utilized seven different machine learning techniques such as Elastic net (ELNET), Support vector regression (SVR), Gaussian process regression (GPR), Multivariate Adaptive regression splines (MARS), K-nearest neighbours (KNN), Random Forest (RF) and Cubist for characterizing the fruit growth stages in tomato. Among the different ML models, Cubist was observed to be the best in predicting all the fruit growth stages and ripening stages, during both calibration and validation. From the present study, identification of the fruit developmental stages using image-based techniques could help in robotic fruit harvesting and machine vision-based detection of fruit ripening.

Theme 5: Geoinformatics in Agriculture

Geoinformatics for spacio-temporal trends in crop cultivation on pan India scale

Emerging hot and cold spot analysis along with space time cube and space-time cluster density analysis combining the correlation with remote sensing data products like EVI and LST were used to study the spatio-temporal changes in crop (Rice, Maize, Chickpea, Pigeonpea, Soybean and Sunflower) area, production and yield.

District wise crop production, area and yield on pan India basis from 1999 to 2020was analysed. The major findings were: Rice production in India displayed distinct hotspot and cold spot patterns influenced by climate, water access, soil, and socioeconomic factors. The southern rice-growing region benefited from infrastructure, high-yielding varieties, fertilizers, and credit, enhancing productivity. Sporadic hotspots for maize cultivation in India occured in parts of Karnataka, coastal Karnataka, western Maharashtra, and Madhya Pradesh. Unsuitable conditions with high rainfall areas of eastern India led to the cold spots for maize cultivation. Intensifying hotspots for chickpea cultivation in India were observed in states like Madhya Pradesh, Maharashtra, and Karnataka due to the availability of short-to-medium duration varieties. Due to the leadership role played by Uttar Pradesh in enhancing the pigeon pea production, higher yields were observed in Jharkhand and Bihar. Central India, particularly Maharashtra within the Deccan Plateau, serves as a hotspot for pigeonpea cultivation due to its semi-arid conditions. Hotspots for Soybean cultivation were concentrated in central India. Sunflower cultivation in India displays dynamic trends due to its contributions from few key states, and low technological prospects, consequently underscoring the crop's importance in the nation's oilseed sector. Thus, the present study revealed the potential of GIS based spatio-temporal analysis when related with additional background information, could segregate the most significant clusters of changes (increase / decrease) happening over the active crop cultivation. The results from this study would help to give better comprehensible directions for deciding the distribution of input resources to enhance the crop area, yield and production in India.

Theme 6: Soil Physics

Development of tillage and residue mulching module in InfoCrop for simulating water and nitrogen productivity in maize and wheat under changing climate

Tillage and crop residue mulching have profound influence on soil properties, crop productivity, and input use efficiencies. The treatments considered in this study comprised of two levels of tillage [conventional tillage (CT) and no-tillage (NT)], residue mulching (with residue mulching (R+) and without residue (R0)], nitrogen [50%, 100% and 150%] recommended doses of nitrogen (RDN)] and irrigation [full irrigation and deficit irrigation] evaluated in a Split factorial design. Results showed that mean weight diameter (MWD), saturated hydraulic conductivity (K_{sat}) and total organic carbon (TOC) was improved under NT and crop residue mulching (CRM) as compared to CT and residue removal, respectively at 0-15 and 15-30 cm soil depths. Bulk density and penetration resistance under NT was lower than that of CT by 6.2 and 8-35%, respectively at sub-surface region. While implementing the residue mulch module(InfoCrop model V2.1), the focus was on the effect of mulch on soil evaporation and the subsequent effects of changed soil water properties by employing the parameters like time and amount of residue application, and the extent of residue mulching coverage. The modified InfoCrop model was calibrated and validated using field experiment data for the years 2019-20 and 2020-21. The evaluation of modified InfoCrop model showed that it could account 93 and 84% variation in the observed grain yield with an RMSE of 374 and 382 kg/ha and nRMSE of 7.7 and 8.6% for maize and wheat, respectively. The InfoCrop model also showed satisfactory result for validation of WP and NP (R^2 of 0.92 and 0.96 for maize and 0.82 and 0.97 for wheat, RMSE of 0.09 kg/m^3 and 3.1 kg grain/kg N for maize and 0.11 kg/m^3 and 4.67 kg grain/kg N for wheat, and nRMSE of 6.3 and 8.5% for maize and 7.5 and 10.7% for wheat, respectively). Thus, the incorporation of tillage and residue mulching module to InfoCrop opens up opportunities to assess the impact of different agronomic management practices.

Development of a prototype field-scale soil moisture monitoring system from satellite measurements

Downscaling of land surface temperature (LST) from space-borne imagery is crucial for many finer-scale applications such as monitoring the state of crops and vegetation, soil moisture estimation, or as an indicator of the physics of land-surface processes at local to global scales. However, downscaling accuracy is impeded by several geographical and environmental factors. The proposed methods in this study focused on downscaling the Landsat-8 thermal band (~30 m) data to 10 m using covariates from Sentinel-1 & 2. The study also compared the random forest (RF), thin plate spline (TPS), and thermal sharpening (TsHARP) based LST downscaling techniques to improve the accuracy of soil moisture retrieval in comparatively homogeneous (IARI and UBKV farms dominated by wheat and rice crops) and heterogeneous (CAZRI with dryland crops and agroforestry) agricultural farms, also characterized by different agroclimates. The accuracy significantly improved from soil moisture estimation at 30-m (satellite LST-NDVI relation) to 10-m resolution with downscaled LST. The random forest (RF) model trained with remotely sensed auxiliary covariates showed strong consistency between downscaled and *in-situ* observations and followed, for the most part, the spatiotemporal patterns of soil moisture. Consideration of a large number of training variables enhanced the accuracy of soil moisture estimation through RF. The performance of TsHARP at IARI was poor in the early (limited crop growth) and late (senescence) in accordance with NDVI, which was low during these periods. The TPS appeared to perform better than TsHARP under a variety of conditions. In CAZRI, the average correlation coefficient was higher (0.73±0.03) with a lower RMSE (0.09±0.01). Similarly, the variability of prediction by RF was lower in UBKV, although the TPS had shown less error (MBE) compared to the TsHARP. The soil water index, a satellite proxy to the field soil moisture (on a scale of 0 to 1) effectively captured the spatiotemporal changes, however, its translation to actual soil moisture needs further reappraisal.

Simulation of greenhouse gases emissions in wheat under different tillage, residue and nitrogen management

Efficient management of the critical inputs in agriculture viz., water, nutrient and energy can help in mitigating the climate change by curtailing GHG emissions. Filed data were collected from the ongoing long-term tillage experiment under maize-wheat system. The treatments comprised of tillage levels: Conventional Tillage (CT) and No Tillage (NT), residue levels: Maize residue @ 5t/ha (R+) and no residue (R0) and nitrogen: 60, 120, and 180 kg/ha. Results showed that soil physical properties viz., BD, MWD, WSA, porosity, SHC; soil chemical properties viz., SOC, TOC, DOC, MBC, SOC and soil biological properties viz., beta glucosidase, glomalin and fluorescence diacetate (FDA) improved under NT with crop residue mulching application compared to CT without residue. NT with residue mulching enhanced the passive/recalcitrant pool of carbon in soil. All the organic nitrogen fractions were greater under NT with crop residue mulching except Hydrolysable Ammonia Sugar Nitrogen (HASN) as compared to CT without residue. The CO_2 emissions decreased while the N_2O emissions increased in NT as compared to CT. Based on the simulation in DNDC95 model nomographs were developed between grain yield and CER under different management practices and based on these nomographs best management practices were optimized to achieve higher CER with minimum yield penalty. It was suggested that that in dry year under NT the best treatment is No till with crop residue mulch @ 2.5t/ha and five irrigations and 180 kg N/ha and in case of CT, the best treatment is conventional tillage with crop residue mulch @ 2.5t/ha and five irrigations and 90 kg N/ha. For a wet year it was observed that under NT the best treatment is No till with crop residue mulch @ 5t/ha and two irrigations and 60 kg N/ha and in case of CT, the best treatment is conventional tillage with crop residue mulch @ 2.5t/ha and three irrigations and 180 kg N/ha.

Farm-Scale irrigation scheduling based on evapotranspiration and soil moisture through open-source multi-sensor satellite data Synergiess

Open-source multi-satellite synergy (Landsat 8/9 and Sentinel 2) for frequent evapotranspiration (ET) retrieval, and machine-learning algorithms [Boruta-Random Forest, Boruta-Cubist, Boruta-Gradient Boosting Machine

(GBM), RF, Cubist, GBM] were used to retrieve profile soil moisture based on remote sensing, soil physical properties, and elevation information in this study. To monitor ET estimation in real-time, the study used Surface Energy Balance (SEB) models based on optical-thermal bands (Landsat 8/9) and Optical Trapezoidal Model-based Evapotranspiration (OPTRAM-ET) model based on optical bands (Sentinel 2). Six SEB models using remote sensing observations were evaluated where SEBAL had the highest correlation coefficient (r) of 0.93 and a root mean square error (RMSE) of 0.58 mm d^{-1}, while OPTRAM-ET also provided reliable ET estimation with r = 0.89 and RMSE = 0.9 mm d^{-1}. GBM and RF ML algorithms with selected covariates using Boruta performed best (r ~ 0.83 and RMSE ~ 2.9%) in capturing soil moisture profiles. Landsat remote sensing was more accurate in estimating soil moisture profiles than Sentinel-2. Remote sensing indices MNDWI, SRPI, NPCI, VARI, SIPI, and NDVI2 showed strong correlations with soil moisture in the root zone. For depths over 100 cm, soil properties were more important than remote sensing parameters. Integrating ET and profile soil moisture from satellite estimates into a field water balance model allowed for more accurate estimates of the depth and timing of irrigation water requirements (IWR), leading to potential water savings of up to 36%. It was probable that more water could be conserved during the early stages of growth, as nearly 55% more water was applied in this phase. The study has used satellite estimates of ET and profile soil moisture to calculate IWR at a spatial resolution of 30 m and an average temporal resolution of 5 days. It has effectively showcased the significance of open-source multi-satellite synergy for irrigation scheduling and water conservation.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Souramita Chakraborty (21595)	M. Sc.	Hyperspectral remote sensing of wheat yellow rust (*Puccinia Striiformis f. sp. tritici.*)	Dr. D. K. Das	ICAR-IARI, New Delhi
2.	Sharan S.P. (21598)	M. Sc.	Effect of zinc oxide nanoparticles on biophysical parameters and biofortification in rice	Dr. Achchhelal Yadav	ICAR-IARI, New Delhi
3.	Suman (21597)	M. Sc.	Efficacy of nano- vis-à-vis prilled urea on plant biophysical attributes and nitrogen uptake in rice	Dr. Debasish Chakraborty	ICAR-IARI, New Delhi
4.	Pratahbidya Nayak (21737)	M. Sc.	Assessment of fly ash application on soil quality and input use efficiency in maize -wheat cropping system	Dr. K. K. Bandyopadhyay	ICAR-IARI, New Delhi
5.	Alka Rani (10759)	Ph. D.	Agricultural drought monitoring and early warning using meteorological and remote sensing datasets for India	Dr. V. K. Sehgal	ICAR-IARI, New Delhi
6.	Ram Narayan (10968)	Ph. D.	Assessment of wheat stripe rust and chickpea wilt through thermal and optical remote sensing	Dr. P. Krishnan	ICAR-IARI, New Delhi
7.	Sujan Adak (11202)	Ph. D.	Development of tillage and residue mulching module in InfoCrop for simulating water and nitrogen productivity in maize and wheat under changing climate	Dr. K. K. Bandyopadhyay	ICAR-IARI, New Delhi
8.	Debasish Roy (11203)	Ph. D.	Development of a prototype field-scale soil moisture monitoring system from satellite measurements	Dr. Debasish Chakraborty	ICAR-IARI, New Delhi

9.	Mohammed Shafeeq P.M. (11204)	Ph. D.	Geoinformatics for spacio-temporal trends in crop cultivation on pan India scale	Dr. P. Krishnan	ICAR-IARI, New Delhi
10.	Sona Kumar (11432)	Ph. D.	Thermal and visible image based analysis of tomato genotypes to characterize the fruit growth stage	Dr. P. Krishnan	ICAR-IARI, New Delhi
11.	Priya Bhattacharya (11433)	Ph. D.	Simulation of greenhouse gases emissions in wheat under different tillage, residue and nitrogen management	Dr. K. K. Bandyopadhyay	ICAR-IARI, New Delhi
12.	Tridiv Ghosh (11703)	Ph. D.	Farm-Scale irrigation scheduling based on evapotranspiration and soil moisture through open-source multi-sensor satellite data synergiess	Dr. Debasish Chakraborty	ICAR-IARI, New Delhi

Agronomy

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Prof. Y.S. Shivay

Agronomy, as a recognized discipline of the ICAR-Indian Agricultural Research Institute traces its origin to the Crop and Animal Breeding Section started in the Imperial Agricultural Research Institute at Pusa, Bihar in 1905. It assumed the status of a division in the year 1923 to award diplomas, provide training, and manage the institute farm. In 1936, it was recognized as a Research Division with the shifting of the Institute to New Delhi. The mission of the division is to provide leadership in crop and cropping system-based agronomic research by developing new concepts and approaches of sustainable crop production suited to farmers; to develop appropriate crop production technologies to enhance the production and productivity of major cropping systems on a sustainable basis and to provide post-graduate teaching and develop human resources. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Nutrient Management

Effect of multi-micronutrient embedded sulphur on productivity and biofortification of wheat

Continuous use of primary fertilizers depletes secondary nutrients and micronutrients, particularly sulphur, impacting global crop productivity. This study focuses on addressing sulphur and micronutrient deficiencies in wheat, a crucial crop in Indian agriculture. A field experiment at ICAR-Indian Agricultural Research Institute, New Delhi, during Rabi season of the 2022-23 assessed the impact of multi-micronutrient embedded sulphur on wheat productivity and biofortification. Results revealed that RDF + Zn-ES @ 40 kg/ha + S @ 37.5 kg/ha demonstrated superior plant height, leaf area index, and dry matter accumulation, leading to the highest grain yield, straw yield, and biological yield. RDF + Zn-ES @ 40 kg/ha + S @ 37.5 kg/ha + MM-ES @ 37.5 kg/ha showed the highest chlorophyll content and NDVI value. Micronutrient uptake was maximized with this treatment. Post-harvest properties, excluding available sulphur and zinc content, showed minimal variation. Dehydrogenase activity peaked with RDF + Zn-ES @ 40 kg/ha + S @ 37.5 kg/ha. Economic analysis favored Zn-ES @ 40 kg/ha with the recommended fertilizer dose, while RDF + Zn-ES @ 40 kg/ha + S @ 37.5 kg/ha demonstrated maximum yield, statistically comparable to Zn-ES @ 40 kg/ha. In conclusion, for optimal wheat cultivation economics, Zn-ES @ 40 kg/ha with the recommended fertilizer dose is recommended. Despite slightly lower yields, RDF + Zn-ES @ 40 kg/ha + S @ 37.5 kg/ha is a competitive alternative, endorsing both crop production and profitability. This research highlights the importance of integrating micronutrients with sulphur for sustainable wheat cultivation and enhancing overall agricultural productivity.

Effect of organic manures and bio-fertilizers on productivity and profitability of wheat under long-term rice-wheat rotation

The experiment was conducted at ICAR–IARI, New Delhi during the *Rabi* season of 2022–23 to assess the impact of organic manures and bio-fertilizers on wheat productivity and profitability in a long-term rice-wheat rotation. Employing a randomized complete block design with 11 treatment combinations, each replicated thrice, the study evaluated various treatments, including control (T1), FYM at 10 t/ha applied only to wheat (T2), *Leucaena* green leaf manuring to wheat (T3), and combinations of green manure, FYM, and bio-fertilizers. Results indicated that GM + FYM + BF applied to both crops yielded the highest grain yield (4.97 t/ha), surpassing other treatments. These organic nutrient sources also enhanced growth parameters and yield attributes, resulting in significant improvements compared to the control. Applying GM + FYM + BF to wheat and previous rice increased dry matter accumulation, effective tillers, flag leaf length, and grains/spike by 76.6%, 51%, 13.9%, and 32.3%, respectively. Furthermore, the nutrient sources positively impacted soil health, with GM + FYM + BF significantly enhancing DHA (86%), available N (40.6%), total organic carbon (76.8%), and very labile C-pool (57.4%) compared to the control. GM + FYM applied to both crops led to the highest straw yield, available soil P, K, and MBC, showing increases of 72.2%, 95.4%, 63.7%, and 107.3%, respectively, over the control plot. In terms of economic returns, GM + BF applied to both crops recorded the highest net return of ₹97,007/ha (100.4% higher than control), while GM + FYM + BFs applied to both crops achieved the highest gross returns of ₹136,465/ha, representing an 83.7% increase over control. Consequently, GM + FYM + BFs applied to rice and wheat crops emerged as the most suitable treatment, followed by GM + BFs for both crops, for enhancing wheat yields, soil health, and profitability.

Phosphorus management through organic and microbial sources in baby corn (*Zea mays* L.)

The experiment aimed to explore alternative and sustainable phosphorus (P) sources for baby corn (*Zea mays* L.) cultivation, given the limitations of di-ammonium phosphate (DAP), the primary but expensive and imported P source with low recovery efficiency and environmental concerns. The experiment was conducted during the 2022-23 *Kharif* season at ICAR-IARI, New Delhi, using a randomized block design with ten treatments and three replications. Results indicated that applying 27 kg P/ha through phosphate-rich organic manure (PROM) significantly enhanced plant growth, yield attributes, and baby corn yield compared to the P control. This treatment was followed closely by 27 kg P/ha through DAP and 20 kg P/ha through PROM + PSB @ 500 g/ha + AM Fungi @ 12.5 kg/ha. The highest baby corn yield with husk (11.80 t/ha), without husk (2.90 t/ha), and fodder (27.81 t/ha) occurred with 27 kg P/ha through PROM, followed by 27 kg P/ha through DAP and 20 kg P/ha through PROM + PSB + AM Fungi. Phosphorus management with 27 kg P/ha through PROM resulted in the highest gross returns (₹250,880/ha) and net returns (₹200,150/ha), while the highest B:C ratio (3.95) was observed in 27 kg P/ha through DAP. P management treatments significantly increased nutrient concentrations and uptake with the most pronounced effects at 27 kg P/ha through PROM. Microbiological parameters were notably influenced by different P application treatments, with the integrated application of 20 kg P/ha through PROM and PSB + AM Fungi recording the highest values. Agronomic efficiency (46.5%) and crop recovery efficiency (43.9%) were maximized with 20 kg P/ha through PROM + PSB + AM Fungi. In conclusion, phosphate-rich organic manure (PROM) emerges as a viable alternative to DAP, enhancing crop growth, productivity, and soil health.

Tillage and methods of nutrients application effects on productivity of maize (*Zea mays* L.)

Globally, crop production faces the challenge of yield stagnation, prompting the need for sustainable methods to enhance productivity, profitability, and environmental safety. A field experiment at ICAR-IARI, New Delhi, explored different tillage and nutrient application techniques for maize production. The split-plot design included three main tillage treatments (Conventional, Minimum, and Zero tillage) and four nutrient application methods (50% RDF, 75% RDF, 100% RDF band placement, and 100% RDF basal + top-dress broadcasting), replicated thrice. The sandy loam soil with slightly alkaline pH and low organic carbon, available nitrogen, and medium phosphorus and potassium levels formed the experimental backdrop. Minimum tillage, involving a single Rotavator pass after the previous crop harvest, outperformed other tillage practices in terms of crop growth, yield attributes, productivity (6.22 t/ha), and profitability (net B:C 2.18). Minimum tillage yielded 1.44% and 11.66% more grain yield than zero tillage (6.13 t/ha) and conventional tillage (5.57 t/ha), respectively. Regarding nutrient application, the 100% RDF band placement method exhibited superior crop growth, productivity (6.20 t/ha), and economic viability (net B:C 2.16). This method resulted in 2.31%, 4.90%, and 8.39% higher yield compared to 50% RDF point placement (6.06 t/ha), 75% RDF band placement (5.91 t/ha), and 100% RDF broadcasting (5.72 t/ha), respectively. Soil microbial activity at the maize flowering stage was higher with zero tillage than with minimum and conventional tillage. The findings suggest that minimum tillage is a viable, cost-effective option compared to conventional tillage. Both minimum tillage and zero tillage, combined with 100% RDF band placement or 50% point placement of fertilizers, emerged as economically sustainable choices for maize production.

Nutrient management in maize (*Zea mays* L.) under different crop establishment option

A field experiment was conducted in 2022 at ICAR-Indian Agricultural Research Institute's research farm in New Delhi. The soil characteristics before the trial included 0.32% organic carbon, 277 kg/ha available N, 16.85 kg/ha 0.5 M $NaHCO_3$ extractable P, and 270 kg/ha 1 N NH_4OAC extractable potassium. The split-plot design had three main crop establishment methods—conventional tillage without residue, permanent raised bed without residue, and permanent raised bed with residue retention—and four nutrient management options—STBR, STBR+GS, NE, and NE+GS-based recommendations. PRB+R significantly enhanced maize growth parameters, outperforming other methods. NE+GS exhibited the highest growth parameters in maize among nutrient management options. Yield attributes were greatest in the PRB+R treatment, with significantly higher maize grain yield (6.43 t/ha) compared to other methods. NE+GS led to the highest maize grain yield (6.17 t/ha), surpassing other nutrient management options. PRB+R resulted in the maximum gross and net returns, with the highest net benefit-to-cost ratio (B:C) among establishment methods, while NE+GS had the highest net B:C ratio among nutrient management options. PRB+R combined with NE+GS demonstrated the highest nitrogen, phosphorus, and potassium uptake. Retaining crop residue reduced soil temperature during maize's reproductive phase. PRB+R showed higher values for soil organic carbon, available nitrogen, phosphorus, potassium, microbial biomass carbon, and FDA compared to other establishment methods. In conclusion, growing maize using the PRB method with 3 t/ha residue retention and nutrient application following the NE+GS prescription is the most effective approach for sustainable productivity, profitability, and soil and ecological health in maize cultivation.

Precision nitrogen management in rice for improving productivity and resource-use efficiency in the NEH Region

A field experiment at ICAR–Research Complex for North-Eastern Hill Region (ICAR–RC–NEHR), Meghalaya, in the 2022 kharif season studied the impact of various precision nitrogen management practices on rice growth, yield, quality, nutrient dynamics, and soil properties. The experiment, in a thrice-replicated randomized complete block design, compared the Recommended Dose of Nitrogen (RDN), Soil Test Crop Response-based N (STCR), and other precision practices. STCR-based nitrogen management (95 kg N/ha) demonstrated superior results, closely followed by 30% basal + SPAD ≤ 37, 30% basal + SPAD ≤ 35, and 30% basal + LCC < 4. Parameters like growth indices, yield attributes, grain yield (4.84 t/ha), straw yield (6.04 t/ha), biological yield (10.88 t/ha), and various quality traits were highest under STCR, with 75% RDN + 2NU standing at par with RDN. STCR showed higher production efficiency (32.3 kg/ha/day) and monetary efficiency (Rs 739/ha/day), followed by SPAD ≤ 37, SPAD ≤ 35, and LCC < 4. Partial factor productivity and physiological-use efficiency of applied nutrients were higher in 50% RDN+2NU. Energy input-output analysis favored STCR, with SPAD ≤37 and LCC < 4 following closely. STCR and RDN had the highest and specific energy, respectively. Precision N management practices had a non-significant effect on soil pH, soil organic carbon, and available P and K, but available N was higher in STCR-based plots. In conclusion, the rice variety Shahsarang 1 performed well under SPAD ≤ 37, RDN, and STCR-based nitrogen application. SPAD-based N application exhibited better outcomes than RDN and was comparable to STCR, with a saving of 16–31 kg N/ha. Additionally, applying 75% RDN with 2 nano-urea sprays performed similarly to 100% RDN, suggesting a potential avenue for further exploration in integrating nano-urea for improved rice productivity in the north-eastern region of India.

Nutrient management in organic rice under NEH region

In the North Eastern Hill (NEH) region of India, where rice plays a pivotal role in the local economy, a field experiment was conducted during the 2022 *Kharif* season at the ICAR Research Complex, Meghalaya. The objective was to identify an optimal combination of organic nutrient sources for improved growth, yield attributes, productivity, grain quality, soil health, and net returns under organic rice cultivation. The experiment, utilizing a factorial randomized block design with 12 treatment combinations, involved two rice cultivars (Shahsarang 1 and Lumpnah) as Factor A and five organic nutrient management practices as Factor B. These practices included 100% recommended dose of N (RDN) through farmyard manure (FYM), 100% RDN through vermicompost (VC), 50% RDN through FYM + 50% RDN through VC, 75% RDN through FYM with two sprays of vermiwash and cow urine, and 75% RDN through VC with similar sprays at 30 and 60 days after transplanting, along with a control laid out with 3 replications. Results indicated that the Shahsarang 1 cultivar outperformed Lumpnah in various growth parameters, responding particularly well to the 75% RDN through VC + vermiwash + cow urine treatment. This treatment also resulted in increased panicles per square meter, filled grains per panicle, higher spikelet fertility, and elevated grain and straw yields (4.32 t/ha and 7.65 t/ha, respectively) in Shahsarang 1. Additionally, the organic treatments contributed to fewer chaffy grains, reduced breakage, and a higher head rice recovery percentage. The 75% RDN through VC + vermiwash + cow urine treatment exhibited significantly higher gross returns (₹1,03,428/ha) and net returns (₹44,488/ha). Among the cultivars, Shahsarang 1 demonstrated cost-effectiveness. Soil health parameters, including soil organic carbon (SOC) content and available NPK, were maximized under the 75% RDN through VC + vermiwash + cow urine treatment, followed closely by FYM + vermiwash + cow urine and FYM + VC.

Effect of organic nutrient sources on rice varieties in NEH region

A field experiment was conducted during the 2022 *Kharif* season at the ICAR Research Complex for the NEH Region in Meghalaya, India, to identify effective combinations for enhancing growth, yield, productivity, grain quality, soil health, and net returns in organic rice cultivation. The experiment employed a factorial randomized block design with 10 treatment combinations, featuring two rice cultivars (Shahsarang 1 and Megha aromatic 1) as Factor A and five organic nutrient management practices as Factor B. Practices included applying 100% recommended dose of nitrogen (RDN) through Poultry manure (PM), Pig manure, Farm yard manure (FYM), Green leaf manure (*Tephrosia purpurea*), and control (without organic treatment), replicated three times. The soil, sandy clay loam, exhibited high organic carbon (1.86%) and low available nitrogen, phosphorus, and potassium, with a pH of 4.8. Results highlighted Shahsarang 1's superior performance in growth metrics, particularly when subjected to RDN through poultry manure, followed by pig manure. Shahsarang 1 under RDN through poultry manure exhibited higher panicles per square meter, filled grains per panicle, grain weight per panicle, grain yield (4.9 t/ha), and straw yield (8.3 t/ha). Organic treatments led to reduced chaffy grains, decreased breakage, and higher head rice recovery. RDN through poultry manure resulted in substantial gross returns (₹1,16,640/ha) and net returns (₹66,800/ha), positioning Shahsarang 1 as a cost-effective option. Soil health improvements, including organic carbon and nutrient availability, were most pronounced under RDN through poultry manure, followed by pig manure. Organic treatments positively impacted soil microbial biomass carbon and rhizosphere activity, while slightly reducing soil pH. In conclusion, applying RDN through poultry manure proved effective for organic rice cultivation in the NEH region, demonstrating significant improvements in production, grain quality, net returns, and soil health. The findings emphasize the potential of organic nutrient management for sustainable agriculture in the specific conditions of the NEH region.

Effect of planting density and nitrogen management on hybrid maize (*Zea mays*) in Eastern India

A field study was conducted in Jharkhand during the *Kharif* season of 2022 to investigate the impact of planting density and nitrogen management on maize growth, yield, resource-use efficiency, and soil health. The study comprised three planting densities (D1: 67.5 cm × 20 cm, D2: 67.5 cm × 22 cm, D3: 67.5 cm × 25 cm) and five nitrogen (N) management practices (control, farmer's practices, RDN-conventional, 75% RDN-SSB (sub-surface band placement), RDN-SSB) arranged in a split-plot design and replicated three times. Results demonstrated that improved planting densities (especially D2) and the N management practice RDN-SSB significantly enhanced maize growth parameters, including leaf area index, dry matter, and plant height, compared to farmer's practices/ RDN-conventional and D1. Notably, the combination of RDN-SSB with D2 exhibited significantly superior yields in terms of stover, cob, and grain. N uptake by leaves, stover, and stem was notably higher with RDN-SSB. The NPK content in maize grain and stover was higher with D3 and RDN-SSB, with the latter showing higher NPK uptake. Agronomic efficiency, apparent nitrogen recovery, and partial factor productivity of applied nitrogen were significantly improved with RDN-SSB. RDN-SSB led to the highest balance of NPK in the soil. Planting density D2 significantly enhanced net returns and benefit-cost ratio (BC ratio), which was comparable to D1. Among nitrogen application practices, RDN-SSB resulted in the highest net returns (₹1,60,872) and B:C ratio (3.34). The combination of D2+RDN-SSB exhibited significantly higher net returns (94.3%) and a B:C ratio of 4.03 compared to farmer fertilization practices with spacing of 67.5 cm × 25 cm. In conclusion, maintaining an optimum plant spacing of 67.5 cm × 22 cm (67,000/ha) and nitrogen management through RDN-SSB is recommended for enhancing yield, profitability, resource-use efficiency, and soil health in *Kharif* maize cultivation in eastern India and similar agro-ecologies.

Effect of nano-urea on maize productivity and nitrogen use efficiency in acid soil of Jharkhand

To validate the efficacy of nano-urea under diverse field conditions, an experiment was conducted at ICAR-IARI, Jharkhand, during the *Kharif* season of 2022. The objectives of the experiment were to assess the impact of various nitrogen doses with nano-urea on maize growth, productivity, nitrogen use efficiency, and economic viability. The soil in the experimental field was classified as alfisol, characterized by red color and mild acidity with a pH of 6.3. Implemented in a Randomized Block Design, the experiment comprised 12 treatments, including four nitrogen doses (0, 50, 75, and 100% of recommended N) and three spray combinations (No spray, nano-N, and prilled-urea) with three replications. The recommended nitrogen dose was applied in split, with 1/3 as basal, 1/3 at 32 DAS as top dressing, and 1/3 at 50 DAS as the second top dressing. Nano-N and prilled-urea spray coincided with top dressing at 32 DAS and 50 DAS. Results revealed significantly higher grain yield (6.89 t/ha) under 100% recommended N + 2 nano-urea sprays compared to other treatments, on par with 100% recommended N (6.24 t/ha) and 100% RDN + 2% prilled-urea sprays (6.26 t/ha). Application of 75% recommended N with 2 nano-urea sprays recorded grain yield at par (5.79 t/ha) with 100% recommended N. Net returns and B:C ratio were significantly higher under 100% recommended N + 2 nano-urea sprays, remaining on par with 100% recommended N and 100% RDN + 2% prilled-urea sprays. Application of 75% recommended N with 2 nano-urea sprays recorded net returns and B:C ratio at par with 100% recommended N. In conclusion, the experiment demonstrated the positive impact of nano-urea on maize productivity, nitrogen use efficiency, and economic returns, highlighting its potential as an environmentally friendly alternative in acid soil conditions.

Effect of nano-urea application for enhancing the productivity of rainfed maize

A field experiment was conducted at ICAR-IARI, Jharkhand to investigate rainfed maize productivity, resource use efficiency, and soil chemical and microbial properties. The experiment was laid out in a randomized block design comprising of 10 treatments with 3 replications. Results indicated that each successive level of nitrogen in the form of granular urea increased plant height, Leaf Area Index (LAI), root dry weight, and dry matter accumulation significantly. Foliar application of nano-urea at 30 and 50 DAS with 75% RDN showed almost similar growth attributes aswell as yield attributes with 100% RDN. The highest grain yield (5.80 t/ha) and biological yield (16.88 t/ha) were obtained with 100% RDN which was superior to other nitrogen management practices. Grainyield under 100% RDN was 19.34% higher than 50% RDN + 2 nano-urea spray, and 10.47% higher than75% RDN + 2 nano-urea spray. Partial factor productivity of nitrogen for 50% RDN + 2 nano-urea spraywas 67.02% higher compared to 100% RDN but partial factor productivity of P and K under100% RDNwas 16.38% higher compared to 50% RDN + 2 nano-urea spray. Higher nitrogen application with one life-saving irrigation to the field resulted in higher water productivity (0.77 kg/m^3). The highest ANUE and ANR was recorded under 50% RDN + 2 nano-urea spray whereas the seed dressing with nano-urea + 2 NUS showed higher NER and PEN. Application of nano-urea increases the cost of cultivation and the highest return was observed under 100% RDN. The highest net B:C ratio (2.49)was recorded under the application of 100% RDN and followed by 50% RDN + 25% RDN + 1 nano-urea spray (2.18). Based on the one-season experimentation, the application of 50% RDN (basal) + 25% RDN (30 DAS) + 1 NUS (50 DAS) in rainfed maize resulted comparable yield with 100% RDN, so 25% RDN can be saved.

Optimization of nitrogen for contrasting genotypes in wheat-maize cropping system

A field investigation was conducted at the research farm of ICAR-IARI in New Delhi during the *Rabi* (2020-21 and 2021-22) and *Kharif* seasons (2021 and 2022). The results showed that the genotypes and nitrogen levels significantly improved the growth and physiological parameters, productivity, and quality of wheat and maize during both years of investigation. HDCSW 18 genotype recorded significantly the highest grain yield and economic profitability in 2020-21, as well as the highest straw yield and maximum SMBC and SMBN. HD 3226 recorded the maximum plant height (2021-22), leaf number and root diameter and also produced the highest grain yield and fetched maximum net returns and B: C ratio in 2021-22. Longer roots with greater root volume and mass density were noted in HD 3117. However, plant growth parameters were higher at 240 kg N/ha. Grain yield, harvest index and soil urease activity were maximum at 160 kg N/ha in both the years. Whereas, straw yield, nitrogen content and uptake, ammonia and nitrous oxide emission, and crop lodging were observed significantly higher at 240 kg N/ha. PJHM 1 recorded the highest growth attributes and root parameters. DKC 9164 recorded the highest grain and stover yields, net returns and B: C ratio, protein content and nitrogen uptake and uptake efficiency. Among the nitrogen levels, the application of 240 kg N/ha recorded significantly higher values of maize growth and physiological parameters, stover yield, protein and nitrogen content and nitrogen uptake. Maximum values of root length density, mean root diameter, root volume density, root mass density and urease activity were exhibited at 120–160 kg N/ha. Hence, the application of 200 kg N/ha to maize recorded significantly higher grain yield, harvest index, net returns (₹91.1 and 97.2 ×10^3/ha) as well as B: C ratio (2.44 and 2.55) during both years.

Effect of legumes and nutrient management on soil health and productivity of organic rice-wheat system

In this comprehensive field study conducted at the ICAR-Indian Agricultural Research Institute in New Delhi, India, the impact of legumes and nutrient management practices on soil health and productivity in organic rice-wheat systems was investigated across summer, *kharif*, and *rabi* seasons. The experiment employed a strip plot design with fourteen treatment combinations, integrating legume-inclusive cropping systems and organic nutrient management practices. The study's key vertical strip treatments included basmati rice-wheat-*Sesbania* and basmati rice-wheat-mungbean cropping systems, while horizontal strip treatments encompassed control, farm yard manure (FYM), vermicompost (VC), FYM + crop residues (CR), VC + CR, FYM + CR + biofertilizers (BF), and VC + CR + BF. Results indicated substantial improvements in growth parameters, yield attributes, and overall yields of basmati rice and wheat due to legume inclusion and organic nutrient management practices. *Sesbania* green manure, when introduced in the basmati rice-based cropping system, notably enhanced growth parameters and yields. Among the organic nutrient management practices, VC + CR + BF emerged as the most effective, showcasing the highest values for growth parameters and yield attributes, resulting in superior grain and straw yields for both crops. Furthermore, the RWS system demonstrated higher gross and net returns compared to the RWM system. The VC + CR + BF treatment consistently exhibited the highest returns in basmati rice and wheat. Macro and micronutrient concentration, uptake, water productivity, grain quality, and soil physico-chemical properties all favored the RWS system, with VC + CR + BF being the optimal organic nutrient management practice. Overall, the study concluded that the RWS system, combined with VC + CR + BF, represents the most favorable treatment combination for achieving enhanced productivity, profitability, grain quality, and soil health in basmati rice and wheat cultivation. The findings contribute valuable insights for sustainable agricultural practices in organic farming systems.

Nutrient management in direct seeded rice (*Oryza sativa* L.)-zero-till wheat (*Triticum aestivum* L.) system

A field experiment was conducted at the ICAR-Indian Agricultural Research Institute, New Delhi, during the *kharif* seasons of 2018 and 2019, as well as the *rabi* seasons of 2018-19 and 2019-20. The study aimed to evaluate the performance of direct-seeded rice and zero-till wheat in a cropping system using various nutrient management strategies. The randomized block design included twelve treatments: soil test-based NPK (STB-NPK), nutrient expert-based NPK [NE (LCCN)-NPK], recommended doses of fertilizers (RDF), and state-recommended NPK, along with nutrient omission treatments (N0PK, NP0K, and NPK0). Among precision nutrient management techniques, STB-NPK followed by NE-(LCCN) NPK significantly enhanced growth, yield attributes, grain and straw yields, nutrient concentration, and uptake in both rice and wheat. This combination also improved the grain and cooking quality of basmati rice and wheat crop protein content. Precision nutrient management increased nutrient use efficiency for both crops. NE-(LCCN) NPK showed improved partial factor productivity (PFP) and agronomic efficiencies (AE) for N, P, and K. RDF treatment demonstrated the highest PFPK and AEK. In terms of water productivity for direct-seeded basmati rice, STB-NPK and NE-(LCCN) NPK treatments exhibited the highest irrigation water productivity (IWP), total water productivity (TWP), and crop water use efficiency (CWUE). Dehydrogenase enzymatic activity (DHA), soil microbial biomass carbon (SMBC), and soil organic carbon (SOC) content after wheat harvest favored STB-NPK and NE-(LCCN) NPK treatments. NE-(LCCN) NPK significantly reduced cumulative seasonal N_2O emission and flux compared to STB-NPK and RDF treatments in both rice and wheat fields. Economically, STB-NPK treatment yielded the highest net return, net B-C ratio, system net return, and system net B-C ratio, statistically equivalent to NE-(LCCN) NPK treatment for both crops. In conclusion, over two years, STB-NPK treatment enhanced growth, productivity, and profitability, with NE-(LCCN) NPK treatment excelling in nutrient use efficiency and N_2O emission reduction in direct-seeded rice-zero till wheat systems.

Microbial mediated in-situ rice residue management and its effects on soil health and productivity of rice-wheat system

A two-year field experiment investigated microbial-mediated in-situ rice residue management and its impact on productivity and soil health in a rice (*Oryza sativa* L.)-wheat (*Triticum aestivum* L.) cropping system (RWCS) at the ICAR-Indian Agricultural Research Institute, New Delhi, India. The study, conducted during the *Kharif* and *Rabi* seasons of 2019-20 and 2020-21, employed a split-plot design with main plot treatments of aerobic rice (AR) and conventional transplanted rice (CTR) during *Kharif*, and seven sub-plot treatments in wheat during *Rabi*. Results demonstrated that CTR outperformed AR in terms of plant growth, growth indices, and yield attributes, resulting in significantly higher grain yield. Among sub-plot treatments, paddy straw incorporation + Pusa decomposer + urea @ 10 kg/ha (PSI + PD + Urea @ 10 kg/ha) yielded the highest wheat grain yield and net returns in 2020-21. AR saved 30.2–33.2% of total water compared to puddled transplanted rice. Water productivity and irrigation water use efficiency were significantly higher in AR than in CTR. Global warming potential (GWP) and methane emissions (CH_4) were higher in CTR than AR, while energetic values were higher in CTR. In-situ rice residue management options had positive effects on wheat growth, yield attributes, yields, and economic returns. For wheat, PSI + PD + Urea @ 10 kg/ha produced the highest grain yield and net returns. The increase in grain yield over control ranged between 10.9 to 11.0% in both years. This treatment also recorded the highest nitrogen concentration and uptake in grain, along with improvements in soil organic carbon, available macro and micro-nutrients, and various soil microbial activities, including enzymes. The study on residue degradation of paddy straw through the litter bag technique revealed that Pusa decomposer involving treatments showed significantly better results under in-situ rice residue decomposition.

Effect of summer green manuring and nano-zinc oxide coated urea on productivity and nutritional quality in basmati rice-wheat cropping system

The rice-wheat cropping system (RWCS) is vital for ensuring food security in India and South Asia, but it grapples with challenges like stagnant yields and environmental concerns. To address these issues, a two-year study (2020-2022) at ICAR–Indian Agricultural Research Institute, New Delhi, India investigated the impact of summer green manuring (SGM) and zinc fertilization (ZnF) modules on the *Basmati* rice-wheat cropping system. In a split-plot design, *Sesbania* and cowpea were compared to fallow conditions (main plots), along with various zinc fertilization (ZnF) modules (subplots). Application of SGM significantly increased *Basmati* rice grain yield by 13.2% and 12.3% in 2020 and 2021, respectively, compared to fallow. Zinc application with urea enhanced rice yield by 9.56% and 10.5% compared to urea alone, and by 33.7% and 33.8% compared to bulk ZnO. SGM positively influenced Zn, Cu, Mn, and Fe in rice, with combined zinc and urea application notably increasing Zn and Fe concentrations. *Sesbania* residue incorporation led to the highest rice protein content. Additionally, SGM had a significant residual effect on succeeding wheat, resulting in 18.1% more grains per spike compared to the control. Wheat parameters such as grain yield, straw yield, biological yield, and harvest index improved by 9.31%, 4.18%, 6.51%, and 2.87%, respectively, compared to fallow. Effective sources for improving wheat protein and micronutrient content were higher 0.2% nano zinc-coated urea (NZnCU) and 1% bulk zinc oxide-coated urea (BZnCU). *Sesbania* with 0.2% NZnCU proved the most effective in terms of yield response, micronutrient uptake, and protein accumulation in both *Basmati* rice and wheat. In conclusion, this study emphasizes the role of nano zinc oxide-coated urea and *Sesbania* green manuring in improving yield response, micronutrient availability, and protein content in both *Basmati* rice and wheat. Importantly, this approach offers a 20% reduction in zinc dose, providing a cost-effective solution for farmers.

Evaluation of rice and wheat genotypes for higher nitrogen use efficiency

A two-year field investigation at the ICAR-Indian Agricultural Research Institute in New Delhi assessed the impact of nitrogen (N) levels on ten rice and wheat genotypes across *rabi* and *kharif* seasons. The split-plot design included N0 (control), N60 (half of recommended N), and N120 (recommended N) levels in main plots. Sandy clay loam soil with pH 7.8, 4.71 g/kg organic carbon, 208 kg/ha available N, 15.54 kg/ha available P, and 254.2 kg/ha available K were used. N120 and N150 emerged as the most effective N levels, enhancing growth parameters, root traits, yield attributes, and nutrient concentration in both rice and wheat. N120 (120 kg N/ha) and N150 (150 kg N/ha) resulted in the highest grain, straw, and biological yield for both crops. Notably, 'Nidhi' and 'Daya' rice genotypes responded positively to N120, while 'HD 3249' and 'HD 3117' wheat genotypes excelled with N150. 'Nidhi', 'Daya', 'HD 3249', and 'HD 3117' genotypes demonstrated superior agronomic efficiency, crop recovery efficiency, partial factor productivity, and N response. The highest nutrient use efficiencies in both crops were achieved with N rates of 120 kg N/ha and 150 kg N/ha. Among genotypes, 'Daya', 'PB 1728', and 'PBW-343' exhibited the highest chlorophyll content. Maximum protein content and NPK uptake occurred with N applications at 120 kg/ha and 150 kg/ha. 'Nidhi', 'Vasumati' (Rice), 'HD 3249', and 'HD 3117' (Wheat) displayed peak NPK concentrations in grain and straw, with 'HD 3249' having the highest protein content. Genotype 'Nidhi' recorded the highest hulling, milling, and amylose %. In conclusion, applying 120 kg N/ha in rice and 150 kg N/ha in wheat enhanced productivity, quality, profitability, and soil health. 'Nidhi' and 'Daya' rice genotypes, along with 'HD 3249' and 'HD 3117' wheat genotypes, exhibited superior nutrient use efficiency, making them ideal candidates for achieving higher yields and nutrient use efficiency.

Organic nutrient management in rainfed mustard + chickpea intercropping system

The field experiment conducted at ICAR–Indian Agricultural Research Institute in New Delhi aimed to evaluate the impact of different nutrient management practices and cropping systems on growth, yield, profitability, quality parameters, nutrient uptake, soil properties, and intercropping indices in the mustard + chickpea cropping system. The study included four nutrient management practices (control, inorganic, organic, integrated organic) and four cropping systems (mustard sole, chickpea sole, mustard + chickpea 2:5, mustard + chickpea 5:2). The results indicated that the mustard + chickpea 2:5 intercropping system exhibited the highest growth parameters, growth indices, and yield attributes for both mustard and chickpea. This was attributed to better resource utilization, especially solar radiation and temperature. While the seed and stover yield of mustard were highest in the sole crop, the overall system yield (mustard equivalent yield) was highest in the mustard + chickpea 5:2 intercropping system. Among nutrient management practices, the integrated application of 20 kg N through FYM + LM + MC resulted in the highest growth, yield, uptake, and quality parameters for both crops. Economically, the mustard + chickpea 5:2 intercropping system with integrated organic manure application generated the highest gross returns, net returns, and benefit-cost ratio. Soil microbial biomass carbon and enzymatic activities showed a significant increase when chickpea was grown as an intercrop with mustard, particularly under integrated organic practices. Soil moisture retention was not significantly influenced by cropping systems or nutrient management practices under rainfed conditions. Intercropping indices revealed an advantage for the mustard + chickpea 2:5 system when supplied with a proper combination of organic manures. In conclusion, the study recommended the adoption of the mustard

+ chickpea 2:5 intercropping system under integrated organic nutrient management practices for enhancing growth, productivity, profitability, and soil quality in rainfed conditions. This approach could contribute to improved yields and income for farmers.

Theme 2: Crop Diversification

Effect of plant growth regulators on productivity, resource use efficiency and economics of Indian mustard under limited irrigation agri-horti system

The field experiment was conducted during the *Rabi* season 2022–23 at ICAR-IARI, New Delhi. Utilizing a split plot design, three main plots featured different Agri-Horti systems (AHS): Moringa-based AHS (M1), Phalsa-based AHS (M2), and Karonda-based AHS (M3). Sub-plots involved four plant growth regulator treatments (PGR): S1 (control), S2 (1% KNO_3), S3 (200 ppm SA), and S4 (1% urea spray). Moringa-based AHS demonstrated the highest mean numbers of siliquae/plant (394) and numbers of seeds/siliquae (15), surpassing Phalsa-based AHS (365 and 14) and Karonda-based AHS (354 and 13). The maximum number of siliquae (416) was recorded with 1% KNO_3, statistically superior to 200 ppm SA (390.56), 1% urea (353.9), and control (322.9). Moringa-based AHS exhibited significantly higher seed yield (1880 kg/ha), stover yield (5731 kg/ha), and biological yield (7611 kg/ha), following the trend: Moringa > Phalsa > Karonda. Among PGR treatments, 1% KNO_3 yielded the maximum seed yield (1886 kg/ha), followed by 200 ppm SA (1783 kg/ha) and 1% urea spray (1646 kg/ha), while the control recorded the lowest yield (1344 kg/ha). 1% KNO_3 treatments resulted in 5.77%, 14.5%, and 40.32% higher seed yield compared to 200 ppm SA, 1% urea, and control, respectively. Maximum total N, P, and K uptake occurred with 1% KNO_3, and Moringa-based AHS displayed significantly higher nutrient uptake than Phalsa and Karonda-based AHS. Regarding soil properties, Moringa-based AHS exhibited the highest soil organic carbon, available N, and soil moisture content. Gross returns, net returns, B:C ratio, and profitability index were notably higher with 1% KNO_3 application. Moringa-based AHS outperformed in gross returns, net returns, and B:C ratio, followed by Phalsa and Karonda-based AHS. In conclusion, Moringa-based AHS and 1% KNO_3 application proved to be superior in enhancing Indian mustard productivity, resource use efficiency, and economic returns under limited irrigation conditions.

Productivity and resource use efficiency of pearl millet [*Pennisetum glaucum* (L.)]-based intercropping systems under zero tillage

A filed experiment was conducted in the 2022 *kharif* season study at ICAR-IARI, New Delhi, to assess the tillage practices and intercropping impact on crop performance. Using a split plot design with two tillage practices (zero tillage + residue 3 t/ha and conventional tillage) and seven intercropping systems, replicated thrice, the results showed significant benefits from zero tillage + residue 3 t/ha. This approach improved growth parameters, yield attributes, yields, net returns, nutrient uptake, water productivity, microbial biomass, and partial factor productivity for all crops (pearl millet, cowpea, and mungbean) compared to conventional tillage. Additionally, nutrient uptake, water productivity, microbial biomass, and partial factor productivity were notably higher under zero tillage + residue 3 t/ha. Pearl millet, cowpea, and mungbean exhibited significantly higher grain yield (1.37 t/ha), green pod yield (5.47 t/ha), and seed yield (0.70 t/ha) under zero tillage + residue 3 t/ha, with substantial increases in grain, stover, and biological yield over conventional tillage. Pearl millet equivalent grain yield, gross returns (₹101139/ha), net returns (₹63077/ha), and benefit-cost ratio (2.65) were also significantly higher under zero tillage + residue 3 t/ha. Pearl millet + cowpea (1:2) intercropping stood out with higher yield attributes, comparable to sole pearl millet. Sole cowpea and mungbean showed improved growth and yield attributes when intercropped with pearl millet. Cowpea achieved the highest green pod yield (6.43 t/ha) in sole cowpea, while mungbean under intercropping systems displayed superior growth attributes. Pearl millet + cowpea (1:2) intercropping demonstrated superior pearl millet equivalent grain yield (4.73 t/ha), net returns (₹84285/ha), and B:C ratio (3.18), comparable to sole cowpea. In conclusion, pearl millet + cowpea (1:2) intercropping under zero tillage + crop residue 3 t/ha demonstrated the most effective approach for higher growth, yield, nutrient uptake, water productivity, and net returns in rainfed agriculture.

Effect of row arrangements in maize-based intercropping systems on productivity and profitability in Eastern India

A field study was conducted at the ICAR-IARI, Jharkhand during the *kharif* season of 2022, to evaluate various cropping systems involving pure stands and intercrops of maize, green gram, and cowpea. The experiment, arranged in a randomized complete block design with five replications, comprised nine treatments, including pure stands of maize, green gram, and cowpea, as well as intercrop stands with different planting arrangements. The results revealed that plant height and dry matter accumulation were influenced by cropping systems, with the pure stand of maize exhibiting the highest values. In terms of grain yield and yield attributes, the cropping geometry did not significantly affect pure maize stands or additive stands. However, replacement stands showed varied grain yields based on planting density. Pure maize stands demonstrated the highest grain yield (7.03 t/ha), comparable to additive stands with cowpea (6.96 t/ha) and green gram (6.93 t/ha). Among replacement stands, maize with cowpea (RS-I and RS-II) produced relatively higher grain yields than those intercropped with green gram. Intercropping systems significantly increased nitrogen (N), phosphorus (P), and potassium (K) uptake in grain and stover, with maize + cowpea additive stands displaying the highest values. The trends were consistent for other nutrients such as sulfur (S), zinc (Zn), iron (Fe), copper (Cu), and manganese (Mn). Similar observations were made for green gram and cowpea, with pure stands exhibiting higher nutrient uptake. Cropping system indices and production economics favored intercrop stands over pure stands. Maize equivalent yield, system productivity, and profitability were highest with maize + cowpea additive stands, suggesting economic benefits. Net returns were also maximum with maize + cowpea additive stands, emphasizing the economic viability of this intercropping system in Eastern India. The study recommends intercropping maize with legumes, particularly cowpea, at additive stands to enhance farmer income in the region.

Sustainable intensification options for rice-wheat system in North-West India

Stagnant yields and groundwater risks persist, aggravated by climate change, posing a threat to food security. On-station experiments suggested sustainable options for non-basmati rice, but a technology adoption gap exists. On-farm study was conducted in Karnal, Haryana, from 2019–20 to 2020–21 for participatory technology development. The study featured six cropping scenarios (Sc), including CT-rice followed by wheat (CTRW), CT-rice followed by zero till (ZT)-wheat and mungbean (CTR-ZTWMb), ZT-direct seeded rice followed by ZT-wheat and mungbean (DSR-ZTWMb), ZT-maize followed by ZT-wheat and mungbean on permanent raised bed (PB) (ZTMWMb), ZT-maize followed by ZT-mustard and mungbean on PB (ZTMMuMb), and ZT-soybean followed by ZT-wheat and mungbean on PB (ZTSWMb). Sc2 to Sc6 integrated best residue, water, and nutrient management practices. These scenarios were replicated at four farmers' fields in a randomized complete block design. Results from the two-year on-farm study indicated DSR-ZTWMb significantly improved rice growth parameters over CTRW, while CTR-ZTWMb exhibited better wheat attributes. Maize and soybean in diversified systems showed slightly higher growth and yield attributes in the second year. Intensification through conservation agriculture (CA) within the rice-wheat system (CTR-ZTWMb and DSR-ZTWMb) and diversification with maize or soybean (ZTMWMb, ZTMMuMb, and ZTSWMb) achieved statistically comparable yields to traditional CTRW. Soybean had the lowest rice equivalent yield (REY), but CTR-ZTWMb and DSR-ZTWMb increased net returns. In diversified systems, wheat growth and yield attributes significantly improved on PB. System REY increased in diversified systems, with ZTMMuMb showing the highest improvement. Water use decreased in diversified systems, with significant improvements in water productivity. Soil health parameters, including available N, P, K, and SOC, increased significantly in diversified systems. Weed density and environmental footprint decreased with ZT and residue retention treatments. In conclusion, diversification and conservation agriculture-based intensification offer viable alternatives to traditional rice-wheat systems in the IGP, enhancing productivity, net returns, and sustainability.

Integrated farming system for sustainable livelihood and income of marginal landholders in North-West India

The study conducted at the experimental site of ICAR-IARI, Pusa, New Delhi, from *Kharif* 2020 to summer 2022, focused on the challenges faced by small and marginal farmers, who constitute 86% of total landholders in India. The average landholding of these farmers, at 0.39 ha per landholder, is insufficient to meet family livelihood and nutritional security. To address these concerns and align with government schemes like PM-KISAN, DFI, and PM-KSY, the study aimed to assess the productivity, profitability, and employment generation of various cropping systems and integrated farming systems (IFS). The experiment was laid out in a randomized complete block design with seven cropping systems, including diverse combinations like baby corn-mustard-baby corn, maize-onion, okra-cole crops-vegetable cowpea, bottle gourd-early vegetable pea-late wheat, cowpea-marigold-vegetable mustard, rice-wheat cropping system (RWCS), and maize-wheat cropping system (MWCS). An integrated farming system unit, comprising open-field vegetable cultivation, protected vegetable cultivation, agri-horti system, mushroom production, beekeeping, and vermicomposting, was also evaluated for system productivity, profitability, employment generation, livelihood security, water usage, and energy efficiency. Results indicated that the okra-cole crops-cowpea system was efficient in achieving higher productivity, sustainability livelihood index, and employment generation over the two years of study. On the other hand, cowpea-marigold-vegetable mustard resulted in higher profitability. Both systems outperformed the cereal-centric RWCS and MWCS in various aspects. The integrated farming system module, encompassing field crops, open-field vegetable cultivation, protected vegetable cultivation, mushroom production, beekeeping, and vermicomposting, showed significantly higher productivity, profitability, and employment generation over the two years. The M10 module (VP+PVC+FC+AHS+MP+BK+VC) was found to be superior in the livelihood index. This integrated approach also demonstrated better water productivity, nutrient recycling, partial nutrient budget, and human nutrition balance compared to RWCS. In conclusion, the study suggested that integrating diverse components in farming enterprises, especially for marginal farmers, could enhance productivity, profitability.

Studies on root-shoot behaviour of maize and wheat genotypes under varying sowing dates

The experiment conducted at ICAR-IARI in New Delhi during *Kharif* and *Rabi* 2020–21 and 2021–22 aimed to assess the impact of sowing dates and genotypes on agronomic, physiological, and root-system traits for maize and wheat in a split-plot design. Timely sowing exhibited a significant grain yield advantage of 16–19% for maize and 17–20% for wheat compared to late sowing. Key genotypes, including AH-4271 and AH-4158 for maize and HD-2967 and HD-3249 for wheat, demonstrated superior grain yield. Timely sowing increased net returns by 25.9–30.4% for maize and 25.3–28.2% for wheat. Post-anthesis dry matter accumulation was 16% higher for maize and 15–22% for wheat with timely sowing, improving nutrient acquisition for both crops. Hybrids AH-4271 and PJHM-1, along with HD-3226, exhibited enhanced root-morphological traits under tube study conditions. Late sowing in wheat advanced days to physiological maturity by 12 days and reduced the grain filling period by 5-9 days. AH-4271 and HD-2967 recorded the maximum geometric mean productivity for maize and wheat, respectively. AH-4158 and HD-2967 were identified as the most stable genotypes. Late sowing in wheat resulted in higher canopy temperature and reduced canopy temperature depression. Timely sowing increased wheat chlorophyll content by 7–12% and 7.2–7.9% at anthesis and dough stages, with HD-2967 exhibiting the highest content. Additionally, wheat genotypes grown under well- and deficit-watered conditions showed superior performance in root-system traits, dry matter accumulation, nutrient acquisition, yield, and water productivity. HD-3249 emerged as the superior genotype across various agronomical and physiological traits under both water conditions. In conclusion, adopting timely sowing for maize and wheat, combined with suitable genotype selection, holds the potential to sustain and enhance genetic yield in semi-arid Indian ecologies.

Theme 3: Irrigation Management

Precision nitrogen management in direct-seeded rice-wheat system under different crop establishment methods and irrigation regimes

A 2-year field study was conducted at ICAR-IARI, New Delhi, during the *Kharif* and *Rabi* seasons of 2019–20 and 2020–21. The clay loam soil at the experimental site had low to medium fertility. The study focused on two direct-seeded rice (DSR) establishment methods (conventional-till and zero-till) with three irrigation scenarios and three nitrogen (N) management options. The wheat crop included zero till-wheat (ZT-wheat) with similar irrigation and N management variations. Results indicated that conventional-till DSR (CT-DSR) exhibited higher plant height, dry matter accumulation (DMA), leaf area index (LAI), tillers, root length, net photosynthetic rate (Pn), and photosynthetic active radiation (PAR) interception, leading to 1.9%, 15.3%, and 121.1% higher grain yield, net returns, and net energy compared to zero-till DSR (ZT-DSR). Assured irrigation and nitrogen management guided by Nutrient Expert® (NE®)+SPAD meter saved N and produced higher yields and returns. In wheat, double zero-till (ZT) recorded higher growth parameters and 6.7% higher grain yield over ZT-wheat. Irrigating at 25% DASM and NE+SPAD meter-based N management resulted in increased wheat yields and returns. The study compared CT-DSR–ZT-wheat with ZT-DSR–ZT-wheat, revealing higher system productivity, net returns, and water productivity in the former. However, ZT-DSR–ZT-wheat showed marginally higher soil organic carbon (SOC) and higher soil available N, P, and K. Assured irrigation in DSR and 25% DASM in wheat exhibited higher system efficiency and energy compared to other scenarios. NE+SPAD meter-based N application reduced costs and energy input but maintained high productivity and efficiency. The combination of CT-DSR × assured irrigation × recommended dose of N and CT-DSR × 40% DASM+Si (80 kg/ha) × NE+LCC emitted lower N_2O emissions in DSR. In conclusion, CT-DSR–ZT-wheat with assured irrigation and NE+SPAD-meter-based N application proved the most productive and profitable option. ZT-DSR–ZT-wheat with assured or mild stressed irrigation and NE+SPAD-based N supply is also viable.

Productivity and quality of nano-urea fertilized transplanted rice under varying irrigation regimes

A field experiment was conducted at ICAR-Indian Agricultural Research Institute, New Delhi, India during the *Kharif* seasons of 2021 and 2022, to determine the effect of nitrogen rate, sources, and varying irrigation regimes on *basmati* rice (*Oryza sativa* L.). The experiment consisted of 12 combinations of three irrigation regimes *viz.,* irrigation at 1, 3 and 6 days after drying of surface water (1DADSW, 3DADSW and 6DADSW) allotted to main-plots and four N-management options including 100% recommended dose of N: (RDN); 75% RDN + nano urea (NU) with 2 sprays (75%RDN + NU); 50% RDN + NU spray (50% RDN+NU) and the control (no-N) allotted to sub-plots, all set in a split-plot design replicated thrice. Irrigation at 6DADSW reduced the grain yield by 13–19% over 3DADSW and a more substantial decrease of 23–28% compared to 1DADSW. RDN led to increments of 14.5% and 41.5% grain yield over 50% RDN + NU and control (N0) respectively, though it was statistically at par with 75% RDN + NU. Further, 75% RDN + NU moderately increased grain lengths (8.83 mm, 9.09 mm) over RDN, 50% RDN + NU, and significantly over control. Grain protein content increased with frequent irrigation and increasing N-rates; however, amylose content followed the reverse trend. RDN consistently had significantly lower amylose content compared to 50% RDN + NU and control. Highest grain and straw N, P and K uptake were observed with irrigation at 1DADSW and RDN. The highest gross return, net return, B:C ratio and monetary efficiency were also observed with irrigation at 1DADSW and RDN. Agronomic efficiency followed the trend as 50% RDN + NU> 75% RDN + NU>RDN. The maximum agronomic efficiency (29.5 kg of grain increased/kg N applied) was observed with the interaction of irrigation at 1DADSW and 50% RDN + NU.

Precision nutrient and irrigation management in soybean and wheat under system of crop intensification

A field experiment conducted at ICAR-IARI, New Delhi, during the *kharif* and *rabi* seasons of 2020-2021 and 2021-2022 aimed to assess the impact of precision nutrient and irrigation management on soybean and wheat under the System of Crop Intensification (SCI). The experiment, utilizing a split-plot design, involved three irrigation regimes (standard flood irrigation, sprinkler irrigation at 80% ETC, and sprinkler irrigation at 60% ETC) and five precision nutrient management protocols (SCI protocol, RDF with SPAD-based top-dressing, 75% RDF with SPAD-based top-dressing, and 50% RDF with SPAD-based top-dressing). The study found that both precision nutrient management (PNM) and irrigation practices significantly improved crop growth parameters, yield attributes, and grain yield in soybean and wheat. Sprinkler irrigation at 80% ET_C exhibited superior results in terms of crop growth parameters and growth indices over flood irrigation. Precision nutrient management protocols, especially PNM3, showed positive effects on various physiological parameters, photosynthetic parameters, root attributes, and yield. Yield attributes and grain yield were significantly higher under sprinkler irrigation at 80% ET_C for both crops. Quality parameters like crude protein, gluten content, and protein yield were also enhanced with this irrigation practice. PNM3 consistently showed higher quality parameters for both wheat and soybean. The study revealed that SCI methods, coupled with sprinkler irrigation at 80% ET_C and PNM3, produced superior yields and quality in soybean and wheat over conventional practices. The combination of Sprinkler irrigation at 80% ET_C and PNM3 emerged as the most effective in terms of yield and quality for both crops. Additionally, these practices demonstrated better resource-use efficiency, improved soil properties, and higher economic returns. In conclusion, integrating SCI with sensor-based precision nutrient and irrigation management, specifically Sprinkler irrigation at 80% ET_C and PNM3, proved to be a viable and effective approach for enhancing crop productivity, resource-use efficiency, and soil health in soybean and wheat crops grown in sequence.

Theme 4: Conservation Agriculture

Conservation agriculture effects on productivity and nitrogen use efficiency of maize (*Zea mays* L.)

A field experiment was conducted at the research farm of ICAR-IARI, New Delhi, India during the *kharif* season of 2022, to study the effect of tillage and nitrogen levels on yield and nitrogen dynamics of maize crop grown in a long-term conservation agriculture-based maize-chickpea-*Sesbania* system along with simulation modeling using DSSAT CSM model (Ceres-Maize). The study employed a split-plot design with three tillage practices [conventional tillage with residue (CT), zero tillage with residue (ZT), and permanent beds with residue (PB)] as main plot treatments and in sub-plots three nitrogen levels [control (without N fertilization), 50% of recommended dose of nitrogen (RDN) @ 75 kg/ha, 100% recommended dose of N @ 150 kg N/ha] with three replications. Results showed that both tillage and nitrogen management options had a significant effect on maize growth, yield attributes, grain and biomass yield, and nitrogen and radiation use efficiency. CA-based zero till flat (ZT+R) plots demonstrated superior plant height at early growth stages, while permanent beds (PB+R) exhibited significant growth at later stages. Nitrogen management showed a clear correlation between the rate of application and enhanced plant growth. Most of the yield-attributing characteristics remained unaffected (except grains/row and grains/cob) due to different tillage practices. However, nitrogen application at 100% recommended dose displayed significant improvements across multiple yield attributes of maize, including cobs per square meter, cob length, grain rows per cob, and grain weight per cob (except grain rows/cob). The findings of the present study highlighted the significance of efficient nitrogen management for enhanced maize productivity, resource use efficiency and profitability under a long-term conservation agriculture-based maize-chickpea-*Sesbania*. The DSSAT-CERES-Maize model was effectively used to simulate crop phenology, leaf area index, yield, and soil N dynamics. The model's predictions are closely aligned with observed values, affirming its accuracy and applicability in predicting maize growth and yield.

Weed and nitrogen management under a long-term conservation agriculture-based maize-wheat-greengram cropping system

Conservation agriculture (CA) is seen as a sustainable alternative to intensive tillage, countering the resource degradation caused by conventional agriculture. Shifting from the traditional rice-wheat system to a maize-wheat system under CA, incorporating legumes, aims to boost productivity, sustainability, soil quality, and ecological balance. However, the benefits of CA might take time to manifest and thus require long-term assessment. A study conducted over two years at the ICAR-Indian Agricultural Research Institute aimed to evaluate tillage, residue management, nitrogen application, and weed control's impact on weed dynamics, crop growth, profitability, and soil properties within a CA-based maize–wheat–greengram system. The experiment employed various treatments: zero tillage (ZT) with residue retention and different nitrogen doses, conventional tillage (CT) with full residue incorporation and nitrogen application. Weed control involved herbicide applications tailored to specific crops. Results favored the CA-based system, demonstrating better weed suppression and higher crop productivity under ZT with 100% or 75% nitrogen compared to CT with 100% nitrogen. The maize-wheat-greengram rotation showed superior productivity under ZT with 100% nitrogen, followed closely by ZT with 75% nitrogen. Improved productivity correlated with enhanced water, nutrient, and energy-use efficiencies. Long-term CA practices enhanced soil health, indicated by improved soil properties and microbial diversity. It suggested a potential reduction in synthetic fertilizer application due to increased soil organic matter (SOM) and nutrient reserves from continuous crop residue recycling. The study emphasized the necessity of efficient weed control strategies within CA, showing that herbicide application, especially a sequential pre- and post-emergence approach, significantly boosted yields, profitability, and resource-use efficiencies. Ultimately, the study recommended a multi-faceted integrated approach: combining zero tillage, residue retention, diversified crop rotation, appropriate nitrogen application, and strategic herbicidal weed control. This approach aims to sustainably manage crops and weeds within the maize-wheat-greengram system in the north-western Indo-Gangetic Plains of India for long-term viability.

Sustainable intensification of conservation agriculture-based pearlmillet-chickpea cropping systems for improving productivity and resource use efficiency in semi-arid ecologies

Pearl millet–based cropping systems with intensive tillage operations prior to crop establishment have limited sustainable productivity in low-irrigation conditions of semi-arid ecologies, such as north Indian plains. Adoption of zero tillage with residue retention (ZT+R) and diversification with the inclusion of summer pulse crops has the potential to improve the cropping system's sustainability. We compared two improved management practices, zero tillage (ZT), and ZT+R, to conventional tillage (CT), across three pearl millet-based cropping systems: PM–CP, PM–CP–MB and PM–CP–FPM a two-year experiment. Experimental treatments were compared in terms of pearl millet productivity, nutrient biofortification and greenhouse gas emissions. Results showed a significant increase in pearl millet yield attributes, grain and stover productivity, nutrient uptake, and micronutrient biofortification in the PM–CP–MB cropping system under ZT+R, relative to other treatment combinations. The study highlights that intensification of PM–CP system using summer crops enhanced pearl millet productivity across diverse tillage systems. Overall, zero tillage practice combined with diversified pearl millet-based cropping systems could be a suitable approach towards sustainable intensification of agriculture in the semi-arid North Indian plains.

Developing intensification options to enhance productivity and resource use efficiency of conservation agriculture-based pearl millet-mustard cropping system

To combat micronutrient malnutrition and improve yields in rainfed cropping systems, this study explores climate-smart strategies like conservation agriculture and intensified millet cropping. ZT (zero tillage) systems with intercropping of legumes (clusterbean, cowpea, and chickpea) significantly increased productivity (7-12.5%), micronutrient biofortification [Fe (12.5%), Zn (4.9–12.2%), Mn (3.1–6.7%), and Cu (8.3–16.7%)], protein content (2.2–9.9%), oil content (1.3%) and fatty acid profile of pearl millet grains compared to conventional tillage (CT)based systems with sole cropping. Zero Tillage (ZT) systems consistently outperform conventionaltillage, with a significant increase in mustard grain yield, major nutrient content (phosphorus andpotassium), and micronutrient levels (iron, zinc, manganese, and copper). Mustard grain yield in ZT-P + CB-M surpasses conventional tillage. In conclusion, ZT with residue-recycling and legumeintercropping is a recommended approach for enhancing pearl millet in South Asian rainfed agro-ecosystems. System productivity (PEY and MEY) over the two-year study, with ZT-PCWM and ZT-PCLM exhibiting significant improvements of approximately 70.35% to 93.97% in the *Kharif* season and ZT-PCLM and ZT-PMC showcasing remarkable enhancements of approximately 57% to 130% in the *Rabi* season. The combination of ZT with intercropping and residue inboth seasons significantly affects the soil bulk density, soil moisture extraction, MBC and carbon pools. The soil aggregate size distribution was higher with residue retention in zero tillage. ZT- PCLM consistently delivered higher gross returns, net returns, benefit-cost ratio, and lower input-cost ratio compared to other treatments, with notable grain yield increases over the control treatment (CT-PM). In contrast, Zero Tillage with intercropping and Crop Residue Management (ZT-PM) excelled in terms of Net Returns and ICR. Overall, these results emphasize the economic advantages of ZT-PCLM and ZT-PM in enhancing pearl millet crop profitability.

Modelling the impact of tillage and nitrogen management on yield and nitrogen dynamics in a long-term conservation agriculture-based maize-wheat system

A field experiment was conducted at the research farm of ICAR-IARI, New Delhi, during the *kharif* and *rabi* seasons of 2020-21 and 2021-22. Results showed that both tillage and nitrogen management options had a significant impact on maize growth, yield attributes, grain and biomass yield, nitrogen and radiation use efficiency in both seasons. CA-based-PB plots recorded the highest values of leaf area index (LAI), grain, and biomass yield for both crops whereas some fluctuations were observed in partial factor productivity and apparent nitrogen recovery. Among nitrogen management options, N150 recorded highest grain yield, biomass yield, and the highest net return and profitability. Overall, CA-based PB and ZT practices combined with RDN (N150) resulted in better crop growth parameters, yield attributes, yields, profitability, efficient nitrogen use and higher radiation use efficiency. The DSSAT CSM model accurately simulated days to anthesis and physiological maturity, LAI, crop growth, and grain and biological yield. The simulation results aligned with the observed soil nitrate concentration across all treatments. The model accurately captured the differences in nitrate concentration among CT and ZT and different nitrogen options, demonstrating its ability to predict the dynamics of nitrate in soil. Both crops showed a substantial increase in nitrogen uptake during the initial days, with a sharp increase observed after the application of fertilizer. The model's predictions were consistent with this trend. The model precisely simulated different appendages of nitrogen dynamics on real real-time basis which indicated the robustness and reliability of the model. This study highlights the importance of adopting CA practices along with N150 and USG as nitrogen management options for improving maize and wheat growth, yield, and profitability. It also suggests that the simulation by the DSSAT CSM model can serve as a reliable tool in real-time tillage and nitrogen management.

Nitrogen and sulphur management in maize-mustard cropping system under conservation agriculture

Conservation Agriculture (CA) minimizes soil disruption, maintains soil cover through residue or cover crops, and employs efficient crop rotation to conserve resources and sustain productivity. This study, spanning the 11th and 12th years of a long-term CA-based maize-mustard cropping system, assessed the impact of nitrogen (N) and sulphur (S) on maize and mustard. Results highlighted that specific CA practices, CA4 and CA3, exhibited superior characteristics such as plant height, dry weight, root development, and grain yield compared to other CA and conventional tillage (CT) systems. Particularly, CA4 showed notable improvements, increasing root characteristics by 15.7–31.1% over CT and significantly enhancing grain yield, leading to increased profitability due to higher yields and reduced cultivation costs. These CA practices also significantly improved water productivity by considerable margins, showing increased partial factor productivity (PFP) of nutrients and better soil physical properties, enhancing soil health. CA4 specifically stood out, showcasing substantial enhancements in soil organic carbon, microbial biomass, and enzyme activities, promoting soil health and nutrient availability. Moreover, this study demonstrated that CA practices improved soil available sulphur, heat soluble sulphur, and SO_4-S content, benefiting the overall soil structure and health. Notably, the CA4 system, a triple zero-tillage system with residue retention and legume integration, consistently outperformed other CA practices, emphasizing its potential for sustainable agriculture. The study highlighted the efficiency of nitrogen and sulphur management in this CA system, allowing for improved productivity and nutrient use efficiency. Furthermore, it emphasized that adopting a CA-based maize-mustard cropping system with adjusted N and S doses might offer sustainable production benefits in the Indo-Gangetic plains of India, showcasing enhanced yield, income, resource-use efficiency, and soil improvement.

Effect of nitrogen placement methods on crop productivity and resource use efficiency in mustard and its carry-over effect on mungbean under conservation agriculture

A two-year field experiment at ICAR-Indian Agricultural Research Institute, New Delhi, investigated the impact of nitrogen placement methods on mustard and its carry-over effect on mungbean under conservation agriculture (CA). The study involved three crop establishment practices (CEP: ZT+R, ZT-R, CT) and four nitrogen placement methods (NPM: control, RDN-conventional, RDN-SSB, 80% RDN-SSB). ZT+R and RDN-SSB significantly improved growth parameters, lowered canopy temperature depression (CTD), and enhanced crop growth and relative growth rates in both mustard and mungbean. The interaction of ZT+R and RDN-SSB resulted in superior yield attributing characters and significantly higher mustard seed yield in ZT+R by 14.3–28.5% compared to ZT-R and CT, while in RDN-SSB, it was 7.3–9.1% higher than other treatments. Similar trends were observed in mungbean with ZT+R and RDN-SSB. ZT+R and RDN-SSB increased nitrogen content in mustard seeds and stalks. In mungbean, ZT+R recorded higher nitrogen content compared to CT, while RDN-SSB had the highest total nitrogen uptake. ZT+R incurred lower system cultivation costs compared to CT. The combination of ZT+R with RDN-SSB reported higher mustard equivalent yield and system net returns, demonstrating economic efficiency. ZT+R had lower carbon input and system global warming potential, indicating environmental benefits. The ZT+R and ZT-R showed significantly higher total water productivity and economic water productivity compared to CT, with better soil moisture content in the upper profile at flowering stages. ZT+R exhibited improved soil properties, including higher soil organic carbon, lower bulk density, and enhanced microbial activity. In conclusion, adopting zero tillage with residue retention and subsurface nitrogen placement in the mustard-mungbean sequence enhances productivity, profitability, and resource use efficiency while reducing environmental impact. This approach, particularly with subsurface band placement, has the potential to save 20% nitrogen compared to conventional methods, making it suitable for semi-arid Indo-Gangetic plains and similar agro-ecologies.

Theme 5: Weed Management

Integrated weed management in maize under conservation agriculture-based maize-wheat-mung bean system

The rice-wheat cropping system, covering 10.5 million hectares in the Indo-Gangetic plains, grapples with declining productivity and sustainability. Both rice and wheat yields stagnate, necessitating an alternative like maize-wheat-mung bean under conservation agriculture (CA). In the *kharif* seasons of 2022-23, ICAR-Indian Agricultural Research Institute conducted a field experiment in New Delhi, exploring weed management in maize cultivation within the maize-wheat-mung bean system. The split-plot design included main plots with different maize cultivation methods (Conventional tillage maize - M1, Conventional tillage maize with green manure - M2, zero tillage maize with residue retention - M3, zero tillage maize with *Sesbania* co-culture - M4) and sub-plots with weed control treatments (Un-weeded check - S1, Pre +1 HW - S2, Pre + Post (Tembotrione) @120 g/ha - S3, Pre + Post (Premix Meso+Atra) @120 g/ha - S4, Weed-free check - S5). M4: ZT-M+BM significantly reduced broad-leaf weed, narrow-leaf weed, sedges, and total weeds by 28.4% at 60 DAS compared to M1: CT-M. Sequential herbicide application of Atrazine @ 750 g/ha+Pendimethalin @ 750 g/ha (pre) followed by Tembotrione @ 120 g/ha (post) exhibited a 78.5% reduction in weed population and an 81.3% reduction in dry weight compared to the un-weeded check. The highest grain yield (6.72 t/ha) was achieved with ZT-M+BM, a 17.7% increase compared to CT-M. The weed-free check plot showed a 25.43% increase in grain yield compared to the un-weeded check, surpassing other weed management methods. ZT-M+BM displayed superior values for cob length, cob girth, cob weight, shelling percentage, number of grains per cob, and 100-grain weight, while CT-M exhibited the lowest values for these attributes. The sequential herbicide application yielded significantly higher grain yields (6.32 t/ha). In conclusion, combining ZT with brown manure and sequential herbicide application can enhance weed control and maize productivity in the CA-based system of the North-Western Indo-Gangetic plains of India.

Integrated weed management in Indian mustard (*Brassica juncea* L.) under NEH region

A field experiment was conducted during *Rabi* season of 2022-23 at the experimental farm of ICAR research complex for North East Hill region (ICAR-RC-NEH), Umiam, Meghalaya. The experiment was laid out in a randomized block design and replicated thrice. The application of pendimethalin @ 0.75 kg/ha as pre-emergence followed by one-hand weeding at 30 DAS was found very effective in controlling all major weeds such as *Ageratum conyzoides, Alternanthera sessilis, Panicum repens,* and *Cynodon dactylon* found in the field. This treatment produced 44.03% higher seed yield of Indian mustard over the weedy check. After this, the pre-emergence application of oxadiargyl @ 45 g/ha followed by one-hand weeding at 30 DAS was found effective in reducing weed density, dry weight, nutrient uptake by composite weed species and increasing nutrient uptake by crop, and enhanced crop growth parameters. The highest yield attributes like primary and secondary branches, silique/plant, and seeds/siliqua were observed in the application of pendimethalin @ 0.75 kg/ha as pre-emergence followed by one-hand weeding at 30 DAS. Plots having season-long weed-free conditions recorded 57.6% increase in seed yield of Indian mustard as compared to plots having season-long weed competition (UWC). Different weed management options provided yield advantages in between the range of 6.06 to 44.03% over the weedy check. The highest net return (Rs 25,800/ha) was obtained under pendimethalin @ 0.75 kg/ha as pre-emergence followed by one-hand weeding at 30 DAS which was closely followed by oxadiargyl @ 45 g/ha as pre-emergence followed by one hand weeding at 30 DAS (Rs 24,400/ha). The B:C was highest in pendimethalin @ 0.75 kg/ha as pre-emergence followed by one-hand weeding at 30 DAS owing to high gross return (Rs 51,800/ha) as compared to the cost of cultivation (Rs 25,900/ha) than other treatments, which was comparable to oxadiargyl @ 45 g/ha as pre-emergence followed by one hand weeding at 30 DAS.

Effect of mulching and herbicide use for weed management in maize (*Zea mays* L.)

A field experiment was conducted at ICAR-NIBSM, Raipur, during the rainy season of 2022. A split-plot design was employed with main plots assigned to different paddy straw mulch treatments (8 t/ha straw mulch - M1, 5 t/ha straw mulch - M2, and no mulch - M3). Subplots involved five weed management treatments: atrazine 1 kg/ha PE (T1), atrazine 1 kg/ha PE followed by tembotrione 120 g/ha at 25 DAS (T2), atrazine 1 kg/ha PE followed by topramezone 30 g/ha at 25 DAS (T3), weed-free (T4), and weedy check (T5). Atrazine 1 kg/ha PE followed by tembotrione 120 g/ha at 25 DAS (T2) exhibited effective control of diverse weed flora, achieving a higher weed control efficiency (81.4%) compared to atrazine 1 kg/ha PE followed by topramezone 30 g/ha at 25 DAS (76.8%) at 40 DAS. The yield attributes and overall maize yield were significantly influenced by both paddy straw mulch and various weed management practices. The treatment with 8 t/ha straw mulch recorded higher values for key yield attributes such as number of cobs/plants, cob length, cob girth, rows/cob, grains/row, and grains/cob. The highest grain yield (5.68 t/ha), stover yield (6.96 t/ha), and biological yield (12.66 t/ha) were observed under the 8 t/ha straw mulch treatment. Weed-free conditions resulted in the maximum yield (6.18 t/ha) among the herbicide treatments, with atrazine 1 kg/ha PE followed by tembotrione 120 g/ha at 25 DAS statistically superior to other herbicide treatments. The interaction effect between straw mulch and weed management treatments was significant for grain yield. The atrazine 1 kg/ha PE followed by tembotrione 120 g/ha at 25 DAS treatment demonstrated the highest total nutrient uptake by maize, including N, P, and K. Economically, atrazine 1 kg/ha PE followed by tembotrione 120 g/ha at 25 DAS exhibited the maximum net return (Rs 76,610/ha) and net benefit-cost ratio (1.97).

Effect of nutrient management and herbicide interaction in weed management of maize (*Zea mays* L.)

A field experiment was conducted at ICAR-NIBSM, Raipur, in the *kharif* season of 2022. A split-plot design with three main plots focusing on different nutrient management (NM) treatments: 100% recommended dose of nutrients (RDN; M1), 50% RDN (M2), and control with no nutrient application (M3). In the sub-plots, five weed management (WM) treatments were employed: atrazine (T1), atrazine followed by (*fb*) tembotrione (T2), atrazine *fb* topramezone (T3), weed-free with two hand weedings at 20 and 40 DAS (T4), and weedy check (T5). T2 demonstrated high effectiveness in controlling diverse weed flora, achieving an 80.1% weed control efficiency, comparable to T3 (77.0%) at 40 DAS. The combined influence of NM and WM significantly impacted various aspects of maize growth and yield. The application of M1 resulted in 13.97% and 23.25% more cobs per plant than M2 and M3, respectively. The weed-free (WF) treatment exhibited the highest number of good cobs per plant (1.3/plant). In terms of herbicide treatments, T2 showed statistical superiority over T1 alone but was on par with T3 in terms of cobs per plant. The highest grain yield (GY; 6.85 t/ha) and stover yield (SY; 10.01 t/ha) were recorded under the full RDN. Among WM treatments, the WF treatment had the maximum GY (6.99 t/ha) *fb* other treatments. T2 treatment showed higher GY (6.20 t/ha) and SY (9.23 t/ha) compared to T1 as pre-emergence and T3. The interaction effect between NM and WM treatments was found to be non-significant. In the treatment of T2, the highest total N uptake by grain (104.0 kg/ha), total P uptake (50.0 kg/ha), and K uptake (32.0 kg/ha) by maize were recorded. Maximum net returns (Rs 88,820/ha) were achieved with the T2, which also had the highest net B:C ratio (2.15).

Interactive effect of crop establishment methods and weed management options on weed interference, productivity and profitability in maize-wheat system

A comprehensive two-year study was conducted at ICAR-IARI, New Delhi, focusing on maize and wheat production within this system. The study assessed three crop establishment methods (bed planting with residue, zero tillage with residue, conventional tillage with residue) and five weed management options (pyroxasulfone in pre- and post-emergence, atrazine followed by tembotrione, weedy check, weed-free check). Bed planting with residue notably reduced weed density and dry matter compared to other methods. Effective weed management strategies, particularly the sequential use of pyroxasulfone followed by tembotrione in maize and pyroxasulfone followed by metsulfuron + carfentrazone in wheat, demonstrated exceptional higher efficacy, achieving high weed control efficiency and weed control index. Bed planting with residue showed superior crop growth parameters, yield attributes, and grain yield in both maize and wheat compared to other establishment methods. Economic analyses highlighted bed planting with residue as the most profitable method, offering the highest gross returns, net returns, and net benefit: cost ratio for both crops. Among weed management options, the sequential herbicide treatment of pyroxasulfone followed by tembotrione in maize and pyroxasulfone followed by metsulfuron + carfentrazone in wheat was economically viable, resulting in substantial increases in gross returns and net benefit. Bed planting with residue improved nutrient uptake and consistently maintained higher soil moisture content, positively impacting crop growth. Soil microbial parameters, including microbial biomass carbon and dehydrogenase enzyme activity, responded positively to bed planting with residue and selected weed management options, indicating enhanced soil microbial activity. Importantly, herbicide residues in maize and wheat grains and soil samples remained below detectable levels, underscoring the safety and compliance of the herbicide application. Overall, the study suggests that adopting bed planting with residue and specific weed management strategies can enhance crop productivity, resource-use efficiency, soil health, and economic returns in the maize-wheat cropping system.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the Student & Roll No.	MSc/ PhD	Title of the thesis	Chairperson	Institute
1.	Shubham Grover (21607)	M.Sc.	Effect of multi-micronutrient embedded sulphur on productivity and biofortification of wheat	Dr. R.S. Bana	ICAR-IARI, New Delhi
2.	Shwetansh (21608)	M.Sc.	Conservation agriculture effects on productivity and nitrogen use efficiency of maize (*Zea mays* L.)	Dr. C.M. Parihar	ICAR-IARI, New Delhi
3.	Soumya Prakash Bhoi (21609)	M.Sc.	Effect of plant growth regulators on productivity, resource use efficiency and economics of Indian mustard under limited irrigation agri-horti system	Dr. S.S. Rathore	ICAR-IARI, New Delhi
4.	Sougata Roy (21610)	M.Sc.	Integrated weed management in maize under conservation agriculture-based maize-wheat-mung bean system	Dr. Kapila Shekhawat	ICAR-IARI, New Delhi
5.	Bipasha Das (21611)	M.Sc.	Effect of organic manures and bio-fertilizers on productivity and profitability of wheat under long-term rice-wheat rotation	Dr. Vijay Pooniya	ICAR-IARI, New Delhi
6.	Subrata Bag (21612)	M.Sc.	Phosphorus management through organic and microbial sources in baby corn (*Zea mays* L.)	Dr. Yudh Vir Singh	ICAR-IARI, New Delhi
7.	Dhanavath Prakash (21614)	M.Sc.	Productivity and resource use efficiency of pearl millet [*Pennisetum glaucum* (L.)]-based intercropping systems under zero tillage	Dr. Raj Singh	ICAR-IARI, New Delhi
8.	Prakash Sonnad (21735)	M.Sc.	Tillage and methods of nutrients application effects on productivity of maize (*Zea mays* L.)	Dr. Teekam Singh	ICAR-IARI, New Delhi
9.	Chappali Harendra (21745)	M.Sc.	Nutrient management in maize (*Zea mays* L.) under different crop establishment option	Dr. Rajiv Kumar Singh	ICAR-IARI, New Delhi
10.	Ayekpam Dollina Devi (50074)	M.Sc.	Precision nitrogen management in rice for improving productivity and resource-use efficiency in the NEH region	Dr. Anchal Dass	#ICAR-IARI, Assam
11.	Rohitash Doodwal (50075)	M.Sc.	Nutrient management in organic rice under NEH region	Dr. Samrath Lal Meena	#ICAR-IARI, Assam
12.	Abhishek Patidar (50076)	M.Sc.	Effect of organic nutrient sources on rice varieties in NEH region	Dr. Shiva Dhar	#ICAR-IARI, Assam
13.	Devendra Kumar Dadhich (50077)	M.Sc.	Integrated weed management in Indian mustard (*Brassica juncea* L.) under NEH region	Dr. Rajvir Sharma	#ICAR-IARI, Assam
14.	Tanmay Das (60096)	M.Sc.	Effect of nano-urea application for enhancing the productivity of rainfed maize	Dr. Teekam Singh	#ICAR-IARI, Jharkhand
15.	Inuganti Kavya (60097)	M.Sc.	Effect of row arrangements in maize-based intercropping systems on productivity and profitability in Eastern India	Dr. Amal Ghosh	#ICAR-IARI, Jharkhand

16.	Indrani Saha (60098)	M.Sc.	Effect of planting density and nitrogen management on hybrid maize (*Zea mays*) in Eastern Indian	Dr. Shankar Lal Jat	#ICAR-IARI, Jharkhand
17.	Satyam Rawat (60099)	M.Sc.	Effect of nano-urea on maize productivity and nitrogen use efficiency in acid soil of Jharkhand	Dr. Rajiv Kumar Singh	#ICAR-IARI, Jharkhand
18.	Diyan Mandal (80010)	M.Sc.	Effect of mulching and herbicide use for weed management in maize (*Zea mays* L.)	Dr. Probir Kumar Ghosh	**ICAR-NIBSM, Raipur
19.	Shruti Sanjita Giri (80011)	M.Sc.	Effect of nutrient management and herbicide interaction in weed Management of maize (*Zea mays* L.)	Dr. Anil Dixit	**ICAR-NIBSM, Raipur
20.	Shanti Devi Bamboriya (10768)	Ph.D.	Optimization of nitrogen for contrasting genotypes in wheat-maize cropping system	Dr. Shiva Dhar	ICAR-IARI, New Delhi
21.	Kavita Kumari (10769)	Ph.D.	Productivity and quality of nano-urea fertilized transplanted rice under varying irrigation regimes	Dr. Anchal Dass	ICAR-IARI, New Delhi
22.	Anita Kumawat (10770)	Ph.D.	Effect of legumes and nutrient management on soil health and productivity of organic rice-wheat system	Dr. Dinesh Kumar	ICAR-IARI, New Delhi
23.	Rahul Sadhukhan (10982)	Ph.D.	Nutrient management in direct seeded rice (*Oryza sativa* L.) zero till wheat (*Triticum aestivum* L.) system	Dr. Dinesh Kumar	ICAR-IARI, New Delhi
24.	Suman Sen (11150)	Ph.D.	Weed and nitrogen management under a long-term conservation agriculture-based maize–wheat–greengram cropping system	Dr. T. K. Das	ICAR-IARI, New Delhi
25.	Radheshyam (11217)	Ph.D.	Sustainable intensification options for rice-wheat system in North-West India	Dr. Shankar Lal Jat	ICAR-IARI, New Delhi
26.	Vijay Pratap (11219)	Ph.D.	Precision nitrogen management in direct-seeded rice-wheat system under different crop establishment methods and irrigation regimes	Dr. Anchal Dass	ICAR-IARI, New Delhi
27.	Manu S M (11220)	Ph.D.	Microbial mediated *in-situ* rice residue management and its effects on soil health and productivity of the rice-wheat system	Dr. Yudh Vir Singh	ICAR-IARI, New Delhi
28.	Mukhtar Ahmad Faiz (11372)	Ph.D.	Sustainable intensification of conservation agriculture based pearlmillet-chickpea cropping systems for improving productivity and resource use efficiency in semi-arid ecologies	Dr. R.S. Bana	ICAR-IARI, New Delhi
29.	Kirttiranjan Baral (11445)	Ph.D.	Effect of summer green manuring and nano-zinc oxide coated urea on productivity and nutritional quality in basmati rice-wheat cropping system	Dr. Y.S. Shivay	ICAR-IARI, New Delhi
30.	Akshay Kumar Yogi (11448)	Ph.D.	Developing intensification options to enhance productivity and resource use efficiency of conservation agriculture-based pearlmillet-mustard cropping system	Dr. R.S. Bana	ICAR-IARI, New Delhi
31.	Shyam C S (11449)	Ph.D.	Integrated farming system for sustainable livelihood and income of marginal landholders in North-West India	Dr. S.S. Rathore	ICAR-IARI, New Delhi

32.	Kamlesh Kumar (11452)	Ph.D.	Modelling the impact of tillage and nitrogen management on yield and nitrogen dynamics in a long-term conservation agriculture-based maize-wheat system	Dr. C.M. Parihar	ICAR-IARI, New Delhi
33.	Sandeep Gawdiya (11453)	Ph.D.	Evaluation of rice and wheat genotypes for higher nitrogen use efficiency	Dr. Dinesh Kumar	ICAR-IARI, New Delhi
34.	R Rustum Zhiipao (11454)	Ph.D.	Studies on root-shoot behaviour of maize and wheat genotypes under varying sowing dates	Dr. Vijay Pooniya	ICAR-IARI, New Delhi
35.	Arkaprava Roy (11456)	Ph.D.	Nitrogen and sulphur management in maize-mustard cropping system under conservation agriculture	Dr. T.K. Das	ICAR-IARI, New Delhi
36.	Sachin K. S. (11457)	Ph.D.	Precision nutrient and irrigation management in soybean and wheat under system of crop intensification	Dr. Anchal Dass	ICAR-IARI, New Delhi
37.	Sasmita Tripathy (11719)	Ph.D.	Organic nutrient management in rainfed mustard + chickpea intercropping system	Dr. Samrath Lal Meena	ICAR-IARI, New Delhi
38.	Sunil Kumar (11725)	Ph.D.	Interactive effect of crop establishment method and weed management options on weed interference, productivity and profitability in maize-wheat system	Dr. Ramanjit Kaur Randhawa	ICAR-IARI, New Delhi
39.	Smruti Ranjan Padhan (11730)	Ph.D.	Effect of nitrogen placement methods on crop productivity and resource use efficiency in mustard and its carry over effect on mungbean under conservation agriculture	Dr. Shankar Lal Jat	ICAR-IARI, New Delhi

#IARI off campus

**Outreach Institute

Environmental Sciences

11

Prof. Dinesh Sharma

Environmental pollution and climate change are the two major problems confronting agriculture today. Environmental impacts of agriculture and vice versa have raised serious questions about the sustainability of agricultural production systems because of widespread deterioration of soil, water and air quality. Climate change, caused by the increased concentration of greenhouse gases in the atmosphere, has emerged as one of the most prominent global environmental problems. To address these challenges Division of Environment Science a multi-disciplinary division was established at Nuclear Research Laboratory Building, Indian Agricultural Research Institute, New Delhi 110 012. The Division of Environmental Sciences has ambitious programme of collaborating with the public, private and civil society organizations to develop and demonstrate the technologies on-farm and promote them to enhance resilience of Indian agriculture and improve the livelihood of farmers. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Climate Change and Agriculture

Response of different duration varieties of Indian mustard to climatic risks

Climate change is reducing the ideal growing period for mustard, necessitating the development of improved crop management strategies. The interaction between sowing times and varieties determines the crop growth and productivity, as exemplified by medium duration and early sown, which achieved outstanding yield and total dry matter which provided 33.7% yield advantage over timely sown condition. The study indicated the importance of identifying region specific suitable sowing and variety combinations for achieving higher yields in mustard. For instance, Aligarh, had highest yield increase 45.86% with four irrigations and a late-sown medium duration variety, Amritsar had 45.36% with four irrigations and planting a late-sown long-duration variety and Bharatpur had 18.9% increase over the current yield was achieved with four irrigations and a timely-sown long-duration variety. This study highlighted the use of simulation analysis for identifying best combination of sowing time and varieties to optimize yield and also for providing valuable insights for better adaptation strategies in changing climates.

Assessing the productivity and plant nutrients in wheat at elevated ozone and carbon dioxide interaction under different nitrogen management

A study was conducted in Genetic H field, Environmental science, IARI during the *rabi* season, 2022-23, to quantify the impact of elevated O_3 and CO_2 interaction on growth, productivity, macro and micro nutrient status of wheat under different N management practices. Wheat crop (variety HD3086) was grown in Free Air Ozone-Carbon dioxide Enrichment rings (FAOCE) rings with two levels of ozone (O_3) (elevated 60 ±10ppb and ambient) and two levels of carbon dioxide (CO_2) (elevated, 550±25 ppm and ambient) concentration and their interaction with four nitrogen fertilizer treatments i.e., 100% RDN (120kg ha-1), 125% RDN, 100%RDN+ 1 spray of nano urea and no nitrogen (control).Elevated O_3 level significantly decreased growth parameters like photosynthesis rate, LAI, leaf chlorophyll, NDVI and yield attributes like grain yield, straw yield, HI, spike and grain number in wheat crop. In elevated O_3 plus CO_2 interaction treatment grain yield was more by 7.8% than that of ambient with recommended dose of N application Available N of soil was less in elevated O_3 plus CO_2 treatment than ambient. Application of higher dose of N improved soil available N status. Thus, it can be concluded that application of one spray liquid nano urea along with recommended N dose can increase grain N status and recovery efficiency of N in wheat under elevated O_3 and CO_2 condition.

Optimization of microclimatic conditions for capsicum (*Capsicum annum* L.) under protected cultivation through quantified response to temperature and water regimes

Capsicum is highly susceptible to extreme low and high temperatures as well as frost and requires fairly warm climate. Protected cultivation offers the sustainable solution for offseason cultivation and provides optimum conditions for crop growth. In a study to quantify crop response to temperature shocks at different stages in different water regimes and to optimize the micro-climate conditions for greenhouse grown capsicum, results indicated that the yield per plant decreased in plants exposed to temperatures of 36.8/17.6°C with non-mulch condition but with mulch and yield increased at same temperature. Parthenocarpy was highest in temperature regimes of 29/11°C in open field, while mulching can reduce this. Greenhouse grown plants had higher LAI, TDM, cumulative fruit number and fruit weight (>80%) than the open field grown ones. Mulching can enhance the fruit yield >70% in open or greenhouse condition Based on the simulations using the calibrated and validated capsicum model, the best combination of microclimatic conditions to get the higher capsicum productivity in greenhouse are 700 CO_2 ppm, 350 μ mol $m^{-2}s^{-1}$ PAR, temperatures of 32/13 °C. These combinations increased the fruit yield per plant to about 2.5 times (4.59 kg/plant) than the current best conditions provide in the greenhouse, where the average fruit yield realized is 1.7 kg/plant.

Combined effect of drought and heat stress on quinoa in marginal environments

Climate change poses a significant threat to crop production and food security, particularly in marginal environments characterized by drought, heat, and various challenges such as rapid population growth and limited resources. Quinoa (*Chenopodium quinoa*) is emerging as a promising alternative crop that can adapt to these harsh conditions, offering a solution for climate change adaptation. However, quinoa plants often face simultaneous exposure to multiple abiotic stresses, including water stress and heat stress, which can severely impact their growth, physiology, and productivity. To address these challenges, a pot experiment was conducted with four treatments: Control (normal conditions), drought (moisture deficit), heat (high temperature), and heat + drought, each replicated eight times. These stresses were applied at different growth stages (vegetative, flowering, and grain-filling) to assess their impact on quinoa. The results revealed that the combined stress of drought and heat had a more detrimental effect on quinoa compared to individual stresses, with the flowering and grain-filling stages being the most sensitive. These findings provide valuable insights for researchers and farmers, highlighting the need to optimize crop production techniques for quinoa in marginal environments. Quinoa's resilience to climate-related stresses makes it a promising candidate for sustainable agriculture and food security in the face of ongoing climate change.

Elevated carbon dioxide responsiveness of soybean genotypes differing in tolerance to soil moisture deficit conditions

The current experiment was conducted in the greenhouse and Walk-in-plant growth chamber at ICAR-National Abiotic Stress Management Institute, Baramati with two treatments of well-watered (35-37% soil moisture) and soil moisture deficit condition (15-17% soil moisture) after 7 days of water withholding at the flowering (R1) stage for drought stress and two treatments of Ambient carbon dioxide (400 ppm) and Elevated carbon dioxide (600 ppm) at the flowering (R1) stage. Soybean was significantly negatively affected by drought stress morphologically, physiologically, and biochemically and the effect varied with genotypes. EC 389399, AGS 205, MACS 1028, and PS 1024 showed higher RWC, cooler canopies, higher Photosystem II efficiency, and higher canopy greenness compared to check varieties both under irrigated and drought stress. Photosynthetic pigments were not significantly affected by elevated carbon dioxide, AGS 205, and EC389399 only showed a significant increase with 2.49 and 2.37 mg/g-FW of total chlorophyll content under elevated carbon dioxide. The number of pods per plant and seed yield (g/plant) were significantly affected by elevated carbon dioxide and did not significantly affect the number of seeds per pod and Hundred seed weight (g). AGS 205 and EC389399 showed a higher number of pods per plant (23 and 22.7) and seed yield (10.02 and 10.11 g/plant.

Effect of rice straw biochar application to rainfed paddy soil on net ecosystem carbon balance and global warming potential

A field experiment was conducted with five treatments and four replications in randomized block design. The treatments were T1 (Soil application of Biochar@5t/ha with recommended dose of NPK 80:40:40); T2 (Soil application of Biochar@10t/ha with recommended dose of NPK 80:40:40); T3 (Farmers practice of NPK dose 40:30:0); T4 (recommended dose of NPK 80:40:40) and T5 (Control i.e., no application of NPK and Biochar). The result showed significant impact of biochar on GHG emission, soil physic-chemical properties and NECB ($p<0.05$). The cumulative N2O emission ranged from 3.99±0.18 kg ha-1 in T4 to 1.15±0.06 kg ha-1 in the control treatment (T5). Biochar applied treatments showed 33% (T1) and 46% (T2) lower emission compared to the recommended practice (T4) as well as farmers' practice (6.7-24.7%). The methane emission was found slightly lower (7.5-8.8%) in biochar-applied treatments (T1 and T2) compared to recommended practice (T4), however the difference was insignificant. The addition of biochar reduces global warming potential (GWP) by about 33.7% in T2 and 25.5% in T1 compared to T4 treatment. The NECB of T1 and T2 was 275.6% and 541.8% respectively higher than T4. This study revealed that the use of paddy straw asbiochar can reduce overall GWP and can enhancethe NECB of the rainfed paddy ecosystem in the acidic soil of Jharkhand.

Interactive effect of elevated carbon dioxide and temperature on greenhouse gas (GHG) emission in rice and its simulation

A study was conducted for two consecutive years during the *kharif* (July to October) season of 2019 and 2020 inside the Open Top Chamber (OTC) at the Genetic-H field of ICAR-Indian Agriculture Research Institute (IARI), New Delhi. Rice seedlings of four varieties namely Pusa Basmati 1509, Nagina 22, Pusa 44, IR 64 Drt 1 were transplanted inside the OTCs. Two levels of CO_2 viz. ambient (410ppm) and elevated (550 ± 25ppm) as well as two temperature levels *i.e.,* ambient temperature and elevated temperature (+ 2.5 to +3.1 °C) were maintained inside the OTCs. Reduction in grain yield with 3°C temperature rise ranged from 8.4 % to 12.8 % in different rice varieties. In elevated CO_2 plus high temperature treatment, reduction in grain yield ranged from 4.7 % to 8.2 %. Hence, elevated CO_2 concentration of 550 ppm was able to reduce the negative effects of high temperature in rice. In Nagina 22, increased temperature had less harmful effect. Elevated temperature increased the spikelet sterility in all rice varieties. The Infocrop-Rice model was able to satisfactorily simulate crop phenology, leaf area, total dry matter, grain yield, CH_4 and N_2O emission in rice crop both under ambient and elevated CO_2 plus high temperature condition. Simulated results suggest, yield will decrease while CH_4 emission would increase under elevated CO_2 and high temperature condition and N_2O emission would slightly decrease in north-western IGP.

Amelioration of ozone stress in chickpeas through nutrient and microbial intervention

A pot experiment was conducted for two years (2020-2021) under ambient and elevated level of ozone in FAOE (Free air ozone enrichment) to study the interactive effect of nutrient and PGPR (Plant Growth Promoting Rhizobacteria) on growth and yield of chickpea. Chickpea variety *Pusa 3043* crop grown with PGPR treated and untreated seed and three fertilizer dose (100% urea N, 75% urea N and 50% urea N) under ambient and elevated O_3 was exposed to eight different treatment combinations during October to March month of 2020 and 2021. Significant decrease of crop growth and biochemical parameters was observed in chickpea grown under elevated O_3. Significant decline in photosynthetic rate (6.4%) and (5.6%) in 1st and 2nd year respectively and it increased by 22.8% under nutrient and O_3 interaction in the presence of PGPR treated seed treatment. The No. of nodules ranged between 82 to 155 in the different treatments. The presence of PGPR along with nutrients increased the No. of nodules by 35% under elevated ozone condition. Significant changes in ascorbic acid (16.2%) and melanoldialdehyde (MDA) content (21%) was observed under EO_3 as compared to ambient treatment. A combination of both PGPR outperformed the individual PGPR, showing a 19% yield increase over RDF. This proves the potential of seed treatment with PGPR (RPAN8 and An-Rh) in ameliorating tropospheric ozone induced stress in chickpea.

Theme 2: Environmental Pollution and Waste Management

Effect of organically amended Linz-Donawitz slag on wheat (T*riticum aestivum* l.) crop growth, yield and grain quality

A pot experiment was conducted to study the effect of vermicompost and biochar-amended LD slag on soil properties, wheat crop growth, yield, and grain quality. A significantly higher grain yield was observed in T7 (540.1g/m2), which is 26.63% higher than in T10. While highest straw yield was observed in T7 (642.14g/m2), which is 22.2% higher than in T10. The available nutrients, physiological, and yield attributes were positively correlated with grain and straw yield. T7 showed higher N% and crude protein % in grain. The nutritional composition order was Mg>Ca>Mn>Fe>Zn>Cu in grain. The heavy metals Cd, As and V were not detected in the grain. The heavy metal in the grain was found in the order of Sr>Ni>Cr>Pb>Co. The Cr in grain was significantly higher in T9 over the control. However, all the heavy metals were below the standard permissible limits. This study indicated that the biochar and vermicompost amended LD slag gave better yield and grain quality than the LD slag alone. This study also suggests that the bio-amended LD slag can be used for sustainable agriculture.

Production and evaluation of biofuel briquettes made from rice straw by using suitable binding material

A briquette is a compacted block of combustible biomass material such as coal dust, that is used as kindling and fuel for a fire. The objective of this research is to investigate to produce low cost biofuel briquettes from rice straw using suitable binder in different ratios. To characterize rice straw-based biofuel briquettes produced by mechanical press method. Under this research thirty different samples had been taken in the different combinations for rice straw and binding material under the variation of particle size, binding material concentration and type. This study concluded that briquettes produced from rice straw of particle size (PS) 2 mm bonded by 30% paper pulp and rice straw of PS-5 mm bonded by 30% cow dung + paper pulp mixture have higher calorific value of (4253 kcal/kg) , which was followed by treatments rice straw of PS-1mm bonded by 20% cow dung (4232 kcal/kg) > RS of PS - 1mm bonded by 20% CD > RS of PS- 5mm bonded by 30% PW (4210 kcal/kg) > RS of PS- 5mm bonded by 10% PW (4199 kcal/kg), which are quite higher than commercially available cow dung briquettes (3456 kcal/kg). They are also significantly more environmentally friendly than traditional firewood. Briquettes burn more effectively and cleanly than firewood because they are more energy dense and often drier.

Impact of plant and microbe derived biostimulants' formulation on chickpea (*Cicer arietinum*) under water stress

This study delves into the development and assessment of germination potential and physiological processes in chickpea plants stimulated by a dual approach of plant and microbial bio stimulation—Aloe vera leaf extract and *Trichoderma asperellum*. Among treatments, *Trichoderma asperellum* exhibited the most positive influence on various growth parameters. *T. asperellum* treated plants displayed enhanced gas exchange parameters—stomatal conductance (59% & 71%), transpiration rate (29% & 48%), and intercellular CO2 concentration—coupled with increased photosynthesis rate (24.72% & 33%) and water use efficiency (21.6% & 34.9%) in the combination (*T. asperellum* + AvLE) treatment under irrigated and rainfed conditions. Remarkably, *T. asperellum* strains also exerted a positive influence on yield attributes. Increased numbers of branches per plant (5), pods per plant (13% & 26%), higher test weight, and enhanced seed yield (39% & 47%) were prominent outcomes of *T. asperellum* treatment and combination (*T. asperellum* + AvLE) treatment yielded higher Harvest Index (38% and 37%) in irrigated and rainfed conditions. Additionally, pest infestation and disease occurrence were notably lower in chickpea plants treated with biostimulants compared to untreated controls. As such, the observed results indicate that seed priming using plant and microbe-derived biostimulants, either individually or in tandem, holds promise for augmenting yield under water stress conditions.

Metal oxide nanoparticle production from agricultural byproducts and their application in removal of arsenic contaminated water

This study investigated the synthesis of ZnO and CuO nanoparticles from the agricultural by products such as maize husks and banana peels and further characterized using FT-IR, UV-Visible Spectroscopy, Zeta (ζ) Potential, XRD, SEM, TEM techniques etc, to evaluate the properties of synthesized nanoparticles. Batch adsorption experiments were performed using these synthesized nano adsorbents by following Box-Behnken Design (BBD) which is a statistical tool of Response Surface Methodology (RSM) to remove Arsenic from spiked water by optimizing parameters such as adsorbent dose, pH, and contact time respectively. From the conducted experiments it was concluded that the ZnO nanoparticles, obtained from banana peel and maize husk extracts, exhibited their highest Arsenic removal efficiencies of 94.7% and 97.7% respectively whereas the CuO nanoparticles derived from banana peel and maize husk extracts shown a maximum removal efficiency of 96.6% and 98.6 % respectively , when subjected to a combination of variables consisting of an adsorbent dosage of 30, a pH level of 6, and a contact time of 60 minutes. Hence The synthesis of metal oxide nanoparticles from agricultural byproducts like banana peel and maize husk not only effectively confronted the issue of Arsenic pollution but also contributed to the valorization of agricultural waste, thus enhancing the Sustainability and utility of these resources.

Pb & Cd responsiveness study of soybean genotypes differing in soil moisture deficit stress tolerance

In the current study, water stress tolerance of 20 soybean genotypes was assessed utilising drought-adaptive and drought tolerance genotypes. Soybean genotypes were assessed for Relative Water Content (RWC), canopy temperature, canopy greenness, and photosystem-II efficiency under well-watered and limited water conditions, along with drought tolerant check varieties JS-7105, JS-9752, and drought sensitive check varieties JS-9560 and NRC-7Through this we found two genotype TGX317-37E and EC-391181 were promising as they outperformed all the other genotypes including check. They showed cooler canopy temperature, higher canopy greenness, more chlorophyll content, lower proline accumulation, higher root and shoot biomass as compared to remaining genotypes. According to the results of the current study, soybean genotypes with lower canopy temperatures, higher PS-II efficiency, higher RWC, higher canopy greenness, higher chlorophyll content, and lower proline accumulation may be regarded as suitable plant types for conditions of water scarcity and lead and cadmium contamination.

Effect of particulate matter associated polycyclic-aromatic hydrocarbons and heavy metals on growth and nutraceutical properties of tomato (*Solanum lycopersicum*)

Atmospheric concentrations of PM10 and associated polycyclic aromatic hydrocarbons (PAHs) heavy metals (HMs) were quantified to study the air pollution load of two distinct location of Delhi viz. (1) Agricultural farms of Indian Agricultural Research Institute (IARI) and (2) Yamuna flood plains (YFP). Tomato crop was grown for studying their response to air pollutant at both sites The heavy metals concentration trend at both location was in the order of Zn > Fe > Pb > Ni > Cd. The concentration of Pb, Ni, and Cd was significantly less at IARI in comparison to YFP. The significant decline in photosynthetic rate (11%, 16%), Stomatal conductance (18%, 20%), and transpiration rate (33%, 37%) in tomato plant recorded at 60 DAT at YFP site compare to IARI in 2020-21 and 2021-22 respectively. The oxidative stress (O-2, H_2O_2, lipid peroxidation) and Production of enzymatic antioxidant (SOD, CAT, Peroxidase) and non-enzymatic (ascorbic acid) antioxidant to counter oxidative stress were was significantly higher at 60 DAT at YFP site compare to IARI. The mineral profile (N, P, K, Ca, Mg, Fe, Zn) of tomato leaf was significantly lower at YFP site. The dietary value (Total antioxidant, vitamin C, lycopene) and mineral profile (P, K, Ca, Mg, Fe, Zn) of tomato inferior at YFP site.

Pollutants source apportionment and suitability of groundwater for agricultural and domestic use in Southwest peri-urban area of Delhi

Assessment of groundwater quality was carried out by collecting 61 groundwater samples in the pre-monsoon and post-monsoon. The pH values indicated that the groundwater is moderately acidic to alkaline (6.6–8.7) in both the seasons. Using irrigation water quality indices such as sodium adsorption ratio (SAR), sodium percentage (Na%), residual sodium carbonate (RSC), kelly's ratio (KR), magnesium hazards (MH), and permeability index (PI) the groundwater found unsuitable for irrigation in both seasons. Batch experiments were conducted using design of experiment software, revealing that the Langmuir isotherm and pseudo-second order reaction best fitted the experimental data. Among all nano-adsorbents, CTS-GO-TiO2 exhibited the highest nitrate removal efficiency (83.54 mg/g) and fluoride removal efficiency (74.10 mg/g) under optimum conditions. Subsequently, the study also explored continuous fixed-bed column experiments using CTS-GO-TiO2 adsorbent, which showed higher removal efficiency for nitrate and fluoride.

Effect of bioaugmented Linz-Donawitz slag on soil physicochemical properties, crop yield and grain quality in rice-wheat cropping system

Laboratory batch scale anaerobic digestion experiments were conducted to prepare bioaugmented LD slag in different combinations of cow-dung (CD) and Biochar (BC). Digested bioaugmented products were applied to crops. A crate experiment was conducted at the Genetic-H farm of the Indian Agricultural Research Institute (IARI), New Delhi, in Kharif and Rabi for two consecutive years (June 2021-April 2023) in the rice-wheat cropping system for assessing crop growth, yield and grain quality. The soil nutrients were influenced by bioaugmentation and were positively correlated with the grain yield. Heavy metals content in soil (Cr and V) was significantly higher in unamended LD slag than bioaugmented LD slag and was not correlated with grain yield. An increase in grain yield of about 25.4% in rice and 26.49% in wheat was calculated in bioaugmented LD slag@2t/ha+ BC@1t/ha compared to 100%RDF. The synergetic effect of bioaugmented cow-dung, LD slag and biochar with 100%RDF over the standalone application for achieving higher yield and stable crop production in the rice-wheat system. The soil under experimentation was found under the low ecological risk index category, indicating that the bioaugmentation didn't pollute the soil. Utilizing bioaugmented LD slag with biochar instead of direct slag could be a sustainable management strategy because the synergetic effect of cow-dung, LD slag and biochar provides more nutrients, increasing crop yield and bioaugmented biochar immobilizes heavy metal uptake in grain and straw.

Theme 3: Ecosystem Services

Impact of elevated ozone, carbon dioxide, and their interaction on pollination ecosystem services in Indian mustard

Tropospheric ozone (O_3) is a phytotoxic air pollutant becoming a global concern and CO_2, a potent GHG escalating due to human activities causing substantial climate change. Thus the study was aimed at quantifying the impacts of elevated O_3 (65±10 ppb) and CO_2 (550±10 ppm) with interaction (O_3*CO_2) on pollination ecosystem services of Indian mustard under free air ozone enrichment (FAOE) and free air carbon dioxide enrichment (FACE). The pistil metabolomics study revealed that the sucrose, sulfur metabolism and amino acids declined in elevated O_3 and CO_2 resulting in reduced pollinators' attraction towards mustard flowers. The colour intensity of flowers also declined in eO_3 which affected the foraging rate of pollinators in elevated O_3, CO_2 and interaction. The total antioxidant capacity of pollen and pistil was high in $eO_3 > eO_3{*}eCO_2 > eCO_2$. The photosynthetic activity and stomatal conductance in mustard declined by about 17% and 32% furthermore seed yield by 28% under elevated O_3 treatments. Contrarily, CO_2 enrichment treatment nullified the O_3 effects on yield by a maximum of 11% and increased the photosynthetic rate in eCO_2 by 12%. Pollination service is a unique ecosystem service and the valuation provides the primary idea to help policymakers to evaluate the monetary loss resulting from the impact caused by future climatic conditions of tropospheric ozone and carbon dioxide enrichment.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Divya Sinha (21639)	M.Sc.	Response of different duration varieties of Indian mustard to climatic risks	Dr. S. Naresh Kumar	ICAR-IARI, New Delhi
2.	Keetrhikumar M (21640)	M.Sc.	Assessing the productivity and plant nutrients in wheat at elevated ozone and carbon dioxide interaction under different nitrogen management"	Dr. Bidisha Chakrabarti	ICAR-IARI, New Delhi
3.	Avinash C (21642)	M.Sc.	Effect of organically amended Linz-Donawitz slag on wheat (*Triticum aestivum* L.) crop growth, yield, and grain quality	Dr. Shiv Prasad	ICAR-IARI, New Delhi
4.	Lokesh Kumar Meena (21643)	M.Sc.	Production and evaluation of biofuel briquettes made from rice straw by using suitable binding material	Dr. Renu Singh	ICAR-IARI, New Delhi

5.	Suchitra Kunduru (21644)	M.Sc.	Impact of plant and microbe Derived biostimulants formulation on chickpea (*Cicer arietinum*) under water stress	Dr. Anita Chaudhary	ICAR-IARI, New Delhi
6.	Shevakula Manasa (21749)	M.Sc.	Optimization of microclimatic conditions for capsicum (*Capsicum annum* L.) under protected cultivation through quantified response to temperature and water regimes	Dr. S. Naresh Kumar	ICAR-IARI, New Delhi
7.	Mutra Bala Krishna Reddy (60102)	M.Sc.	Effect of rice straw biochar application to rainfed paddy soil on net ecosystem carbon balance and global warming potential	Dr. Dipak Kumar Gupta	#ICAR-IARI Jharkhand
8.	Sai Kiran Burji (60103)	M.Sc.	Metal oxide nanoparticle production from agricultural byproducts and their application in removal of arsenic contaminated water	Dr. Anita Chaudhary	#ICAR-IARI Jharkhand
9.	Ashok Kumar Subudhi (70011)	M.Sc.	Combined effect of drought and heat stress on quinoa in marginal environments	Dr. Dinesh Kumar Sharma	**ICAR-NIASM Baramati
10.	Nandimandalam Charishma (70012)	M.Sc.	Elevated carbon dioxide responsiveness of soybean genotypes differing in tolerance to soil moisture deficit conditions	Dr. Ajay K Singh	**ICAR-NIASM Baramati
11.	Prerna Kumari (70013)	M.Sc.	PB & CD responsiveness study of soybean genotypes differing in soil moisture deficit stress tolerance	Dr. Ajay K Singh	**ICAR-NIASM Baramati
12.	Partha Pratim Maity (11246)	Ph. D.	Interactive effect of elevated carbon dioxide and temperature on greenhouse gas (GHG) emission in rice and its simulation	Dr. Bidisha Chakrabarti	ICAR-IARI, New Delhi
13.	Chandra Prakash (11249)	Ph. D.	Effect of particulate matter associated polycyclic-aromatic hydrocarbons and heavy metals on growth and nutraceutical properties of tomato (*Solanum Lycopersicum*)	Dr. Shakeel A. Khan	ICAR-IARI, New Delhi
14.	Sethupathi N (11369)	Ph. D.	Amelioration of ozone stress in chickpea through nutrient and microbial intervention	Dr. Dinesh Kumar Sharma	ICAR-IARI, New Delhi
15.	Divya Pooja B (11490)	Ph. D.	Effect of bioaugmented Linz-Donawitz slag on soil physicochemical properties, crop yield and grain quality in rice-wheat cropping system	Dr. Shiv Prasad	ICAR-IARI, New Delhi
16.	Mamta Bisht (11492)	Ph. D.	Pollutants source apportionment and suitability of groundwater for agricultural and domestic use in Southwest peri-urban area of Delhi	Dr. Manoj Shrivastava	ICAR-IARI, New Delhi
17.	Gayathri J (11494)	Ph. D.	Impact of elevated ozone, carbon dioxide and their interaction on pollination ecosystem services in Indian mustard	Dr. Dinesh Kumar Sharma	ICAR-IARI, New Delhi

#IARI off campus

**Outreach Institute

Microbiology

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Prof. Rajeev Kaushik

The Division of Microbiology focuses on basic, applied and strategic research on microorganisms of agricultural importance. The Division is the national lead centre for advancing knowledge and understanding of the microbial domains for agricultural application which includes utilization of microbial gene- and metabolite pool for plant growth promotion as well as protection, natural resource management and value addition of biomass through microbial means. The mandates of the Division are to undertake research, teaching, and extension in the field of beneficial microorganisms; to serve as the lead centre in the country; to decide national priorities for Agricultural Microbiology. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Microbial Management of Abiotic Stress in Agriculture

Development of rhizobacterial bioformulation for water deficit stress alleviation in mustard and assessing its impact on soil health

Drought stress is one of the major abiotic stresses affecting agriculture and is a significant concern for global food security. Mustard is the second most important oil seed crop in India which is often affected by drought stress, especially in arid and semi-arid regions of its cultivation. Plant growth-promoting bacteria (PGPR) have emerged as an essential tool in sustainable agriculture and have proven to be promising where various biotic and abiotic stresses are concerned. A field experiment was conducted to evaluate the medium-term (three years) application of rhizobacterial inoculants viz., *Bacillus* spp. MRD-17, *Bacillus aryabhattai* NSRSSS-1, and *Bacillus casamancensis* MKS - 6 on soil parameters and growth and productivity of mustard under varied irrigation levels. Plant physiological attributes and yield were enhanced, while catalase activity was reduced in inoculated treatments, especially under rainfed and one-irrigation conditions.Inoculation had a beneficial effect on soil biological properties.There was an increase in soil aggregation in different fractions in MRD-17 and NSRSSS- 1 inoculated treatments.The most promising rhizobacterial strain *Bacillus* sp. MRD–17 was formulated into eighteen different combinations of emulsion-based liquid formulations and shelf life was studied for one year. The combinations T4 (B1) and T18 (B2) were found to be the best bioformulations which maintained the cell count (> 9 cfu/ml) and plant growth-promoting properties of bacteria (IAA, GA, and EPS production; and ACC deaminase activity) at the end of one year of storage and also improved fresh weight and dry weight of the mustard seedlings. Influence of treatment with bioformulations B1 and B2 *Bacillus* sp. MRD – 17) and bioformulation B3 (on mustard, under water deficit stress conditionswere determined in pot house, field, and hydroponic experiments. Under pot house and field experiments (two successive trials), inoculation with rhizobacterial bio formulations improved the plant physiological and biochemical attributes and root system architecture in mustard plants under water deficit stress. Plant and seed nutrient content, growth, and yield were also improved in the inoculated treatments, under stress. The soil biological properties such as dehydrogenase activity, FDAse activity, alkaline phosphatase activity, MBC, and soil organic carbon also improved significantly under field trials. Bioformulation B3 showed the best performance in most parameters. Under the hydroponics experiment the effect of all these three bioformulations on the phytohormone status and expression of drought-responsive genes in mustard seedlings was evaluated. There was an increase in IAA and GA, while reduction in ABA levels in the seedlings in inoculated treatments under osmotic stress. There was upregulation in the expression of drought-responsive genes such as *BjNCED3*, *BjAREB1*, *BjDREB1-2*, *BjNAC14, BjDHN1, BjP5CSB,* and*BjFeSOD* under osmotic stress, while inoculation led to their down-regulation. However, the expression of *BjPIP3* was upregulated in inoculated treatments compared with uninoculated under osmotic stress conditions. Thus, the application of rhizobacteria showed promising potential for improving crop yield in drought-stressed areas.

Microbiome-mediated management of heat stress in wheat (*Triticum aestivum*)

India's wheat (*Triticum aestivum*) production has been declining due to an increase in temperature, where every 1°C rise above average causes a yield reduction of 4.1% to 6.4%. Nowadays, studies on plant microbiomes have gained increased attention and their role in managing stress by modulating enzymatic actions or producing plant growth hormones has been explored. Accordingly, we hypothesized that the construction of small microbial communities (SMCs), based on a combination of culturable and metagenomics approaches would induce tolerance to heat stress in wheat.In this study,the abundance and diversity of wheat seed endophytic bacteria (WSEB) and wheat-associated bacteria (WAB) were investigated from heat^S (heat susceptible, GW322) and heat (heat tolerant, HD3298 and HD3271) varieties by culturable and unculturable approaches. The metagenomic analysis of seed microbiota unveiled the predominance of Proteobacteria. Whereas culturable analysis results evidenced that the diversity was more in the heat^S variety than the heat. Further morphotyping and environment adaptive functions were evaluated based on their tolerance to temperature, salt, drought, and pH, from which the heat isolates were selected.Several plant growths promoting (PGP) functions of the selected isolates were analyzed qualitatively and the results were combined based on the monitor scale for the quantification of IAA,GA,and cytokinin production, N, P, and K solubilizationand siderophore production. Those efficient PGP isolates were identified by 16S rDNA sequencing and found 42 different species in 18 genera.*Bacillus* was found as the most abundant genus of class *Bacilli*, followed by *Gammaproteo bacteria*, *Actinomycetia*, *Alphaproteo bacteria,* and *Betaproteo bacteria*. Then, four different small microbial communities (SMCs) were designed based on function, dominance, and function+dominance phytohormone production by combining the results of culturable and unculturable taxonomic and functional annotation. The SMCs formulated were found to have increased PGP effects over the individual isolates in both the susceptible and tolerant wheat varieties. This was also confirmedby the physiological, biochemical, molecular, biometric, and yield parameters evaluated under controlled (phytotron) conditions with induced heat stress. Also, the SMCs were validated under field conditions by staggered sowing and the results displayed the promising role of SMC treatments in assisting the plants to tolerate heat stress. Hence, this study has comprehensively concluded that the SMCs formulated in this study were highly effective under heat stress conditions for promoting plant growth as well as sustaining production.

Cyanobacteria mediated enhancement of drought stress tolerance in wheat genotypes

In the present study, experiments were conducted to assess the desiccation tolerance of *Anabaena* species and based on physiological parameters and multivariate analysis *A. fertilissima* and *A. variablis* were identified as most tolerant. Ten cyanobacterial strains isolated from the desert areas of Pokhran, Rajasthan, India were identified based on morphological and molecular attributes, and among these isolates, *Nostoc* sp. (SGR3) and *Neowestiellopsis* sp. (SGR8) grew optimally at desiccation level (10% w/v polyethylene glycol). Further, they exhibited high levels of antioxidant activity and plant growth-promoting traits such as nitrogen fixation and ammonia release Therefore, these two strains have been selected for further studies on the management of desiccation stress in wheat. The strains have been grown individually as well as in combination in liquid and soil microcosms and based on the soil chlorophyll content and nitrogenase activity their establishment was confirmed without any antagonism. A pot experiment was conducted to evaluate the role of *Nostoc* sp. (SGR3) and *Neowestiellopsis* sp. (SGR8) in the management of desiccation stress in wheat cultivars. It was observed that due to drought stress (25% FC) growth and several physiological parameters were inhibited. However, inoculation by *Neowestiellopsis* sp. (SGR8) enhanced the growth as well as physiological characteristics in wheat during the tillering and anthesis stages under drought stress conditions. Cyanobacterial inoculation helped the plants to maintain redox status through efficient modulation of antioxidant enzymes. It was also observed that under drought stress cyanobacterial inoculation helped in the maintenance of root system architecture and development of roots. The cyanobacterial inoculation also improved the soil's chemical and biological properties such as available nitrogen, available phosphorous, dehydrogenase activity, and microbial biomass carbon under drought stress. Improvement in the yield parameters was also recorded in wheat plants exposed to drought and cyanobacterial inoculation. Protein profiling through two-dimensional gel electrophoresis and nano-LC-MS/MS showed the differential expression of proteins in wheat related to drought tolerance in response to cyanobacterial inoculation. The overall results show the potential of cyanobacterial inoculation in the effective management of drought stress in wheat.

Exploring seed endophytic bacteria of pearl millet for plant beneficial traits and abiotic stress tolerance

The present investigation aimed at prospecting the seed endophytic bacteria of pearl millet (*Pennisetum glaucum*) for plant-beneficial traits. Seeds of eight Pearl millet cultivars (includingpopular open-pollinated varieties, hybrids, and landraces representing three agro-climatic zones (A1, A, and B) were surfacesterilized and macerate plated on five different media nutrient agar (NA), R2A, trypticase soy agar (TSA) and two pearl millet flour-based media. The highest bacterial population was observed on TSA and NA (copiotrophic media) followed by R2A (oligotrophic media). The highest bacterial population was observed on saprotrophic media. MPMH 21 showed the highest population followed by MBC 2, PILI, PC 612, Pusa 1201, HHB 299, MOONCH, and PC 701. Eighty-six bacterial colonies were purified and characterized for *in vitro* PGP traits, biocontrol potential, osmotic stress tolerance, and extracellular hydrolytic enzymes.The endophytic bacteria exhibited multiple PGP traits with 95%, 43%, 90%, 19%, 34%, 33%, and 65% isolates showing IAA, siderophores, ammonia, P, Zn, K solubilization, and antifungal activity respectively.The isolates could produce esterase (42%) and pectinase (42%) followed by chitinase (34%), amylase (31%), lipase (30%), protease (27%), and cellulase (26%). These features indicate the seed as a hub of agriculturally and industrially important bacteria.Based on *in vitro*traits, 38 endophytic bacterial isolates representing eight pearl millet varieties when identified based on 16S rRNA sequence represented 13 bacterial genera including *Acinetobacter, Atlantibacter, Bacillus, Brucella, Pantoea, Pseudomonas, Staphylococcus, Stenotrophomonas, Exiguobacterium, Kosakonia, Enterobacter, Achromobecter* and *Cronobacter*, indicating structural diversity. *Acinetobacter* was observed in six cultivars indicating its close association with the crop.

Evaluating potential diazotrophic inoculants for boosting the productivity of DSR and transplanted rice under acidic soil conditions

The present investigation was aimed to develop a unique diazotrophic consortium inoculant usingnativebacterialisolates that wouldbebetteradapted to rice cultivation in acidic soils of the Jharkhand region and to evaluate their influence on soil health and rice growth under two planting methods *i.e*., DSR and Transplanted rice. Diazotrophic consortium (F1) was formulated with native bacterial isolates (B1 *Brucella oryzae*, B2 *Brucella ciceri*, B3 *Pseudomonas nitroreducens*) using carriers vermiculite + paddy straw compost (C1) and charcoal (C2). In a pot experiment, it was observed that a C1 carrier-based formulation with 75% N significantly improved IAA levels, nitrate reductase, and glutamine synthetase activities.Superior outcomes in tillering and panicle initiation stages were observed in both Abhishek and IR 64 Drt 1 varieties.Field trials using C1 carriers in DSR and TPR methods showed consistent enhancement in plant and soil parameters.DSR exhibited higher plant enzyme activities, while the Abhishek variety demonstrated elevated IAA levels during tillering.At harvesting, the inoculant outperformed RDF and 75% N+100% PK, resulting in improved nutrient availability and 25% N savings. The study provides useful information regarding the performance of microbial consortia in 2 regional varieties under both DSR and TPR modes of cultivation grown under acidic soils, towards enhanced crop productivity and soil health.

Theme 2: Plant-Microbe Interaction for Crop Growth Promotion

Rice microbiome associated with functional traits of carbon and nitrogen cycling

Soil microbiomes regulate nutrient recycling, crop growth, and ecosystem services in rice fields. The global significance of rice production for food security makes it vital to understand the factors that determine the assembly and functions of the microbiome in the rice rhizosphere. Metatranscriptomics analysis revealed high similarities in the rhizosphere-active microbiomes of neutral and alkaline soils, but acidic soil was markedly distinct. Proteobacteria (18-30%), Actinobacteria (6-10%), Firmicutes (0.4-4.5%), Acidobacteria (1-2.5%), Chloroflexi (0.5-2.5%), and Planctomycetes (0.4-1.8%) were the predominant phyla in the rice rhizosphere. Photoautotrophic organisms were more abundant in the rhizosphere of neutral and alkaline soils than in acidic soil. The rice rhizosphere is a vital methane source and sink, with the prevalence of acetoclastic over hydrogenotrophic methanogens and aerobic and anaerobic methane oxidizers. Nitrogen-fixing microorganisms were more active in the rhizosphere of acidic soil. The transcripts of microbial taxa mediating nitrification, denitrification, anammox, and comammox were more abundant in neutral and alkaline soils. The impact of stoichiometry imbalances on rice microbiomes was explored by altering the soil C:N ratio by two- and five-fold by adding glucose, rice straw, and urea.This study highlighted the potential of straw incorporation to improve the microbiome assembly for optimal functioning of C and N cycling in rice rhizosphere, while excess urea application might enhance N-losses from the soil. Further, the effects of urease and nitrification inhibitors with N-fertilizers on the composition and functions of the rice rhizosphere microbiome were investigated using a split-root experiment. The results indicated that the application of urease and nitrification inhibitors partially alleviated the adverse effects of fertilization by reducing the abundance of genes related to nitrification, denitrification, and anammox while improving the copies of *nifH* and the genes associated with DNRA.Long-term application of inorganic fertilizers and organic manures significantly influenced the diversity of soil microbiome in paddy rice soils.Significant deliverables of this investigation are a root-exudates equivalent (REE) medium and a synthetic microbial consortium to establish a healthy microbiome in the rice roots for sustainable crop production. This study expanded our understanding of active microbial diversity and nutrient cycling processes in the rice rhizosphere, with implications for improving soil fertility and ecosystem sustainability.

Genome-based analyses of rice-actinobacteria interactions

Microbial inoculants produce plant hormones, expand and elongate the root system, elicit induced or acquired systemic resistance, and produce lytic enzyme and antibiotics and 1-amino cyclopropane-1-carboxylate-deaminase

(ACC-deaminase) in the rhizosphere. This study demonstrated the ability of indigenous actinobacterial strains isolated from rice rhizosphere (FT1, FTSA2, FB2, FH7) and endosphere (EB6) regions to promote plant growth. In addition, the molecular mechanisms involved in plant-microbe beneficial effects were investigated using a transcriptional study of a small set of key genes in biosynthesis, signaling, and metabolism of phytohormone pathways. Using molecular (16S rRNA) and chemotaxonomical (FAME) methods, all of the isolates were determined to be members of the genus Streptomyces, with the predominance of iso/anteiso branching C15-C16 long chain fatty acids. This was followed by *in vitro* screening for various plant growth-promoting (PGP) and biocontrol properties. All isolates tested positive for indole acetic acid synthesis, and siderophores, and were antagonistic to *Rhizoctonia solani* AG1-1A, the causal agent of rice sheath blight. The phenotypic characterization of all isolates by BIOLOG Gen III- Microplate revealed their capacity to utilize diverse carbon and nitrogen sources and to endure a variety of pH, osmotic, and temperature challenges. In pot experiment investigations, Streptomyces sp. isolates FTSA2 considerably increased rice plant shoots dry mass, leaf nitrogen, and total biomass, while isolates FB2 and FT1 had higher root dry matter, with FB2 considerably improving the majority of root morphological features.Both FTSA2 and FB2 were able to increase the N and C assimilatory capacities of the roots and shoots, respectively.Whole-genome analysis of Streptomyces sp. FB2 and Streptomyces sp. FT1 showed that these consisted of single circular chromosomes of 7.7 Mb and 6.9 Mb with 71.9% and 73.4% GC content, respectively.Comparative genomic analyses of the genomes under study and selected reference genomes confirmed that isolates FB2 and FT1 belonged to the *Streptomyces nigra* and *Streptomyces albidoflavus* species, respectively. Pan-core genome analysis indicated the presence of 88326 genes in total in the pan-genome of the Streptomyces strains, comprising 682 genes in the core genome, 5733 genes on average in the accessory genome, and 81911 unique genes.Genome mining of strains FB2 and FT1 revealed the presence of genes related to stress adaptations, biocontrol mechanisms, metabolism of carbohydrates, amino acids and secondary metabolites,ethylene, nitrogen, phosphate metabolism, and production of indole-3-acetic acid, and siderophores. AntiSMASH and BAGEL analyses revealed the presence of 17–20 biosynthetic gene clusters (BGCs), including terpenes, PKSs, NRPSs, and RiPPs, which were further verified by BiGSCAPE analysis. RT-PCR analysis corroborated these findings that showed differential gene expression of auxin (OsAUX1, OsIAA1, OsYUCCA1, OsYUCCA3), gibberellin (OsGID1, OsGA20-ox1), and cytokinin (OsIPT3, OsIPT5) pathways in response to specific actinobacterial treatments. However, these *Streptomyces* strains need to be assessed in field experiments either as individual or consortia strains for their potential as bioinoculants.

Evaluation of bio-control potential of Actinobacteria against pathogens causing major diseases in rice

Rice yield is often limited by biotic stresses mainly caused by fungal diseases such as blast (*Magnoparthe oryzae or Pyricularia oryzae*), sheath blight (*Rhizoctonia solani*), and leaf blight (*Xanthomonas oryzae* pv.*oryzae*). In this present study, 19 actinobacterial isolates from the rice-rhizosphere showed the highest fungal growth inhibition of *M. oryzae* such as RSF Tap 13 (58.75 ± 0.72 %), RSF Tap 19 (56.25 ± 2.17 %) and $V_0$7 (52.41 ± 1.40 %) and from the rice-endorhizosphere actinobacterial isolates such as Ha1b (65.00 ± 2.89 %) and Tap 1 (57.13 ± 0.21 %). Out of 19 actinobacterial isolates, two isolates Ha11 and Humic 11b (77.78 ± 0.00 %), and two endorhizosphere isolates, Tap 2V_0(77.78 ± 0.00 %) and Tap 1 (62.22 ± 2.57 %) were found to show superior antifungal activity against *R. solani*. Similarly, there were several potential actinobacterial isolates found with significantly the highest antifungal activity against *Fusarium* sp. and *S. rolfsii.* The actinobacterial isolates showed low to high antibacterial activity in terms of zone of Xoo growth inhibition, of which 6 rice-rhizosphere isolates (Met24, Ha2, Tap 10, RSF Tap4, RSF Met 5 and RSF Tap10) and two of the rice-endorhizosphere isolates, M 9

(25 ± 0.00 mm), and Tap 1 (22.5 ± 1.44 mm) were found with the highest zone of growth inhibition for Xoo. All eight potential actinobacterial isolates belonged to the different species of the genus *Streptomyces*. In the *in-planta* experiments conducted for evaluation against blast disease pathogen (*M. oryzae*), sheath blight disease pathogen (*R. solani*), and bacterial leaf blight disease pathogen (*X. oryzae*pv. *oryzae*) the highest efficacy was shown by the isolate Tap 1. The significant biocontrol activity showed by the selected actinobacterial isolates against rice-fungal and bacterial pathogens was attributed to one or more biocontrol mechanisms including enhanced plant immunity or resistance as well as the plant growth promotion capabilities. Significantly the endorhizosphere isolates showed the highest disease control efficacy against all three diseases of rice such as rice blast, rice sheath blight, and rice bacterial leaf blight.

Studies on AMF-ROC root inoculum-based formulations for improved infectivity and effectiveness

The research laid the foundation to establish and mass multiply the AM fungi in *vitro* encompassing the following achievements**:**a notable increment of root proliferation and growth was attained in M-medium; significant amount of AMF root inoculum has been demonstrated by carbon compounds viz., sucrose: glucose (10:1 g/L); co-application of phytohormones and secondary metabolites (IAA – 2ppm + quercetin – 2.5µM + flavonoids – 5ppm + raffinose – 50mM) aggravated the AMF inoculum production further.

Exploring the potential of P-solubilizing spore-associated bacteria with AM fungi toward growth and P uptake in wheat

Arbuscular mycorrhizal fungi (AM fungi) enhance crop growth by increasing N and P uptake, and disease resistance, but the impact of AM fungi when enriched with its mycorrhizal helper bacteria on P uptake and accumulation in crops is unclear. This study investigated the inoculation of wheat with PUSA Mycorrhiza enriched with MHB isolated from the spore wall of *Rhizophagus irregularis*. Approximately 30 spore-associated bacterial isolates were selected & screened to study their PGP traits from the AM fungi species. All were screened in vitro to study their PGP traits, especially their phosphate solubilization& related traits. The range of Phosphate solubilization in this group of bacteria was 271.18 -352.9 µg mL-1 in both qualitative and quantitative aspects. In vitro assessment of mycorrhization by MHB was studied by spore germination and hyphal growth illustrated their role, both as mycorrhization helper bacteria and mycorrhiza helper bacteria. Based on morphological and 16S rRNA gene sequences, 3 best isolates showing PGPR traits i.e., G1, NSS22, and OSS8S were identified as *Pseudomonas aeruginosa*, *Bacillus licheniformis,*and *Bacillus hynesii*, respectively. In the wheat pot trial, plant growth parameters like shoot length, and shoot dry biomass improved upon in treatments (T4- AM fungi enriched with MHB) and showed the highest dry biomass, IAA production, and chlorophyll content among the inoculated treatments. A significant increase in biochemical activities like Dehydrogenase, ALP, ACP activity, MBC, & glomalin content was observed in comparison to RDF (T2) indicating a synergistic effect of Bacterial inoculation with AM fungi. Root traits showed a significant effect of co-inoculation influencing root architecture. Phosphorus content was considerably enhanced by inoculation in shoots, roots, and grains of wheat. Hence, the dual inoculation of AM fungi with P solubilizing mycorrhiza helper bacteria isolated from AM fungi spores can be advocated as an inoculation mode, to improve P nutrition, plant growth, and vigor.

Influence of *Bacillus cabrialesii* on plant growth and wilt disease control of chickpea challenged with or without *Fusarium oxysporum* f.sp. *ciceris.*

This study presents a comprehensive report on the evaluation of plant growth-promoting and biocontrol traits of strains IS-10 and BATS-13 of *Bacillus cabrales* and the application of strain IS-10 on growth, protection, and yield of two varieties of chickpea pre-challenged with or without *F. oxysporum* f.sp. *ciceris*. The strains possess many plant-growth-promoting attributes such as the production of IAA and hydrolytic enzymes, solubilization of phosphate and zinc, and siderophore production. In this context,biosurfactant analysis revealed the presence of fengyicin and surfactin. In the pot experiment, application of *B. cabrialesii* IS-10 as seed bacterization in sterile soil amended with vermicompost (0.2 %) and gum acacia (0.02 %) in absence of pathogen enhanced mean plant height by 13.47 %, straw yield by 39.17 % and grain yield by 46.8 % over absolute control in Vaibhav variety while in JG-62 variety, plant height increased non- significantly but straw yield and grain yield increased significantly by 39.47 % and 50.32 %, respectively, over absolute control. The above same treatment in the presence of pathogen, seed bacterization by *B. cabrialesii*IS-10 in sterile soil amended with vermicompost (0.2 %) and gum acacia (0.02 %) reduced disease by 20.80 % in Vaibhav and 26.85 % in JG-62 over pathogencontrol and consequently enhanced straw yield and grain yield to 53.92 % and 57.14 %, respectively, over in Vaibhav and 36.6 % and 50.81 %, respectively, over pathogen in JG-62. Such enhancement in plant growth promotion through disease control might be attributed to direct antagonism and enhanced levels of SOD, catalase, peroxidase, and phenylalanine ammonia-lyase in the inoculated plant (leaves & stem) with IS-10 in the presence of pathogen. Overall, *B. cabrialesii*IS-10 improved plant growth and controlled disease induced by *F. oxysporum*f.sp. *ciceris*in chickpeas by a combination of PGP and biocontrol functions operated by bacteria.

Prospecting cowpea germplasm for their innate nitrogen fixation potential and nodulating rhizobial diversity

Cowpea (*Vigna unguiculata)* is a multi-purpose legume, that contains high-quality protein for human consumption, and livestock fodder, and also enriches the soil by re-cycling nutrients and Nitrogen fixation in association with nodulating bacteria. The coverage of this crop is considerable throughout the world and very important in various countries *viz*., Nigeria, Ethiopia, Kenya, Sub-Sahara region, *etc*. A study of the germplasm of crops with respect to the microbial association (mainly endophytes) may give a clue about the significance of symbiosis towards production, and changes of taxa concerning various genotypes. In this study, we have collected 210 cowpea genotypes distributed all over the world, *i.e*., from America (19),Australia (5), Brazil and Malaysia (2), Canada, China, Nepal, Sri Lanka, and Trinidad and Tobago Island (1),Europe (17),India (70), Philippines (27), West Africa (53) and 10 from unknown locations. From those samples, the nitrogen-fixing potential of nodulating genotypes estimated by ARA indicated that the activity ranged from 18.77 to 4652.24 µmole of ethylene/g root fresh wt/hr from European genotypes followed by West Africa (2.22 to 3482.56 µmole) and Indian genotypes were having 9 to 2082.48 µmole of ethylene/g root fresh wt/hr ARA activity. A total of 153 rhizobial isolates were obtained collectively and presumptive tests such as growth on YEMA with BTB, lactose agar, and glucose peptone agar were done for preliminary confirmation of Rhizobia. Further, the confirmatory test was done by checking their nodulation potential, and by carrying out a pot experiment in the National Phytotron Facility, IARI, New Delhi. Out of 153 isolates, 97 have been re-nodulated and found to be symbiotically effective. Plant growth-promoting traits such as nutrient solubilization, production of phytohormone and biocontrol compounds were estimated, and it found that 143 rhizobial isolates were P solubilizers, 6 were K solubilizers, 117 were Zn solubilizers and 141 were producing siderophore. Whereas, production of IAA ranged from 2.24 to 21.53 ppm, while in the case of biocontrol compounds, 33 isolates were positive for ammonia and 43 isolates were positive for HCN production qualitatively, out of which the isolates named 24, 92B, 71A, and 32 and 19 were showing highest HCN production. Further, molecular analysis by BOX-PCR technique was utilized to delete the duplicity of strains, from which 36 rhizobial isolates were shortlisted out of 97 and their *nif*H and *nod*C genes were also amplified. Further, by 16S rRNA gene amplification, the isolates were identified as belonging to *Rhizobium azibense, R. redzepovicii, R.*

qilianshanense, R. indicum , B. radyrhizobiumbrasilens, B. japonicu, B. vigna, B. australiens, and *B. elkanii* as well as *Mycoplanaramosa*.

Axonomic and functional annotation of seed endophytes from parents-hybrid complex of *Zea mays*

Maize (Zea mays L.; 2n = 20) is an important cereal crop of the world, belonging to the tribe Maydeae of the grass family Poaceae. Microbial endophytes help their hosts by assisting in the acquisition of nutrients and growth regulators as well as the control of pathogens. Seed endophytes are of particular interest as they are transmitted from generation to generation via vertical transmission. In this study, a model system of a maize hybrid complex was taken to study the endophytes present in it. Endophytic bacterial load in seeds varied from 0.03x104 to7.75x104 cfu g-1 in PML-93 (F),0.01x104 to 5.04x104 cfu g-1in PML-105 (M), while it varied from 0.32×104 to 3.33×104cfu g-1 of the sample in hybrid PJHM-1 (H).Morphologically diverse 168 putative bacterial endophytic isolates (35 from seed,110 from seedling, and 23 from cob) were obtained. After testing their growth at variable environmental conditions like temperature, moisture, pH, and salt,all isolates were screened functionally for plant growth-promoting traits. Of a totalof 168 isolates36% wasP solubilizing, K(39%), and Zn (42%) solubilizing.Isolates produced hormone IAA ranging up to to77.4 µg/mland fixed N_2up to 148.55µmole ml /hr.Colony BOX PCR and monitor scalewere used to remove the duplicity of isolates at the seedling stage. Finally, 86 isolates (35 from seed, 28 from seedling,23 from cob)were processed for 16SrRNA-based identification.In maize seeds, 84% are of the *Bacillus* genus, followed by *Priestia* (9%) and by Pseudoarthrobacter *and Paraburkholderia* (3.5% each). But at the species level, *Bacillus haynesii was* most common. In seedling stage,the most common bacterial genera were *Bacillus* (50%), followed by *Stenotrophomonas* (17%), *Acinetobacter* (8%), *Klebsiella* (8%),*Kosakonia* (3%), *Pantoea* (3%), *Pseudomonas* (3%), *Paenibacillus* (3%) and *Enterobacter* (3%). At the species level, *Bacillus australimaris* and *Stenotrophomonas maltophilia* were common. In the cob stage, the most common bacterial generawere*Pseudomonas* (34%), *Serratia* (30%), *Bacillus* (21%), *Acinetobacter* (4.3%), *Stenotrophomonas* (4.3%), and *Enterobacter* (4.3%). Butat species level *Bacillus haynesii, Serratianemato diphilia, and Pseudomonas juntendi* were common among all genotypes. But, notably, *Bacillus haynesii was* common in all three stages. *In planta* evaluation of selected isolates, demonstrated their beneficial impact on plant growth and development.

Theme 3: Bioprospecting Microorganisms for Value-added Products and Bioremediation

Standardizing process for xylitol production from corn cobs using *Candida tropicalis*

Crop residues are valuable sources of lignocellulosic biomass that will continue to be available as long as food production for humanity continues. Maize, a cereal crop that serves as a staple food in many parts of the world and is cultivated in numerous countries, holds great importance. The surge in maize production generates substantial amounts of corn cob waste, which can be used as feedstock for the production of various valuable products like xylitol, a compound with a rapidly growing market, and ethanol. In the current study, hemicellulose was extracted from the corn cobs to obtain xylose by subjecting them to acid hydrolysis with 1% H2SO4. Non-Non-conventional yeast strain *Candida tropicalis* Y6 isolated from rotten vegetables was tested for growth and xylose utilization potential on an acid prehydrolysate medium supplemented with mineral salts. *Candida tropicalis* Y6 exhibited high growth and 70% sugar utilization. In a synthetic medium with 10% mixed sugars (Glucose and xylitol), it produced 45 g/l ethanol with efficiency >90% at 48 h, and Xylitol 6.7g/l was also formed. On synthetic medium with xylose as the sole C source, it achieved a maximum conversion efficiency (53%) of xylose to xylitol at 24 hours, with a production of 6.71 g/L of xylitol, and ethanol was also formed. When C. tropicalis Y6 was cultured on corn cob hydrolysate, it produced 0.41 g/L of xylitol along with 0.74 g/L of ethanol under standard conditions. However, its growth and xylose conversion were severely affected in acid hydrolysates possibly due to the presence of inhibitors. The noticeable feature was the high level of ethanol produced in acid prehydrolysate fermentation indicating the expression levels of XR and XDH enzymes under conditions of study.

Exploring diverse nutritional modes to enhance carotenoid production in selected cyanobacteria

Different modes of nutrition significantly affected growth and carotenoid production in both cyanobacterial strains.Mixotrophic mode of nutrition improved the growth and carotenoid production under salinity stress in both the cyanobacterial strains.Among different variables studied, light, light duration, and salinity showed a significant effect on the growth and carotenoid production of Spirulina sp., and further interaction of light and light duration was also found significant.Both enzymatic and non-enzymatic antioxidant level was found to be increased significantly under salinity stress in mixotrophic mode.There was a 5- and 3.43-fold increase in the carotenoid production for *Nostoc* sp. and *Spirulina* sp. respectively.

List of contributing students and Chairpersons of their advisory committee

S. No	Name of the student & Roll No.	MSc/ PhD	Title of the thesis	Chairperson	Institute
1.	Karthika K (21669)	M.Sc.	Studies on AMF-ROC root inoculum-based formulations for improved infectivity and effectiveness	Dr. S.N. Bhowmik	ICAR-IARI, New Delhi
2.	Sangram Garai (21670)	M.Sc.	Standardizing process for xylitol production from corn cobs using *Candida tropicalis*	Ms. Anju Arora	ICAR-IARI, New Delhi
3.	Yamini Yadav (21668)	M.Sc.	Exploring diverse nutritional modes to enhance carotenoid production in selected cyanobacteria	Dr. Pranita Jaiswal	ICAR-IARI, New Delhi
4.	Barnana Maitra (21667)	M.Sc.	Exploring seed endophytic bacteria of Pearl millet for plant beneficial traits and abiotic stress tolerance	Dr. Minakshi Grover	ICAR-IARI, New Delhi
5.	Konderu Niteesh Varma (21750)	M.Sc.	Evaluation of bio-control potential of actinobacteria against pathogens causing major diseases in rice	Dr. V. Govindasamy	ICAR-IARI, New Delhi
6.	Pratibha Brarik (21671)	M.Sc.	Exploring the potential of P-solubilizing spore-associated bacteria with AM fungi towards growth and P uptake in wheat	Dr. Seema Sangwan	ICAR-IARI, New Delhi
7.	Sonam Yangchan (21672)	M.Sc.	Prospecting cowpea germplasm for their innate nitrogen fixation potential and nodulating rhizobial diversity	Dr. Archna Suman	ICAR-IARI, New Delhi
8.	Raghavendra JS (60110)	M.Sc.	Axonomic and functional annotation of seed endophytes from parents-hybrid complex of *zea mays*	Dr. Archna Suman	#ICAR-IARI Jharkhand
9.	Bavana Nallapareddy (60111)	M.Sc.	Evaluating potential diazotrophic inoculants for boosting the productivity of DSR and transplanted rice under acidic soil conditions	Dr. Himani Priya	#ICAR-IARI Jharkhand
10.	Prajwal S.K. (80019)	M.Sc.	Influence of *Bacillus cabrialesii* on plant growth and wilt disease control of chickpea challenged with or without *Fusarium oxysporum*f.sp. *ciceris.*	Dr. Sushil Kumar	**ICAR-NIBSM Raipur

11.	Dhivya Priya T. (11065)	Ph.D.	Genome-based analyses of rice-actinobacteria interactions	Dr. Sangeeta Paul	ICAR-IARI, New Delhi
12.	Baban Preet Kaur (11282)	PhD	Rice microbiome associated with functional traits of carbon and nitrogen cycling	Dr. B. Ramakrishnan	ICAR-IARI, New Delhi
13.	Vikram K.V. (11284)	Ph.D.	Development of rhizobacterial bioformulation for water deficit stress alleviation in mustard and assessing its impact on soil health	Dr. Sangeeta Paul	ICAR-IARI, New Delhi
14.	Sneha GR (11540)	Ph.D.	Cyanobacteria mediated enhancement of drought stress tolerance in wheat genotypes	Dr. G. Abraham	ICAR-IARI, New Delhi
15.	Aswini K (11542)	Ph.D.	Microbiome-mediated management of heat stress in wheat (*Triticum aestivum* L.)	Dr. Archna Suman	ICAR-IARI, New Delhi

#IARI off campus

**Outreach Institute

Soil Science and Agricultural Chemistry

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Prof. Tapan J. Purakayastha

The Division of Soil Science and Agricultural Chemistry has the mandate to carry out research on the fundamental and applied aspects of the physical, chemical and biological properties of soil; fertilizers and manures and their interaction with soil and plant; improvement and maintenance of soil fertility for sustained optimum agricultural production; utilization of organic residues (wastes) as a manure and production of biogas as fuel; soil test crop response correlation studies; advice to the farmers on soil test-based fertilizer recommendations. The post graduate research findings have been grouped under various themes. Significant research findings of post graduate students are enlisted under the following themes:

Theme 1: Synthesis and evaluation of novel fertilizer products

Synthesis and evaluation of bioaugmented zinc oxide coated urea product for its efficacy under wheat crop

Zinc (Zn) is essential for plant, animal, and human development, but Zn deficiency in salt-affected soils harms plant growth and development. Enhancing bioavailable Zn requires solubilizing fixed Zn and reducing fixation of applied Zn fertilizers. Zinc-coated urea improves N and Zn utilization, while cost and availability issues hinder zinc sulfate ($ZnSO_4$) adoption. Insoluble zinc oxide (ZnO) with innovative dissolution techniques and Zn solubilizing bacteria (ZSB) shows potential. In wheat, a key carbohydrate and protein-rich crop, optimal N and Zn management are vital. The study embarks on synthesizing and evaluating bioaugmented Zn oxide-coated urea products, tailored for wheat cultivation. Objectives encompass evaluating Zn solubilizers, synthesizing and characterizing ZnO and Zn solubilizer coated urea, and assessing the impact of these formulations on wheat yield and the uptake of N and Zn. Among 20 bacterial isolates, four strains—*Priestia aryabhattai* WSB119, *Stenotrophomonas pavanii* WSB22, *Bacillus aerius* WSB68, *Klebsiella pneumoniae* M35—displayed superior Zn solubilization potential. Characterization studies revealed the uniformity of coating on urea granules through SEM, crystallinity imparted due to ZnO through XRD. Interestingly, FTIR spectra also revealed some unidentified peaks representing low molecular weight carboxylic acids which were believed to be secreted by zinc solubilizing bacteria that was used for coating of urea. Application of bioaugmented zinc oxide coated urea led to enhanced nutrient use efficiency (N and Zn) in wheat. Despite the insolubility of ZnO, effective urea coating can be achieved through binder-enhanced adherence and incorporation of Zn solubilizing organisms. Notably, selected strains for product formulation exhibited a shelf life of two months at 4°C and room temperature. Yield results substantiate the promise of coated urea, demonstrating comparable yields at 75% N application to those achieved through 100% N urea application. In synthesis, this research unearths the potential of bioaugmented ZnO coated urea as an efficacious nutrient supply strategy.

Evaluation of POLY4 as a source of potassium and sulphur using basmati rice in an Inceptisol

POLY4 is a granular fertilizer containing 19% sulphur (S), 14% potassium oxide (K_2O), 6% magnesium oxide (MgO), and 17% calcium oxide (CaO). In Indian soils, both potassium (K) and sulphur levels have been declining due to nutrient depletion caused by crop uptake. Keeping this in view, the present study has been undertaken. The first objective of this study was to investigate the release of K and S from three different soils (Acid soil of Assam, calcareous soil of Bihar and alkaline soil of Delhi) treated with different dosages of POLY4. The second objective was to assess the impact of POLY4 and other K and S nutrient sources on the fractions of K and S, as well as their uptake by basmati rice. For fulling the first objective, a laboratory study was undertaken to study the release of K and S from the contrasting soils treated different dosages of POLY4 (19 mg POLY 100 g^{-1} soil and 190 mg POLY 100 g^{-1}). In this study it was recorded that significantly higher release of both K and S was in acid soil of Assam. For achieving the second and third objective soil (0-15 cm and 15-30 cm) and plant samples were collected after the harvest of rice from an ongoing POLY4 field experiment started from June 2021 at ICAR-IARI, Pusa, New Delhi. Findings of the present experiment underlines that POLY4 is an effective nutrient source, particularly of K and S, the benefit of which could be harnessed as an alternative non-conventional fertilizer. Therefore, considering the above points among the different dosage of POLY4, treatment with recommended N, P and 100% of K through POLY4 (T5) has been the most effective treatment as a source of K and S under basmati rice in an Inceptisol.

Effects of seaweed extract-based products on nutrient release, use efficiency and grain quality of wheat grown in an Inceptisol

Seaweed extracts have emerged as a promising alternative while requiring no fresh water or arable land and boasting a low carbon footprint. This makes them ideal for carbon-neutral, sustainable farming practices. Keeping this in mind the present study was conducted with two types of products developed by The Indian Farmers Fertiliser Cooperative (IFFCO), *i.e.,* seaweed extract-based *Sagarika* Z++ granules (SG) and *Sagarika* liquid (SL). The SG showed alkaline pH, and is rich in N, P, Ca, Mg, S, Fe, Zn and Cu content, whereas, the SL had neutral pH, and a slightly lesser amount of these nutrients, except a very high K content. The research involved two experiments: an incubation study and a greenhouse pot experiment with wheat as a test crop, both conducted using highly acidic soil (pH 3.87) sampled from ICAR- NBSS & LUP, Assam. The greenhouse study revealed that the application of 75% recommended NPK along with SG @ 10.67mg/kg soil and SL @ 5ml/L of water [75%NPK + SG (10.67) + SL(5)] showed prominent bio-stimulatory effects., The application of seaweed extract-based products promoted an efficient use of fertilizer nutrients. The treatment 75%NPK + SG (10.67) + SL (5) reported similar yield and harvest index, as compared with 100% NPK application. The grain quality of wheat measured in terms of nutrient contents, and biochemical composition of grains showed improvement with the application of seaweed extract-based products. In acidic soils, the application of SG showed an indication of an ameliorative effect, without any visible signs of nutrient mining. Furthermore, the organic nature of SG promoted soil microbiological growth and activities. Therefore, the application of seaweed extract-based granules @ 10.67 mg/kg soil (corresponding to 10 kg/acre) and 2 sprays of seaweed extract-based liquid @ 5 ml/L has the potential for reducing fertilizer NPK application by 25%.

Development of novel phosphatic fertilizer products for enhancing phosphorus use efficiency in maize-wheat cropping system

Controlled release fertilizers (CRFs) are the best techniques to improve nutrient recovery efficiencies as they have a propensity for regulated nutrient delivery that synchronize with plant nutrient requirements. In the present investigation, super absorbent phosphorus (P) loaded nano-clay polymer composite (NCPC), nano-clay bio polymer composite (NCBPC) and self-polymerizing natural oil coated DAP (OC-DAP) were prepared. Bentonite (nano-clay) was used for the preparation of the products. The NCBPC was synthesized by replacing acrylic acid by starch (20% by weight) to reduce the cost of clay polymer composites. Total P content in NCPC and NCBPC was determined and found to be 12.1 and 11.6%, respectively. Nine formulations of oil-coated DAP (OC-DAP) was synthesized using various combinations of oil, clay and DAP and were compared with standard DAP fertilizer in terms of release behaviour of P in alkaline, sodic, calcareous and acid soils. P was added @ 7.61g P kg^{-1} soil through OC-DAPs and DAP. The release of P was highest in DAP treated soils compared to OC-DAP treated soils. However, the P release from OC-DAP treated soils were significantly different by a huge margin than DAP treated soils. OC-DAP_2 was selected for evaluation in greenhouse pot experiment and field study. In a greenhouse pot experiment, the performance of P loaded NCPC, NCBPC, OC-DAP and DAP fertilizer was evaluated using maize as test crop. Results indicate that, NCBPC, NCPC and OC-DAP were able to provide higher P as compared to DAP fertilizer which was reflected in biomass yield and plant P uptake. The P uptake from 75% RDP applied through NCBPC, NCPC and OC-DAP and 100% RDP applied through DAP fertilizer were statistically at par with each other in all the soils. Hence, use of P loaded NCBPC, NCPC and OC-DAP promising for enhancing use efficiency of applied P.

Effect of residue management practices, nitrification and urease inhibitors on soil microbiota, ammonia and greenhouse gas emissions under rice-wheat and maize-wheat cropping systems

Burning of the crop residues is a significant and widespread issue in wheat-based cropping systems of northern and northwestern India, which leads to severe air pollution. Alternatives to burning could be crop residue removal (CRR), incorporation of crop residue (CRI) in the field during land preparation and converting the residue into biochar (BC). On the other hand, poor N management led to significant loss of N through NH_3 volatilization, NO_3^- leaching, and emission of nitrogen oxides. Combined use of using nitrification and urease inhibitors could mitigate all the N loss simultaneously. To address these issues, a laboratory and a field study was designed. For the laboratory experiment, soil was collected from a 10-year residue management field experiment (Crop residue removal, CRR vs. crop residue incorporation, CRI). Neem coated urea (NCU), standard urea (U), urea ammonium sulfate (UAS), and two alternative fertilizers, urea + urease inhibitor NBPT (UUI), and urea + urease inhibitor NBPT + nitrification inhibitor DMPSA (UUINI) were compared to non-fertilized controls for four weeks in incubation under anaerobic condition in a 6×2 factorial CRD. For the field experiment, NCU and UUINI were tested across four long-term crop residue management practices: residue burning (CRB), CRR, CRI, and biochar (BC) in a split-split-plot design under rice-wheat and maize-wheat systems. Residue incorporation increased CH_4 and N_2O emissions, NH_3 volatilization but reduced nitrate leaching, whereas, BC marginally reduced N_2O emission, nitrate leaching, and increased CO_2 and CH_4 emission but did not affect NH_3 volatilization. This study highlights the potential for dual inhibitor to reduce N losses compared to conventional NCU. Biochar emitted similar global warming potential (GWP) compared to CRB, while CRI showed higher GWP over CRB. However, carbon sequestration potential and overall health benefit of CRI and BC, and loss of GHGs during biochar production needs to be carefully evaluated before recommending any residue management to the farmers.

Theme 2: Soil management strategies to enhance SOC sequestration, soil health, and soil resilience

Impact of long-term conservation agriculture on quality and stability of carbon in calcareous soils of eastern Indo-Gangetic plains

Conservation agriculture (CA) has emerged as an alternative approach to address soil degradation, improve productivity, and protect the environment. Soil organic carbon (SOC) is a vital component of soil quality and agricultural system stability. To gain further insights into the long-term impact of CA on the physical and chemical stability of soil carbon, a study was conducted in the calcareous soils of the Eastern Indo-Gangetic Plains. The trial included eight combinations of tillage, crop establishment and residue management options, namely: conventional tilled rice and -wheat (CTR-CTW); CT rice and zero till wheat (CTR-ZTW); direct seeded rice (DSR) and wheat on permanent raised beds (PBDSR-PBW); ZTDSR and CT Wheat (ZTDSR-CTW); ZTDSR and ZT wheat (ZTDSR-ZTW); ZTDSR-ZT wheat with residue (ZTDSR-ZTW+R); unpuddled transplanted rice-ZTW (UpTR-ZTW) and ZTDSR with *sesbania* brown manuring-ZTW (ZTDSR+S-ZTW). The objectives were to examine the impact of CA on soil carbon stability, clay minerals and clay-humus complex stability, and the quality of soil organic matter. Micro-aggregate content was highest in conventionally managed systems. CA practices improved soil aggregate stability, especially at the 0–5 cm depth. The ZTDSR-ZTW + R treatment had the highest mean weight diameter (MWD) value (1.72 mm) at the 0–5 cm depth. While, the CTR-CTW treatment had the lowest MWD value (0.59 mm. The use of zero-tillage, residue retention, and brown manuring resulted in a decrease in soil inorganic carbon (SIC) content at different soil depths. Zero-tillage with residue retention significantly increased SOC content (233%, 166%, and 140% at 0–5, 5–15, and 15–30 cm, respectively), while CT practices led to a depletion of SOC. CA practices increased the Ca^{2+} content in clay-humus complexes, which positively correlated with clay-humus C stability. The findings highlighted the positive impact of CA practices, such as zero-tillage and residue management are the best practices for carbon sequestration in calcareous soils and to improves the quality and thermal stability of soil organic matter.

Biochemical characterization of crop residues and their effects on carbon mineralization in a Typic Haplustept

In the present study, efforts were made to assess the effect of the biochemical composition of different *kharif* crop residues on carbon (C) mineralization, soil carbon fractions and enzyme activities. To achieve the objectives, both soil (0-5 cm depth) and different residues were collected from ICAR-Indian Agricultural Research Institute's research farm, New Delhi. The crop residues were analyzed for elemental and biochemical characteristics. An incubation study was carried out at two temperatures *viz.,* 25 and 35˚C to study C mineralization from different crop residues in soil. The *Sesbania* residue was rich in C, N, P and S, along with the lowest C:N, and lignin content, which reflected in the highest values of PRQI (Plant residue quality index) followed by that under mung bean and pigeon pea. On the other hand, the cotton residues had the lowest values of PRQI, owing to the highest lignin content and C:N, followed by rice and maize residues. The crop residues with a high C content, accompanied by lower values of C:N (mung bean, pigeon pea, *Sesbania*) were most preferred by the microbes for the decomposition process. The lability/quality of *Sesbania* residue might have immensely contributed towards the cellular structures of microbes, in turn diminishing their contribution towards C mineralization and favoring immobilization. The immense enhancement in microbial biomass build-up under *Sesbania*-added treatments reported a significant enhancement in the soil enzymatic activities and less recalcitrant soil organic C (SOC) fractions *i.e.,* SOC_{VL} and SOC_{L}. On the other hand, cotton residues which had a very high amount of complex lignin and polyphenol resisted the microbial attack and resulted in the lowest enzyme activities, SOC_{VL} and SOC_{L}, even at 35 °C. Therefore, brown manuring with *Sesbania* has great potential for use in regenerative agriculture, followed by pulse crop residues, by virtue of their low lignin content.

Aggregation behavior of biochar and its impact on carbon and phosphorus fractions in an acidic Inceptisol under rice-wheat system.

Converting rice straw to biochar offers a potential solution for residue management, and also enhances soil carbon sequestration, nutrient availability and serves as an amendment in acidic soil. Yet, interaction of biochar with low molecular weight organic acids (LMWOAs)/rhizo-secrets of crops that may affect the movement and behaviour of biochar colloids in soil, which has not been investigated thoroughly. To unfold this interaction present study was carried out. To achieve the study, soil samples (0-15 and 15-30 cm depth) were collected during the grain maturing stage of rice (*Kharif* 2022), s from an ongoing field experiment (since 2019-20) at ICAR-Indian Agricultural Research Institute in Jharkhand, India. Treatment consisted; control (unfertilized), recommended NPK + biochar @ 10 t ha^{-1}, recommended NPK + biochar @ 5 t ha^{-1}, recommended NPK, and farmers' practice. Investigation on aggregation behaviour of the biochar colloids in response of LMWOAs namely formic acid, acetic acid and malic acid was carried out. Collected soil samples were analyzed for chemical properties, nutrient availability, acidity forms, carbon and phosphorus fractions. Results revealed that the total carbon content of biochar was (39.9%), and rich in primary and secondary nutrients along with many micronutrients. The findings indicated that the addition of biochar (RP + Biochar @ 10 t ha^{-1}) increased the very labile, less labile, and non-labile C pools in the surface soil by 85.8%, 113% and 70.4%, respectively over control. In nutshell, the profound impact on aggregation of biochar colloids noticed with (LMWOAs)/rhizo-secrets of crops, and the impact was more with decreasing pH, and increasing molecular weight of organic acids. Biochar @ 10 t ha^{-1} superimposed with recommended NPK was most effective to alleviate soil acidity and to enhance carbon sequestration and nutrients availability of acidic Inceptisol.

Assessment of soil health, carbon, nitrogen and phosphorus dynamics in long-term conservation agriculture under rainfed pearl millet-based cropping systems

There is a lack of research on the impact of rainfed conservation agriculture on soil health and nutrient dynamics of carbon, nitrogen, and phosphorus. To address this gap, depth-wise, soil samples were collected from three different tillage practices, namely Zero-tillage with residue retention (ZT+R), Zero-tillage without residue retention (ZT-R), and Conventional Tillage (CT), and three cropping systems, namely pearl millet-chickpea (PM-C), pearl millet-chickpea-fodder pearl millet (PM-C-FPM), and pearl millet-chickpea-mung bean (PM-C-M), from an ongoing rainfed CA experiment situated at ICAR-IARI, New Delhi. The CA practices, *i.e.,* crop residue retention, zero-tillage and inclusion of legumes can reduce soil bulk density, improve soil structure and effectively manage soil compaction. Different tillage and cropping systems significantly impacted the availability and distribution of essential plant nutrients (P, K, S, Cu, Fe, Mn and Zn). The PM-C-M and PM-C in combination with ZT+R enhance soil organic carbon (SOC) and improved soil health. Four soil quality indices (SQI) based on a minimum dataset, two types of scoring functions (linear (L) and non-linear (NL)), and two integration methods, additive (A) and weighted additive (WA) were evaluated. The results showed that SQI-LWA was the most sensitive in detecting changes among treatments. Across all soil depths, ZT+R had the highest SQI-LWA, while CT had the lowest. The study found that the ZT+R system had the highest levels of different pools of SOC, while the PM-C and PM-C-M cropping systems had higher SOC compared to PM-C-FPM. Additionally, the ZT+R system had the highest Carbon Management Index (CMI) values at the 0-5 cm and 5-15 cm soil depths, indicating its effectiveness in managing carbon in the soil compared to the CT system. Tillage and cropping systems significantly impacted soil structure and stability, with ZT+R and PM-C having the highest MWD and GMD values respectively. ZT+R significantly increased soil mineral N content and stock compared to CT across 0-30 cm soil depth. Legume-based cropping systems enhanced N concentration and its availability. The adoption of conservation agriculture practices, such as zero tillage with residue retention under legume-based cropping systems, can enhance soil health and nutrient dynamics of C, N and P and promote sustainable agricultural practices, leading to enhanced food security in these regions.

Impact of long-term conservation agriculture practices on soil carbon and phosphorus dynamics under maize based cropping systems in an Inceptisol

Understanding the long-term impacts of different tillage and cropping system under conservation agriculture (CA) on soil carbon (C) and phosphorus (P) dynamics is crucial to gain knowledge about the distribution of C and P in soil. Hence, the effects of 12 years of CA in an Inceptisol of the Indo-Gangetic Plains on soil organic carbon (SOC) pools, soil phosphorus (P) pool, aggregate associated C and P, available N, P, K, and biological properties were studied under a maize-based cropping system. The results revealed that the permanent bed (PB) plots had 33.5and 32.3% more total SOC concentration than the conventional tillage (CT) flat plots in 0-5 cm and 5-15 cm soil layers, respectively. The cropping system maize-chickpea-*Sesbania* (MCS) had 15.4% higher SOC content in 0-5 cm soil layer. In the topsoil, the proportion of macroaggregates was significantly higher under permanent bed and microaggregates was significantly higher in CT-flat plots. Significant synergistic effects of winter legume (Chickpea) with summer legumes (*Sesbania* and moong bean) in crop rotation were observed on SL-P, labile Po, humic acid-Po, alkaline phosphatase and microbial biomass (MBP) at 0–5 and 5–15 cm soil depths. The ZT-flat tillage practices had the highest large macroaggregate associated Olsen-P values in the 0-5 cm soil layer, while MCS cropping system showed the highest Olsen-P values in different depths. In the 0-5 cm soil layer, the highest Olsen-P in micro aggregates was observed under CT-flat (19.6 mg kg^{-1}), which is statistically similar to ZT-flat (19.5 mg kg^{-1}). The results indicated that the P uptake in maize grain and straw was significantly higher in PB compared to ZT-flat and CT-flat. The results showed that the P uptake in maize grain and straw was significantly higher under MCS and MWMb than other cropping systems. The treatment combinations PB-MCS, ZT-MCS, PB-MWMb and ZT-MWMb performed better in terms of improving nutrient availability and increasing yield besides improving soil quality.

Assessing stability of clay-humus complexes and soil organic carbon fractions under long-term conservation agriculture in an Inceptisol

The objective of this research work was to study the impact of long-term conservation agriculture (CA) on the quality of humic acid in soil under maize-wheat (M-W) and pigeon pea-wheat (P-W) cropping systems. In the present study, the influence of long-term (11 years) CA practices namely, zero-tillage and residue retention (ZT+R) on humic acid (HA) quality and composition, clay-humus carbon (C) stability, C pools and C stock was assessed. For this purpose, the soil samples were collected from M-W and P-W cropping systems under CA farm of the Division of Agronomy, Indian Agricultural Research Institute, New Delhi at different soil depths up to 40 cm. The treatments in the present study consisted of conventional practice (CT), zero tillage (ZT) and zero tillage with residue (ZT+R) with three replications. Results indicated that the treatment ZT+R showed comparatively higher C content and total acidity in the HA fraction. Results of the present investigation further indicated that the retention of crop residue under ZT+R treatment significantly increased clay–humus stability with respect to other treatments in both the cropping systems throughout all the soil depths. The highest magnitude of passive pool of C in soil was associated with ZT+R treatment, indicating the positive influence of CA practice on C sequestration. The C stock was also significantly improved due to CA practice and ZT+R had 19.7% higher C stock over CT in M-W system and 18.8% higher C stock over CT in P-W system. It was also observed that yield of crops was significantly higher under CA practice and significant correlations between yield with different pools of C were observed. From this study, it is concluded that ZT+R treatment can be recommended in CA-based maize-wheat and pigeon pea-wheat cropping systems in the IGP.

Microbial stability and nutrients dynamics of soil under conservation agriculture in an Inceptisol

A long-term field experiment was started under conservation agriculture (CA) at research farm of ICAR-Indian Agricultural Research Institute, New Delhi in the year 2008. The present study was conducted to evaluate the influence of nitrogen (N) management and weedicide application under long-term CA on the activity of different soil enzymes, soil carbon (C) fractions, soil N release and distribution of N and phosphorous (P) fractions in soil. To achieve these objectives, soil samples were collected from two depths (0-5 and 5-15 cm) at harvesting stage of wheat under maize-wheat cropping system. Four nitrogen levels in main plots *viz;* (i) CT_{100}; conventional tillage + residue + 100% recommended dose of N (RDN), (ii) ZT_{50}; zero tillage + residue + 50% RDN, (iii)ZT_{75}; zero tillage + residue + 75% RDN and (iv) ZT_{100}; zero tillage + residue + 100% RDN and four treatments of weedicide application in the sub-plots *viz;* (i) sulfosulfuron + metsulfuron-methyl @ 40 g a.i. ha^{-1} (pre-mix post-emergence) at 30 days after sowing (W_1), (ii) carfentrazone-ethyl + metsulfuron-methyl (20+4 g a.i. ha^{-1}) at 30 days after sowing (W_2), (iii) clodinafop + carfentrazone + metsulfuron-methyl (60+20+4 ga.i. ha^{-1}) at 30 days after sowing (W_3) and (iv) unweeded/control (U) were studied with three replications under the split-plot design. The results indicated that N fractions, CA practice led to an increase in various fractions of N. In case of P fractions, higher amount of soluble and loosely bound P, iron-bound P, aluminum-bound P, reductant soluble P and calcium-bound P were detected in ZT_{100}, than CT_{100} in both the soil depths. Among zero tilled plots, ZT_{100} recorded significantly higher wheat yield (3.76 t ha^{-1}), which was at par with CT_{100} (3.71 t ha^{-1}). Thus, it may be stated that the recommended dose of N with ZT practice enhanced the microbial function, SOC, N and P availability in soil.

Soil organic carbon stabilization in bed planted cotton-wheat system under conservation agriculture in an Inceptisol

In the present study, a ten-year conservation agriculture (CA) field experiment was taken with seven treatments namely, conventional tillage (CT), permanent narrow bed (PNB), permanent narrow bed with residue retention (PNB+R), permanent broad bed (PBB), permanent broad bed with residue retention (PBB+R), permanent flat bed with residue retention (ZT+R) and permanent flatbed (ZT) laid out in a randomized block design with three replications. Results revealed that soil bulk density showed no significant variations among treatments due to long-term CA practices. After ten years of cropping in the Indo-Gangetic plains (IGP), in the topsoil (0-5 cm depth), the PBB+R, PNB+R and ZT+R plots had ~39%, 34%, and 29% more total SOC storage than CT plots (4.84 Mg C ha^{-1}), respectively. Similarly, up to 30 cm depth, the effect of CA was significant with respect to SOC storage, beyond which it was not significant. Plots under PBB+R had 0.85 Mg $ha^{-1}yr^{-1}$ soil organic C (SOC) accumulation rate over conventionally tilled (CT) plots in the 0-30 cm soil depth. Nearly 82% of the total SOC accumulation in the 0-60 cm was observed in the 0-30 cm soil layer. Residue removal decreased the SOC accumulation by ~66, 65 and 53% in PBB, PNB and ZT over PBB+R, PNB+R and ZT+R treatments, respectively, in the 0-30 cm soil layer. The residue retention significantly influenced the labile and recalcitrant C pools of soil, where the PBB+R plots had ~63 and 52% higher labile and recalcitrant C than CT plots, respectively, in the topsoil. The residue retention was positively correlated with soil aggregation, mean weight diameter, C accumulation and thus enhancing more C stability in soil. Overall, raised bed with residue retention had highest C stabilization potential under this cropping system, whereas considering other agronomic parameters PBB+R could be recommended in a cotton-wheat system in the IGP.

Influence of emplacing agro-geotextiles on soil organic carbon stabilization and nitrogen sequestration under conservation-tilled maize based cropping systems in the north western Himalayas

Although agro-geotextile (AGT) emplacement has potential effect to mitigate soil loss and thus increase carbon sequestration, comprehensive information is scanty on the impact of using AGT on soil organic carbon (SOC) sequestration, aggregate-associated C, C stabilization, N sequestration, aggregate stability and C and N cycling enzyme activity in the foot hills of the Indian Himalayan Region. In the present study, the impacts of using *Arundo donax* AGT in different configurations on SOC sequestration, aggregate stability and N sequestration since 2017 under two maize-based cropping systems on a 4% land slope where eight treatments were evaluated. In top soil and 5-cm soil layer, 10 cm thick *Arundo donax* placement at 0.5m vertical interval-pea-wheat treatment (M+AD10G0.5-P-W) had nearly 22% and 23% increase (P=0.05) in total SOC storage than maize-wheat system (M-W). Results revealed that M+ADGT0.5-P-W plots had ~23% increase in SOC storage (27.87 Mg ha^{-1}) compared to M-W in the 0-30cm soil layer. Plots under M+AD10G0.5-P-W and maize-pea-wheat under bench terracing (M-P-W) BT had similar impacts on SOC stocks in that layer after 5 years of cropping. Within soil conservation practices, *Arundo donax* mats emplaced plots had 14% higher labile C pool over control plots. Total SOC values in bulk soils, macroaggregates and microaggregates were ~24%, 20%, and 31%higher, respectively, in plots under M+AD10G0.5-P-W than M-W in the topsoil (0-5 cm depth). The inclusion of post-rainy season vegetable pea in maize-wheat cropping system along with AGT application and crop residue management generated additional biomass and enhanced carbon management index (CMI) by~60% in the plots under M+AD10G0.5-P-W over M-W, although M+AD 10G 0.5-P-W and (M-P-W) BT had similar effects in the 0-5 cm soil layer. The adoption of AGT application under M+AD10G0.5-P-W increased the c POM_M and LF _mM associated C concentrations by~31% and 30% compared to control plots, respectively, in the topsoil. In the M+AD10G0.5-P-W treatment annual mean soil loss decreased by ~92% over M-W treatment. M+AD5G0.5-P-W plots showed comparable effects on soil loss and carbon pools with M+AD10G0.5-P-W plots. We observed that CMI, proportion of macro aggregates, aggregate-associated C, labile C, total SOC concentration (thus SOC accumulation rate) and estimated C input were strongly correlated with mean annual soil loss from 2017 to 2021. Thus, soil aggregation and SOC accumulation are the major mechanisms of soil conservation. The study revealed that emplacement of *Arundo donax* mat and incorporation of a legume in the M-W cropping system, conservation tillage and crop residue retention not only prevented soil loss but also enhanced C stabilization and N sequestration compared to control practice.

Long-term impact of conservation agriculture on dynamics of carbon, nitrogen, phosphorus and sulphur in soil under maize-wheat-mungbean cropping system

The present study endeavours to investigate the impacts of nine years of conservation agriculture (CA), employing various tillage techniques (ZT+R: Zero tillage with residue retention and CT+R: Conventional tillage with residue incorporation) and nitrogen management approaches (Control, RDN, Urea+GS and USG+GS), on aspects of soil organic carbon (C), soil nitrogen (N), phosphorus (P) and sulphur (S) dynamics in an Inceptisol under a maize-wheat-mungbean cropping system. The results revealed that the ZT+R (Conservation agriculture) plot showed significantly higher very labile, labile, less labile and non-labile soil organic carbon pools. Nearly 9.78 and 7.74% significantly higher total soil organic carbon was recorded by CA practices in comparison to CT+R at 0-5 and 5-15 cm soil depths, respectively. Among the subplots, all the nitrogen fertilizers received plots had significantly higher total organic C (mainly the non-labile organic C pool) and TC compared to control treatment. The carbon pool index was significantly enhanced by practicing CA with nitrogen application compared to CT+R and control plots. After 60 days of incubation, the ZT+R plot had nearly 20 and 23% significantly higher cumulative C mineralization over CT+R at 0-5 and 5-15 cm soil depths, respectively. Among subplots, better N management through USG+GS treatment showed significantly higher cumulative C mineralization over both control and recommended dose of N plots. All the N pools, i.e., NH_4-N, NO_3-N, Alkali-$KMnO_4$, Microbial biomass N (MBN), Potentially mineralized N (PMN) and total N were found significantly higher in ZT+R over CT+R plots. The ZT+R and nitrogen applied plots recorded significantly higher NH4–N, NO3-N, Olsen-P and $CaCl_2$-S compared to CT+R and control plots, respectively throughout the incubation period. Overall, the better N management option (USG+GS) under CA practices needs to be considered carefully to optimize the maximum potential of carbon sequestration and major nutrient dynamics (N, P and S) in maize-wheat-mungbean cropping system.

Theme 3: Dynamics of Nutrients and their Interactions in Soil

Phosphorus dynamics in an Inceptisol under different land use systems of semi-arid ecologies

Land use change had significant impacts on soil physicochemical and biological properties. However, in depth understanding of phosphorus (P) dynamics is needed with respect to different land use systems (LUS). Suitable LUS can help in liberating P from fixed reserves and making it available to the plant. Therefore, seven LUSs namely, Subabul (*Leucaena leucocephala*) based silviculture system, Anjan (*Hardwickia binata*) based silviculture system, Desi babul (*Acacia nilotica*) based silvopasture system, Aonla (*Emblica officinalis*) based horti-pasture systems, Neem (*Azadirachta indica*) based silviculture system, Natural grassland (<10% tree cover) and Fallow land (Control) were selected to study their impact on soil properties and P dynamics in a degraded soil (Typic Haplustepts). Soil samples were collected from three different depths *i.e*., 0-15, 15-30 and 30-45 cm from the ICAR-Indian Grassland and Fodder Research Institute, Jhansi, India. Results showed that pH and electrical conductivity increased in different LUSs in comparison to fallow land. Also, all the LUSs significantly improved the organic carbon content in soil as compared to fallow land, irrespective of soil depths. The available nitrogen, available P and available potassium content also showed a significant increase in different tree and grass-based LUSs compared to fallow land across different soil layers. Fractionation study revealed iron P (Fe-P) fraction as the dominant P fraction, followed by aluminium P (Al-P), clearly indicating dominance of Fe and Al oxides in soil. After transitioning from fallow to tree and grassland, the different P fractions in all soils showed a significant improvement. Adsorption-desorption study of P indicated a decrease in adsorption capacity in tree and grass-based LUSs compared to fallow land. Thus, it can be concluded that different tree and grass-based LUSs can be practiced in order to improve P supplying capacity of soil as well as to restore degraded lands in semi-arid ecologies.

Extractability of plant available potassium as influenced by fixation capacity and moisture content of soil

Information on moisture sensitivity of commonly used extractants for plant available potassium (K) in soil is scarce. There is a need to identify an extractant for plant available K that will show minimum deviation in its extractability from moist to air-dry soil. Different extractants viz. 1 N ammonium acetate (NH_4OAc), 0.1 N barium chloride ($BaCl_2$), 0.1 N sodium acetate (NaOAc), 0.01 M organic acid mixture (OAM: mixture of 0.025 M each of citric, malic, tartaric, and oxalic acids), 0.1 N HNO_3, Mehlich 1 (0.05 M HCl + 0.0125 M H_2SO_4), and Cold H_2SO_4 were compared to find out the one that shows the least deviation in K extractability between field-moist and air-dried soils. For this, seven different soils were collected, one each from Bolpur (Alfisol), West

Bengal; Samastipur (Entisol), Bihar; Hazaribagh (Alfisol), Jharkhand; Nagpur (Vertisol), Maharashtra; New Delhi (Inceptisol), Delhi; Rewari (Inceptisol), Haryana; Trissur (Alfisol), Kerala. A greenhouse pot experiment was conducted using all collected soil samples. Harvesting and collection of moist soils were started after the watering at 45 days of sowing. The acidic extractants viz, organic acid mixture, cold sulphuric acid and nitric acid showed lower deviation in K extraction between moist and air-dry soil than other extractants, where organic acid mixture showed the lowest deviation. Among the seven extractants, ammonium acetate, barium chloride, nitric acid and Mehlich extractant showed better correlation with plant K uptake in moist soil than air-dry soil. Sodium acetate extracted K was better correlated with plant K uptake in air-dry soil than in moist soil. The rest two extractants, i.e., the cold sulphuric acid and organic acid mixture showed same correlation with plant K uptake in air-dry and moist soils. The 0.01 M OAM and 0.1 N NaOAc emerged as the least and most soil moisture-sensitive extractants, respectively, of plant available K.

Interactive effect of phosphorus and zinc fertilization on nutrient uptake by mustard grown in acid soils

The interaction between phosphorus (P) and zinc (Zn) in plant and soil influences the growth of crops under different fertilization practices. Mustard (*Brassica juncea* L.), a significant *Rabi* oilseed crop in India requires these nutrients in appropriate quantities for optimum growth. So, this study aimed to investigate the detailed chemistry, particularly sorption-desorption behaviour of Zn under different phosphorus levels and its effects on mustard crop yield, nutrient uptake, and efficiency grown on acid soils. The results indicated that Zn adsorption in acid soils increased with increase in the equilibrium Zn concentrations and was influenced by P and temperature. Both Langmuir and Freundlich sorption models successfully explained Zn sorption in the presence of phosphorus. Increased temperature and phosphorus levels also amplified Zn sorption. High desorption index values indicated hysteretic desorption due to affinity of phosphorus for adsorbed Zn, reducing reversibility. However, significant effects of applied P on plant dry matter yield were observed for both the acid soils. Despite the non-significant impact of Zn application on dry matter yield, the positive effect of Zn application on Zn uptake by the crop was evident. High P application rate resulted in increased mustard stover yield but decreased Zn uptake. Optimal recovery efficiency of applied Zn was achieved with combined application of P (in the form of P_2O_5) at the rate of 20 mg kg^{-1} and Zn at the rate of 2.5 mg kg^{-1}. Application of P at the rate of 40 mg kg^{-1} led to reduced Zn content in post-harvest soils and mustard stover. This study encompasses on P-Zn interactions in acid soils, elucidating the sorption mechanism affecting Zn availability and its uptake under high phosphorus application. This research provides valuable information on optimizing the P and Zn fertilization rate for improved mustard crop nutrition.

Leaching loss of nutrients under different nutrient management options in maize and brinjal grown on an Alfisol

To comprehend the mobilization, adsorption, and nutrient leaching losses, the present study was undertaken in the experimental field of ICAR- RCER, FSRCHPR, Ranchi, Jharkhand to quantify the nutrient leaching and nutrient distribution within the soil profile of post-harvest soil under different nutrient management options. The leachate was quantified from the non-weighing lysimeter with different nutrient management options comprising of control (T_1), inorganic (T_2), organic (T_3), and integrated nutrient management (INM) (T_4) under maize and brinjal crops. The inorganic (T_2) treatment registered the highest amount of nitrogen (both nitrate and ammonium form) leaching, causing 31.27 and 19.95 kg ha^{-1} in brinjal and maize, respectively. The ammonium-nitrogen contribution was approximately 15-20% of total mineral nitrogen loss, while the rest was in nitrate form. The leaching loss of potassium from the inorganic treatment was observed highest and resulted in 19.97 and 13.51 kg ha^{-1} loss in brinjal and maize, respectively. The inorganic treatment caused higher calcium leaching loss and accounted for 23.81 and 14.68 kg ha^{-1} in brinjal and maize, respectively. In the post-harvest soil sample, pH, EC (electrical conductivity), EOC (easily oxidizable organic carbon), AN (available nitrogen), AP (available phosphorus), AK (available potassium), Ex-Ca (exchangeable calcium), AS (available sulphur) were observed highest in the topsoil and then decreased gradually with the increase in soil depth though available nitrogen content was observed highest in 15-30 cm soil layer. Exchangeable calcium and available potassium content were found highest in organic treatment and reflected a stronger bonding of cation with organic matter. From the present investigation, it can be concluded that INM practice enhanced the overall soil fertility and sustainability by increasing the available nutrient content among all the nutrient management options and decreasing the leaching loss of nutrients.

Solubilization of soil phosphorus using rice residues and phosphorus solubilizing microorganisms

Disposal of significant tonnages of rice straw (RS) is expensive, but using it to mobilize phosphorus (P) from inorganically fixed pools in the soil may add value in the Indo-Gangetic Plains. This study was carried out to determine whether the use of RS mixed with phosphorus solubilizing microorganisms (PSM) could solubilize a sizable portion of fixed soil P and affect P transformation, silicon (Si) concentration, organic acid concentrations, and enzyme activity to increase plant growth. For this, soils from semi-arid and humid tropical agro-ecosystems were treated with PSMs, *i.e. Pseudomonas striata* (~10^8 CFU mL^{-1}) and *Aspergillus niger* (~10^8 spores mL^{-1}) and graded doses of RS (at 8, 10, 12, and 14 Mg ha^{-1}) under varying hydrothermal scenarios (temperature and soil moisture suctions), namely, S1 (25°C and 0.033 MPa), S2 (35°C and 0.033 MPa), S3 (25°C and 0.1 MPa) and S4 (35°C and 0.1 MPa). Rice straw application at 12 Mg ha^{-1} with PSMs in soil significantly boosted the Si content, enzyme activity as well as organic acid production during incubation. In pot experiment the performance of rice straw application with PSM and 75% of recommended dose of P application was tested to justify the practical feasibility of RS and PSM application in wheat-rice cropping sequence. According to path analysis, P solubilization by Si and organic acids considerably increased P availability (18-32%) in the wheat and rice rhizosphere. Rice straw at 12 Mg ha^{-1} with PSM and 75% mineral P fertilizer application could solubilize ~ 11 to 15% (*i.e.* 86 to 90 mg P kg^{-1}) inorganic P depending on the soil and environmental conditions. Therefore, cultivators could be advised to use RS at 12 Mg ha^{-1} with PSM with 75% P of mineral P-fertilizer to save 25% P-fertilizer without reducing yield. This can significantly contribute to reducing P-fertilizer import and promoting P circular bio-economy.

Assessing potassium supplying capacity and clay mineral alterations under exhaustive cropping in major soil orders

The present experiment was conducted to compare the extent of potassium release through successive leaching from major soil orders of India, to assess the extent of potassium depletion from soils under exhaustive cropping, and to study the effect of potassium (K) depletion on K supplying capacity and clay minerals in soils at various levels of added K. Five soils (0–15 cm) were collected from New Delhi (alkaline soil; Typic Haplustept), West Bengal (acidic soil; Typic Fluvaquent), Bihar (calcareous soil; Calciorthent), Jharkhand (red soil; Typic Haplustalf), and Madhya Pradesh (black soil; Typic Haplustert). A leaching experiment was conducted where soils were extracted with 0.1 N $BaCl_2$ for 90 times (18 h incubation per leaching). A pot experiment was also conducted with sorghum-Sudan grass hybrid (*Sorghum bicolor* × *Sorghum bicolor* var. sudanese), which was grown for consecutively five times taking similar nitrogen (N) and phosphorus (P) doses but nine varying K levels which were 0% (K0), 40% (K40), 50% (K50), 60% (K60), 70% (K70), 80% (K80), 90% (K90), 100% (K100), and 150% (K150) of the recommended K dose (RDK). Results under the leaching experiment revealed that after 23rd numbers of leaching, a constant K release (13–14 mg kg^{-1}) was obtained irrespective of soil types indicating nonexchangeable-K (NEK) release from the similar K-affinity sites. However, cumulative K release was significantly ($P < 0.01$) higher in black soil than the rest four soils. The findings inferred that severe NEK depletion is only partly reversible which not only deteriorates K-bearing minerals but also affects the plant K availability through declining soil K supplying capacity. Under severe depletion, added K gets fixed, deteriorating the plant K use efficiency. Proper K fertility management does not ensure the positive K balance under intensive cropping but it can maintain better soil K-supplying ability than when cropping without K-fertilization.

Theme 4: Remediation of Polluted Soil and Water

Preparation of clay-based composites and beads for dyes remediation

The present study was carried out to develop and standardize clay-based composites and their beads for treating dye-contaminated (anionic dye Congo red and cationic dye Crystal violet) water. For the preparation of composites, comparative assessment of agricultural waste (Rice husk - RH) and clay mineral (Bentonite - B) before and after calcination (Calcined rice husk – CRH and Calcined bentonite – CB) was done for both the dyes using adsorption experiments. The results revealed that, CRH adsorbent was better than RH (16.6 mg g^{-1} and 18.4 mg g^{-1} for Congo red and crystal violet, respectively) and CB was better than B adsorbent for both the dyes. Composites of different ratios (1:1, 1:2, 1:3) were then prepared from CB and CRH and optimization studies were carried out for dyes removal to assess and compare their adsorption capacity. On the basis of adsorption capacity and maximum utilization of crop residue, 1:3 composite was selected and used for the preparation of beads. The beads were prepared with 1% sodium alginate solution loaded with 2g (2Be), 3g (3Be) and 5g (5Be) of 1:3 composites, respectively. On the basis of adsorption capacity and stability of beads, 3Be was found to have maximum dye removal efficiency for Congo red (28.50 mg g^{-1}) and Crystal violet (32.65 mg g^{-1}). A pot experiment on spinach was conducted on IARI soil (Inceptisol) using completely randomized design. 6 treatments (Normal tap water, untreated congo red containing water, untreated crystal violet containing water, Treated Congo red containing water, Treated crystal violet containing water and Treated mixture of both dyes (CR and CV) containing water) Thus, it can be concluded that the clay based composite beads can effectively remove Congo red and Crystal violet and their mixture from the simulated effluents and treated water can be used as irrigation source which can increase the crop yield without adversely affecting the soil properties.

Preparation and evaluation of phosphorus solubilizing fungus-augmented maize-based biobed for dye remediation and phosphorus solubilization

The study was carried out to develop and standardize clay-based composites and their beads for treating dye-contaminated (anionic dye Congo red and cationic dye Crystal violet) water. For the preparation of composites, comparative assessment of agricultural waste (Rice husk - RH) and clay mineral (Bentonite - B) before and after calcination (Calcined rice husk – CRH and Calcined bentonite – CB) was done for both the dyes using adsorption experiments. The results revealed that, CRH adsorbent was better than RH (16.6 mg g^{-1} and 18.4 mg g^{-1} for Congo red and crystal violet, respectively) and CB was better than B adsorbent for both the dyes. Composites of different ratios (1:1, 1:2, 1:3) were then prepared from CB and CRH and optimization studies were carried out for dyes removal to assess and compare their adsorption capacity. On the basis of adsorption capacity, BBD application and maximum utilization of crop residue, 1:3 composite was selected and used for the preparation of beads. The beads were prepared with 1% sodium alginate solution loaded with 2g (2Be), 3g (3Be) and 5g (5Be) of 1:3 composite, respectively. A pot experiment on spinach was conducted on IARI soil (Inceptisol) using completely randomised design. 6 treatments (Normal tap water, Untreated Congo red containing water, Untreated Crystal violet containing water, treated Congo red containing water, treated Crystal violet containing water and Treated mixture of both dyes (CR and CV) containing water) Pot study indicated significant improvement in plant growth parameters as well as soil properties. Thus, it can be concluded that clay based agricultural waste composite beads can effectively remove Congo red and Crystal violet and their mixture from the simulated effluents with efficient recovery from the aqueous solutions and the treated water can be used as irrigation source which can increase the crop yield without adversely affecting the soil properties.

Risk assessment and mitigation of arsenic contaminated rice soils in Nadia district of West Bengal

The arsenic (As) contamination is a serious environmental issue worldwide. So far, no work has been carried out on fixing the safe level of extractable As in soil of highly contaminated areas of Nadia, West Bengal, India, linking solubility of As in soil, uptake of As by rice and potential health hazard to human. Solubility and free ion activity model was used to predict As content in rice grain, and prescribe the toxic limit of extractable arsenic in soils concerning human health hazard for its intake through rice. Predicted and observed values of As content in rice grain are presented in 1:1 line for FIAM. A ready reckoner was developed to predict HQ of As intake through rice grain based on soil extractable As, pH and OC content using solubility-FIAM parameters. The hazard quotient was used to quantify the risk to human health from ingesting As in rice grain. A maximum permissible limit of extractable As in soil was fixed at the point where the value of HQ exceeded 0.5. An attempt has been made to evaluate the effect of flooding (W1), alternate wet and drying (AWD; W2) water management in combination with phosphate (0.0, 30.0, 60.0 mg kg^{-1}:: P1, P2, P3) and vermicompost (0.0, 2.5, 5.0 g kg^{-1} :: C1, C2, C3) application on the accumulation of As in rice grain and soil solution As extracted with rhizon sampler. The cumulative value for overall lifetime cancer risk ranged from 5.70 × 10-4 to 4.10 × 10^{-3} with a mean value of 1.09 × 10^{-3}. Hazard quotient (HQ) calculated based on As content in brown rice revealed that the mean HQ was 0.58 (0.27 -0.83) which was below 1. The lowest value of As in rice grain was observed with a conjoint application of phosphate and vermicompost (C2 and P2) in AWD water management. The study demonstrated that Alternate wetting drying along with the application of phosphate and vermicompost at the rate of 30 mg kg^{-1} and 2.5 g kg^{-1} in rice, reduces As uptake by the plant.

Immobilization of heavy metals in aqueous and soil system using functionalized clays and ionic liquids

The present investigation was undertaken to enhance the metal sorption capacity of kaolinite and bentonite clay by inorganic as well as organic functionalization and to determine their metal immobilization potential by batch adsorption and pot culture experiments. The commercial kaolinite (NK) and bentonite (NB) was functionalized with iron sulphate (Fe-B), potassium dihydrogen phosphate (P-K), organic functional groups such as guar gum (GG-B), humic acid (HA-B), dimethyl sulfoxide (DMSO-K) and goethite with humic acid (GHA-K and GHA-B) and mixed with ionic liquids namely 1 Ethyl 3 methyl imidazolium chloride (IL1-B), 1 Ethyl 3 methyl imidazolium bromide (IL2-B) and 1 Hexyl 3 methyl imidazolium chloride (IL3-B). Batch adsorption study was conducted to screen efficient functionalized kaolinite and bentonites modified clays. To evaluate the metal immobilization efficiency of functionalized bentonites, pot culture experiment with Indian Spinach (All-Green) as test crop was conducted with soils from irrigated by tannery effluent (Unnao, UP). The soil was amended with efficient modified bentonites (HA-B, GG-B and IL3-B) and compared with normal bentonite (NB) @ 2.5, 5 and 7.5 g kg^{-1}. Amendment of polluted soil with GG-B, HA-B, IL3-B and NB resulted in enhanced metal sorption capacity. The biomass yield (both fresh and dry) of the crops was improved by the modified bentonites at higher dose of application (7.5 g kg^{-1}). Treatment of soils with higher dose (7.5 g kg^{-1}) of bentonites significantly reduced the DTPA extractable metal content in soil. Significant reduction in extractable metal as well as metal content of crop plants was observed in treatments receiving higher dose (7.5 g kg^{-1}) of GG-B and HA-B. Amended soils showed a significant reduction in bio-concentration factor of metals for the crop indicating that metals are efficiently immobilized in the soils by bentonites. Therefore, Hazard quotient (HQ) of leafy parts of spinach was reduced significantly except normal bentonite amended soil.

Bioremediation of metal and metalloid polluted soils

Metals extraction from contaminated soil through plants is considered as one of the potential remediation options. Hence, an attempt has been made to study the effect of selected organic amendments on solubility of cadmium and lead in contaminated soil. The collected bulk soil from Godwa, Udaipur district was used for green house pot experiment using mustard and sunflower as test crops. The effect of selected organic amendments namely *cluster bean* crop residue, FYM, green manure (*Sesbania)* and metal solubilizing bacteria (*Pseudomonas* sp. *PS2-79*) on solubility of metals and metal removal efficiency of accumulator plants in contaminated soil. Results indicated redistribution of metal from non-labile to labile pool occurred in soil as a resultofapplication of different amendments. Cadmium content in water soluble + exchangeable fraction increased to the extent of 12.9, 21.35, 36.8, 116.6, 66.6 and 73.1% in residue *of cluster bean* (T2), FYM (T3), green manure (*Sesbania)* (T4), metal solubilizing bacteria (T5), residue *of cluster bean* + FYM + metal solubilizing bacteria (T6), and green manure + FYM + metal solubilizing bacteria (T7) treated soil, respectively over control. In sunflower soil, water soluble + exchangeable fraction increased to the extent of 8.54, 18.8, 33.3, 105.9, 63.2 and 66.6% in T2 to T7 treated soil, respectively over control. The corresponding value of Pb was 13.6, 22.7, 68.1, 150, 140.9 and 163.6%, respectively. The arsenic polluted soils of Nadia district of West Bengal, namely Ranaghat, Mitrapur, Nonaghata Uttarpara and Arbetai. Bacterial inoculum A (*Pseudomonas* sp. PS2-72) and bacterial inoculum B (*Pseudomonas* sp. PS2-73) used for arsenic volatilization. Bacterial inoculation of B in soils decreased the total arsenic content in the range of 6.90-8.67% over control at 30 days of incubation. Arsenic content in rice straw was reduced by 14 % and in grain by 23.50% by application of mixed bacterial inoculum A and B over control.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Alapati Nymisha, (21712)	M.Sc.	Synthesis and evaluation of bioaugmented zinc oxide coated urea product for its efficacy under wheat crop	Mr. Kapil A. Chobhe	ICAR-IARI, New Delhi
2.	Jyotirmay Roy, (21713)	M.Sc.	Phosphorus dynamics in an Inceptisol under different land use systems of semi-arid ecologies	Dr. D. R. Biswas	ICAR-IARI, New Delhi
3.	Chakrapani Saikrishna Kishore, (21714)	M.Sc.	Preparation of clay-based composites and beads for dyes remediation	Dr. Indu Chopra	ICAR-IARI, New Delhi
4.	Manish Kumar, (21715)	M.Sc.	Evaluation of POLY4 as a source of potassium and sulphur using basmati rice in an Inceptisol	Dr. Shrila Das	ICAR-IARI, New Delhi
5.	Thungashan Kikon, (21716)	M.Sc.	Preparation and evaluation of phosphorus solubilizing fungus-augmented maize-based biobed for dye remediation and phosphorus solubilization	Dr. Indu Chopra	ICAR-IARI, New Delhi
6.	Deepak, (21743)	M.Sc.	Bio-chemical characterization of crop residues and their effects on carbon mineralization in a typic haplustept	Dr. Abir Dey	ICAR-IARI, New Delhi
7.	Himanshu Singh, (21753)	M.Sc.	Extractability of plant available potassium as influenced by fixation capacity and moisture content of soil	Dr. Mandira Barman	ICAR-IARI, New Delhi
8.	Prathyaksha C S, (50081)	M.Sc.	Interactive effect of phosphorus and zinc fertilization on nutrient uptake by mustard grown in acid soils	Mr. Kapil A. Chobhe	#ICAR-IARI, Assam
9.	Bijan Kumar Mondal, (50082)	M.Sc.	Effects of Seaweed extract-based products on nutrient release, use efficiency and grain quality of wheat grown in an Inceptisol	Dr. Abir Dey	#ICAR-IARI, Assam
10.	Subhajeet Sarkar, (60117)	M.Sc.	Leaching loss of nutrients under different nutrient management options in maize and brinjal grown on an alfisol	Dr. Sushanta Kumar Naik	#ICAR-IARI Jharkhand
11.	Sarmistha Priyadarshini, (60118)	M.Sc.	Aggregation behavior of biochar and its impact on carbon and phosphorus fractions in an acidic Inceptisol under rice-wheat system	Dr. Manoj Chaudhary	#ICAR-IARI Jharkhand
12.	Deep Mohan Mahala, (10673)	Ph.D.	Impact of long-term conservation agriculture on quality and stability of carbon in calcareous soils of eastern Indo-Gangetic plains	Dr M. C. Meena	ICAR-IARI, New Delhi
13.	Avijit Ghosh, (10888)	Ph.D.	Solubilization of soil phosphorus using rice residues and phosphorus solubilizing microorganisms	Dr. D. R. Biswas	ICAR-IARI, New Delhi
14.	Amresh Chaudhary, (10889)	Ph.D.	Assessment of soil health, carbon, nitrogen and phosphorus dynamics in long-term conservation agriculture under rainfed pearl millet-based cropping systems	Dr. M. C. Meena	ICAR-IARI, New Delhi

15.	Rahul Mishra, (11122)	Ph.D.	Risk assessment and mitigation of arsenic contaminated rice soils in Nadia District of West Bengal	Dr. S. P. Datta	ICAR-IARI, New Delhi
16.	Ajin S. Anil, (11338)	Ph.D.	Impact of long-term conservation agriculture practices on soil carbon and phosphorus dynamics under maize based cropping systems in an Inceptisol	Dr. V. K. Sharma	ICAR-IARI, New Delhi
17.	Athulya S, (11339)	Ph.D.	Development of novel phosphatic fertilizer products for enhancing phosphorus use efficiency in maize-wheat cropping system	Dr. Mandira Barman	ICAR-IARI, New Delhi
18.	Naveen Kumar A, (11340)	Ph.D.	Immobilization of heavy metals in aqueous and soil system using functionalized clays and ionic liquids	Dr. K. M. Manjaiah	ICAR-IARI, New Delhi
19.	Ganpat Louhar, (11341)	Ph.D.	Bioremediation of metal and metalloid polluted soils	Dr. M. C. Meena	ICAR-IARI, New Delhi
20.	Ranabir Chakraborty, (11605)	Ph.D.	Effect of residue management practices, nitrification and urease inhibitors on soil microbiota, ammonia and greenhouse gas emissions under rice-wheat and maize-wheat cropping systems	Dr. T. J. Purakayastha	ICAR-IARI, New Delhi
21.	Mohankumar K T, (11610)	Ph.D.	Long-term impact of conservation agriculture on dynamics of carbon, nitrogen, phosphorus and sulphur in soil under maize-wheat-mungbean cropping system	Dr. V. K. Sharma	ICAR-IARI, New Delhi
22.	Subhadip Paul, (11612)	Ph.D.	Assessing potassium supplying capacity and clay mineral alterations under exhaustive cropping in major soil orders	Dr. Mandira Barman	ICAR-IARI, New Delhi
23.	Abhishek Das, (11613)	Ph.D.	Assessing stability of clay-humus complexes and soil organic carbon fractions under long-term conservation agriculture in an Inceptisol	Dr. Nayan Ahmed	ICAR-IARI, New Delhi
24.	Vishwanath, (11616)	Ph.D.	Microbial stability and nutrients dynamics of soil under conservation agriculture in an Inceptisol	Dr. V. K. Sharma	ICAR-IARI, New Delhi
25.	Ann Maria Joseph, (11618)	Ph.D.	Soil organic carbon stabilization in bed planted cotton-wheat system under conservation agriculture in an Inceptisol	Dr. Ranjan Bhattacharyya	ICAR-IARI, New Delhi
26.	Plabani Roy, (11875)	Ph.D.	Influence of emplacing agro-geotextiles on soil organic carbon stabilization and nitrogen sequestration under conservation-tilled maizebased cropping systems in the northwestern himalayas	Dr. Ranjan Bhattacharyya	ICAR-IARI, New Delhi

#IARI off campus

Water Science and Technology

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Prof. Susama Sudhishri

The Water Technology Centre (WTC) is an interdisciplinary facility for research, teaching, training, and extension in agricultural water management. The Centre has evolved into a unique institution, addressing a wide range of issues pertaining to water harvesting, conservation, revival of ponds, water management at farms, large irrigation commands, and watershed scales. It has the mandate to conduct basic and applied research on all aspects of water management in agriculture and develop technologies for water conservation, and improved water management; to participate in the post-graduate teaching programs of IARI for developing human resources and organize training programs for the in-service field and research personnel working in the area of water management in agriculture; to disseminate knowledge developed through appropriate documentation and also to different Government programs like Jal Shakti Abhiyan, Amrit Sarovar, PMKSY etc. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Water Harvesting, Conservation and Performance Assessment

Design optimization of water harvesting structures for their efficient utilization in watersheds, Haryana

India faces a critical water challenge, marked by water scarcity and exacerbated by climate change in regions like Mewat, and Haryana. To address this, the study “Design Optimization of Water Harvesting Structures for Its Efficient Utilization in Watersheds” focused on the Nuh watershed. The objectives included (i) preparing a hydrological zonation map of the Nuh watershed, (ii) evaluating the performance of existing water harvesting structures in the Nuh watershed, (iii) optimizing the WHS under different design and management scenarios, ArcGIS 10.8 maps revealed 11.42% high runoff, 50.43% moderate, and 32.41% low runoff. Evaluation of 335 water bodies showed that 75% were 30-50 years old, with decreasing storage. Water availability ranged from 3.2 Mm 3 in 2005 to 2.7 Mm 3 in 2022, with existing structures contributing 2.8 Mm 3 in 2020. The study emphasizes pond revival, structure optimization, and sustainable water management. Using ArcGIS, a protocol for new water bodies classified 10.7% highly suitable, 47.8% moderate, and 30% low. Among 86 proposed, 49 were highly suitable, 2 were very highly, and 86 were moderately suitable. The Water Evaluation and Planning model found a 21% increase in agricultural demand from 2011 to 2050. To address climate change, optimal pond design, guided by probability analysis, suggested a 103.3 mm one-day rainfall for a 25-year return period. The Untka pond study in Haryana highlighted a strong relationship (R 2 value 0.97) between stage and storage. Using a Linear Programming model for crop planning, the 40:20:40 ratio resulted in a net profit of Rs. 4,29,071 ha/year with a water requirement of 14.03 ha-m. Scaling up pond rejuvenation could yield an annual net profit of Rs. 49,38,01,057/- in Nuh, providing insights for water management and increased returns.

Eco Hydrological analysis of water bodies in NCT of Delhi

Delhi faces water challenges: scarcity, depletion, floods, and pollution. Research aims to fill data gaps for effective management: (i) studying the inventory of water bodies using modern tools and (ii) assessing water availability through an ecohydrological model. Waterbody identification utilized a hybrid method with DEM, Sentinel 2A, ArcGIS, and Google Earth Pro. Thematic maps, incorporating elevation, slope, contour, and LULC, were created in ArcGIS. Rainfall data (1990-2022) sourced from FAO gridded data. Isohyets created via ArcGIS and IDW. Runoff in 2022 was assessed using NRCS-CN methods considering hydrologic soil groups and weighted curve numbers. Groundwater data was obtained from the Central Groundwater Board. The study emphasized runoff and groundwater, excluding canals or rivers. Crop water demands were assessed via the Penman-Monteith equation and CROPWAT software. Domestic and livestock needs were determined using per capita methods from the Indiastat portal. The eco-hydrological model WEAP simulated water supply and demand, identifying 488 water bodies, with 21 drying up post-rainfall. Northwest Delhi had the most, and East Delhi had the fewest water bodies. These bodies covered 1.40% of the geographical area, occupying 2092.12 ha, with 59.3% in built-up areas. Annual rainfall ranged from 505 to 709 mm, and surface runoff varied from 58 mm (Central Delhi) to 621.36 mm (Northwest). The WEAP model indicated a total water availability of 28,641.54 Mm3, a total water demand of 379,236 Mm3, and an unmet demand of 350,594.46 Mm3. As demand surpassed availability, the study recommended reviving water bodies through initiatives like Amrit Sarovar, expanding storage through Jal Shakti Abhiyan, and improving water and crop management via PMKSY programs. The bottom-up approach, supported by modern tools such as Google Engine, ArcGIS, and Google Earth Pro, facilitates efficient information gathering and planning.

Irrigation system performance assessment of Narmada Canal Project in Rajasthan using surface energy balance modelling approaches

The agriculture sector relies heavily on water resources, with 85% allocated to irrigation. Despite the significant contributions of canal irrigation and groundwater in agricultural production, India grapples with water stress. Traditional canal systems, designed for equitable water distribution, show supply-based inefficiencies, emphasizing the need for demand-driven systems in changing climates. One major pre-requisite for this transition is accurate estimation of actual evapotranspiration (ETa). This study assesses the applicability of two satellite-based surface energy balance approaches—EEFlux and SETMI—for ETa flux estimation over the Narmada canal command in arid Rajasthan. Cross-comparison of the estimated ETa fluxes through the single source, EEFlux, and the dual-source, SETMI modeling approaches in terms of the five statistical indices recommended EEFlux as the most suitable approach for the water-scarce area, having limited ground (input) data and computational resources. Using EEFlux, crop water demand was computed for evaluating irrigation supply vs. demand gaps and irrigation performance efficiencies across 70 irrigation units during pre- (2013-14) and post-project (2018-19) periods. The analysis illustrated that though the aeolian undulating lift region of canal command was reported to be associated with the highest rise in crop cover during (2018-19), pre-vs post-project agricultural production (10-fold) and hence agricultural income (16-fold) growth were reported to be the highest for the alluvial – moderately good irrigable croplands of the flow region followed by the “Ned” region of the canal command. Thus Ned” region croplands, reported to be associated with the lowest crop yields and moderate agricultural production and income – -growth (i.e., about 7-fold and 12-fold, respectively) were found to be associated with the highest pre-vs post-project agricultural and economic water productivity growth (i.e., 244% and 4-fold, respectively). The investigation thus clearly revealed the great potential of such satellite-based approaches for assessing catchment scale crop water demand and for benchmarking canal irrigation system performance efficiency.

Drought vulnerability assessment using composite drought index

The present study was carried out to assess drought vulnerability in the Karnataka state of India through a composite drought index (CDI) with socioeconomic indicators. The CDI was computed using the Standardized Precipitation Index (SPI), Standardized Water Level Index (SWI), Standardized Reservoir Level Index (SRLI), Normalized Difference Vegetation Index (NDVI), Vegetation Condition Index (VCI), NDVI Anomaly and Evaporative Stress Index (ESI) along with detrended production anomaly (DPA) for the Kharif season. The CDI was developed employing the regression tree analysis using the Cubist algorithm for the period 2001-2019 at a 1km spatial scale. Out of the total 11 models developed, model M9 with DPA as the dependent and SPI-6, SWI Pre-monsoon, SRLI, NDVI Anomaly, and ESI as independent variables were found to be best with a correlation coefficient of 0.84 and model score of 0.69. On validation, the CDI showed a correlation of 0.85 for declared area under drought (AUD) and 0.86 for number of districts which was stronger than the individual indices SPI-6 and ESI. Further, the socioeconomic parameters such as percentage irrigated area, net sown area, cropped area, milk production, per capita income, number of regional rural banks, and number of below-poverty line cardholders were chosen after a literature survey based on the relation with CDI. These were categorized into components of vulnerability viz. sensitivity (S) and adaptive capacity (AC) and assigned weights using principal component analysis (PCA). The CDI was considered for the exposure (E) component and S and AC were calculated as the weighted averages of their respective indicators. The composite drought vulnerability index (CDVI) was computed by applying simple arithmetic operations on E, S, and AC for the period 2010-2016. The developed CDVI identified vulnerability in the state and is a useful tool for effective monitoring and mapping of drought-vulnerable zones.

Application of soil and water assessment tool in simulating water balance and assessing crop water productivity in the Chittar basin of Thamirabarani river

The present study was conducted to address water management challenges in the Chittar River basin. For the study SWAT model was set up and run for 21 years spanning from 2001 to 2021. Model calibration and validation procedures showed close agreement between simulated and observed discharge, affirming the model's accuracy. Monthly water balance components, exhibited a distinct seasonal pattern influenced by the northeast monsoon. Yearly analysis of water balance components highlighted the presence of inter-annual rainfall variability showing substantial impact on other hydrological system elements. The trend and change point analysis of the Karuppanadhi and Gundar dams in the Chittar River basin identified declining inflow trends during specific seasons (*Rabi* for the Karuppanadhi dam and *Kharif* for the Gundar dam). Analysis of crop water productivity for the major crops such as *Kharif* rice, *Rabi* rice, and sorghum was done on both physical and economic basis. Crop water productivity exhibited ranges from 0.46 to 0.74 kg/m³, 0.51 to 0.89 kg/m³, and 0.74 kg/m³ to 1.31 kg/m³ for *Kharif* rice, *Rabi* rice, and sorghum in the river basin. Net economic water productivity varied from 1.59 Rs/m³ to 4.77 Rs/m³, 1.32 Rs/m³ to 5.76 Rs/m³ and 4.13 Rs/m³ to 11.92 Rs/m³ and gross economic water productivity, showed variation from 4.76 Rs/m³ to 14.30 Rs/m³, 3.97 Rs/m³ to 16.19 Rs/m³ and 12.39 Rs/m³ to 35.73 Rs/m³ for *Kharif* rice, *Rabi* rice, and sorghum respectively. The study also assessed the impact of different ponding water depth scenarios (50 mm, 40 mm, and 30 mm) on *Kharif* and *Rabi* rice cultivation. While reducing irrigation depth led to a decrease in crop yield, it significantly improved crop water productivity and other water productivity metrics. Among the scenarios, scenario 3 having a ponding water depth of 30 mm emerged as the most water-efficient, albeit with lower crop yields.

Theme 2: Marginal Quality Water Use in Agriculture

Impact of Heavy Metals Spiked Wastewater Irrigation on Metal Phytoremediation, Soil Health and Productivity of Gaillardia (*Gaillardia pulchella* Foug.)

The study conducted at the Water Technology Centre, ICAR-IARI New Delhi, aimed to explore the influence of heavy metal-spiked wastewater irrigation on Gaillardia, a flowering plant known for its phytoremediation potential. The investigation focused on the impact of various treatments, each replicated thrice in a randomized design, with escalating concentrations of Cd, Cr, Ni, and Pb. The experiment spanned 2.5 months, evaluating plant growth, soil health, and heavy metal accumulation in both. Results indicated that wastewater irrigation positively affected Gaillardia productivity, with treatments involving heavy metal-spiked wastewater demonstrating higher flower yields. Notably, the quality of Gaillardia flowers remained unaffected by heavy metal-irrigated wastewater. However, soil analysis revealed significantly elevated heavy metal concentrations, particularly in Treatment T-7. The concentrations of Ni, Cr, Cd, and Pb varied across plant parts, showcasing a trend of increasing values from T1 to T7. Gaillardia exhibited remarkable tolerance, with Ni concentrations ranging from 0.94 to 6.11 mg/kg in flowers, 31.17 to 99.90 mg/kg in shoots, and 16.80 to 81.75 mg/kg in roots. Similarly, Cr and Pb concentrations followed increasing patterns across plant parts. While Cd levels remained relatively low, Gaillardia's ability to endure heavy metal-spiked wastewater without compromising productivity underscored its phytoremediation potential. The study implies a potential detrimental effect on soil health due to heavy metal irrigation. Nevertheless, *Gaillardia pulchella* Foug. emerged as a promising candidate for phytoremediation in contaminated environments, showcasing its resilience to heavy metal-spiked wastewater. These findings suggest a nuanced interplay between plant tolerance and soil health in the context of wastewater irrigation enriched with heavy metals.

Impacts of maize residue incorporation on nickel translocation in Ni-spiked wastewater irrigated wheat

In the face of freshwater scarcity, wastewater reuse for irrigation is inevitable in peri-urban agriculture. Long-term usage of untreated or partially treated wastewater leads to a build-up of heavy metals like nickel and poses health hazards. To formulate guidelines and devise a mitigating strategy for irrigation usage of nickel-polluted wastewater, accumulation, and translocation of nickel in soil and plant along with health hazards were estimated in an experiment conducted at ICAR-IARI, Research Farm in *rabi* 2023 by raising wheat on soils irrigated with wastewater containing five levels of Ni @ 0, 2, 5, 10 and 20 mg $l^{-1}$with and without incorporation of maize residue @ 10 Mg ha^{-1}. Grain yields obtained with wastewater irrigation containing 0, 2, and 5 mg l^{-1} of Ni were at par but reduced by 19 and 31% at 10 and 20 Ni mg l^{-1} compared to the yield obtained at 2 mg l^{-1} Ni spiking level. The corresponding decrease in straw yield was 19 and 27%. Wheat yields were not influenced by maize residue incorporation. Graded levels of Ni in wastewater irrigation resulted in a significant decrease in NPK accumulation but a significant increase in Ni accumulation in wheat. Incorporation of maize residue in soil showed a significant reduction of 21-26% in nickel uptake in wheat compared to no residue incorporation. The contents of DTPA extractable Ni were 1.9, 2.3, 3.1, and 4.0 times higher in plots irrigated with 2, 5, 10, and 20 ppm Ni spiked wastewater compared to control in surface 15 cm soil. Soil incorporation of maize residues reduced the DTPA extractable Ni by 31% in the 0-15 cm soil layer. The health hazards like hazard quotient, enrichment, and translocation factor were the minimum in control (0 mg l^{-1}) and increased with an increase in nickel concentration in wastewater irrigation.

Theme 3: Efficient Irrigation Technologies for Enhancing Water and Crop Productivity

Impact of drip fertigation on GHG emission and crop productivity of tomato

Drip irrigation is crucial for successful crop cultivation, addressing global challenges like water scarcity, food security, and poverty. Acknowledged for efficiency, drip systems minimize losses, enhancing irrigation water application efficiency (Vinot et al., 2014). The impact of water management on greenhouse gas (GHG) emissions in different crops is significant. Implementing effective irrigation scheduling reduces over-irrigation, while advanced methods like drip irrigation curb water wastage and GHG discharge. Additionally, skillful fertilizer management plays a role in limiting nitrous oxide emissions resulting from excessive use (Yang et al., 2012). The present study focuses on understanding crop response, GHG emissions (specifically N_2O), and water productivity in drip-fertigated tomato crops subjected to various irrigation and fertilizer treatments. The field experiment conducted at PFDC, Water Technology Centre research field, ICAR-IARI, New Delhi during the rabi season of 2022-2023, aimed to assess the crop response and N_2O emissions under different fertilizer and irrigation levels. Three irrigation levels with 100% ETc, Drip with 80% ETc, and surface irrigation flooding along with three fertilizer doses-100% RDF, 80% RDF, and no fertilizer were tested, each replicated three times. CROPWAT 8.0 monitored irrigation scheduling, while nitrous oxide emissions were analyzed using gas chromatography. Results indicated that treatment T_2-100% ETc x 100% RDF exhibited the highest yield increase (46.42 t/ha), closely followed by T_5-80% ETc x 100% RDF with a non-significant difference of only 2.5%. T_5 also demonstrated 21% higher irrigation water productivity and 22% better economic water productivity compared to T_2, despite using less water. Surface irrigation resulted in higher nitrous oxide emissions compared to drip irrigation, emphasizing the environmental benefits of efficient water and fertilizer management. Notably, the study suggests that maintaining yields in 80% ETc is achievable with reduced GHG emissions, offering a sustainable approach to crop cultivation.

Soil matric potential-based irrigation scheduling in drip fertigated Pakchoi (*Brassica rapa* subsp. chinensis L.) crop

In the Rabi season of 2022-2023, a field experiment at the Water Technology Centre, Indian Agricultural Research Institute, New Delhi, focused on Pusa Pakchoi-1. The study aimed to assess soil matric potential and water requirements under drip fertigation. Four matric potential thresholds (-10kPa, -20kPa, -30kPa, -40kPa) were combined with varying fertigation rates (100%, 75%, and 50% of recommended dose). Digital tensiometers monitored soil moisture, triggering irrigation when matric potential exceeded limits. Results revealed significant effects on Pakchoi growth and yield. Irrigation frequency ranked I1 (-10kPa) > I2 (-20kPa) > I3 (-30kPa) > I4 (-40kPa). Tensiometer-controlled fertigation consistently reduced water usage (95.6mm to 104.8mm). Irrigation depth increased with lower matric potential, from 6.24mm (-10kPa) to 12.49mm (-40kPa). Water use efficiency followed a similar pattern, peaking at -20kPa. Surprisingly, max irrigation at -10kPa didn't yield the highest crops, possibly due to excess moisture hindering aeration and nutrient leaching. Optimal parameters (plant height 28.2cm, leaf count 19, leaf weight 30.1cm, plant weight 550.2g, yield 55.2t/ha) resulted from -20kPa matric potential and 100% fertilization, enhancing aeration and nutrient distribution. In conclusion, digital tensiometer-driven irrigation improves water efficiency in Pakchoi under drip irrigation, emphasizing precise management's importance and highlighting matric potential and fertilization impact on growth and yield. This study underscores the potential of precise irrigation strategies to enhance water efficiency in Pakchoi cultivation under drip irrigation.

Modeling Soil Water and Nutrient Dynamics under Drip Irrigation in Broccoli (*Brassica oleracea* L. var. *italica* Planck)

An effort was made to estimate broccoli crop evapotranspiration, develop region-specific crop coefficients using a weighing-type field lysimeter, study the response of broccoli to varying irrigation and nitrogen levels, and simulate soil moisture, nitrogen dynamics, and broccoli yield. The field experiment was conducted for the broccoli (*Brassica oleracea L. var. italica Planck*) cultivar Palam Samridhi at the research farm, WTC, ICAR-IARI, New Delhi, India during *rabi* seasons in 2016-17 and 2017-18. Three irrigation levels *viz.,* full irrigation (100 % of field capacity (FC) (I_1), 75 % of FC (I_2), and 50 % of FC (I_3) and four nitrogen levels viz., 50 % of the recommended dose of nitrogen (RDF) (N_1), 75 % RDF (N_2), 100 % RDF (N_3), and 125 % RDF (N_4) were used. It was observed that the single crop coefficient (K_c) for broccoli during *rabi* 2016-17 was 0.68, 0.84, 1.04, and 0.94, for initial, development, mid-season, and late season stages, respectively. In the dual crop coefficient approach, the value of basal crop coefficient (K_{cb}) was 0.30, 0.66, 0.97, and 0.84 and the soil evaporation coefficient (K_e) was 0.42, 0.23, 0.18, and 0.23 for initial, development, mid-season and late season stages, respectively. The study revealed that all the crop growth and yield attributes were found to be best under the I_1N_4 treatment. The water use efficiency was found best in I_2N_4 treatment. Predicted soil moisture was in agreement with the observed soil moisture content and a high coefficient of determination (R^2) was found for 0-15 cm depth near/at the emitter (0.84 to 0.90). The maximum and minimum prediction errors in yield simulation were observed in I_3N_3 (9.55%) and I_1N_1 (1.33%) treatments, while for biomass, the errors occurred in I_3N_4 (8.27%) and I_2N_1 (1.52%) treatments, respectively.

Irrigation water security index for District Bahraich, Uttar Pradesh, India

Bahraich, an aspirational district of Uttar Pradesh faces significant challenges such as uneven water resource distribution, inefficient irrigation methods, over-dependence on groundwater, frequent floods and droughts, and limited access to information and resources. In the light of above problems, a study was conducted for 2018-22 with objectives 1) To assess crop water footprint of major crops, 2) To assess the water availability, quality, productivity, disaster, and water governance parameters of the study area 3) To develop irrigation water security index for the district Bahraich. Crop water footprint (CWF) consists of green, blue, and grey water. Green CWF (CWFg) for all crops of kharif was found to be higher compared to rabi crops, whereas blue CWF (CWFb) for rabi season was found to be higher compared to kharif except for potato and sugarcane. However, nitrogen was selected as the only source of pollutants to bring polluted water at the natural concentration level i.e., grey CWF (CWFgrey). For the estimation of total available water resources, groundwater resource was estimated using water level fluctuation (WLF), runoff using GIS coupled with curve number, and canal water volume using equivalent length factor (ELF) methods. This study revealed that the contribution of groundwater was more than 52.5%, whereas runoff (45.61%) and canal water (1.89%). A blockwise irrigation water security index (IWSI) with five criteria and many sub-criteria was created using multiple criteria decision analysis (MCDA) and the normalizing technique. Mihipurwa, Mahsi, and Nawabganj are identified as 'high-security' blocks in terms of water security, with governance and management achieving the intended results. Fakherpur and Jarwal are considered 'low-security', with management and governance needing improvement. Tejwapur, Payagpur, Risia, Huzoorpur, Shivpur, Chittaura, Kaisarganj, Balha, and Bisheswarganj are classified as 'medium-security', with governance and management instruments in place but not yet yielding desired results. Neither block qualified for the 'very high or very low' rank of IWSI. This will help the authority to prioritize resources for efficient management of water resources and achieve water security.

Water and nutrient dynamics in drip fertigated maize-wheat-moong bean system

Enhancing irrigation and nutrient use efficiency using drip fertigation is accentuated to address the rising water scarcity and escalating fertilizer prices. Impacts of surface drip (SDI) and subsurface drip (SSDI) with two levels of irrigation schedules (0.6 and 0.8 etc) and four fertilizer levels (0, 60, 80, and 100% recommended doses of NPK fertilizers) were assessed on water-saving, crop and water productivity, water and nutrient dynamics, nutrient use efficiency, energy and monetary benefits of wheat-moong bean-maize (WMbM) system in a field study carried out for two years at Indian Agricultural Research Institute farm. The results were compared with the conventional local practice of surface flood irrigation and soil application of recommended fertilizer doses. The irrigation water applied in WMbM through drip at 0.8 ET_c (336-274 mm) was 44 and 58% lower compared to conventional surface irrigation (600-660 mm) in the 2019-20 and 2020-21 seasons, respectively. Compared to fertilizer control (NPK_0), fertigation doses of 60 (NPK_{60}), 80 (NPK_{80}), and 100% (NPK_{100}) RDF resulted in significant yield gain of 36, 55 and 67% in wheat; 25, 31 and 34% in moong bean, 33, 49 and 62% in maize and 32, 51 and 58% system wheat equivalent yields, respectively. The system crop water productivity was also enhanced from 1.18 kg m^{-3} in the control plot (no NPK). The agronomic efficiency of N, P, and K in maize was 1.26, 1.00, and 1.26 times higher than that of wheat and 2.21, 11.03, and 13.8 times higher than found in moongbean. The energy efficiency indicators were in the order of maize>wheat>moongbean. The fertigation doses of NPK_{80} or NPK_{100} applied at 0.8 ET_c through subsurface drip fertigation resulted in higher crop productivity, water productivity, net income, better discounted BCR, and lower payback period showing it more profitable compared to surface irrigation (conventional method) in maize-wheat-moongbean system.

Simulating water productivity of purple broccoli under different water regimes and nitrogen levels using the AquaCrop model

A two-year experiment at PFDC, Water Technology Centre, IARI, New Delhi, assessed the impact of irrigation and nitrogen (N) on broccoli. The split-split plot design included drip (DR) and furrow irrigation (FU) as main factors, full irrigation (100% ETC) and limited irrigation (75% ETC) as sub-factors, and three nitrogen doses (N) of 125%, 100%, and 75% of the RDN as sub-sub-factors, replicated thrice. DRI1F2 treatment recorded significantly the highest yield (29.23 t ha-1 and 29.95 t ha-1) for two years. DRI2F1 showed the highest water use efficiency (WUE) (266.81 and 284.78 kg ha-1 mm-1) and irrigation water productivity (IWP) (30.62 and 143.26 kg/m3). DRI1F3 had the highest Nitrogen Partial Factor Productivity (NPFP) (457.96 and 466.61). The AquaCrop model demonstrated good accuracy (R2 values: 0.91 for yield, 0.89 for biomass, 0.86 for water productivity). Calibration and validation indices were satisfactory, with r values of 0.94 and 0.91 for yield, KGE values of 0.90 and 0.91, and MBE values of 0.72 and 0.80. A water-yield production function with a second-degree polynomial relationship, exhibiting significantly higher R2 values, was identified. DRI2F2 treatment recorded significantly higher net income (₹4,43,668 & ₹5,63,358 ha-1) and a B: C ratio of 3.7 and 4.5 for both years, indicating economic viability. DRI1F2 treatment proved most effective in yield, while DRI2F1 demonstrated superior WUE and IWP. The AquaCrop model's accurate predictions and the establishment of a water-yield production function contribute to optimizing broccoli cultivation practices, with DRI2F2 treatment emerging as economically viable.

Development of filter for drip nutrition with biogas digestate

India's abundant indigenous bioenergy resources, such as biomass and biogas, produce valuable by-products like nutrient-rich biogas slurry (1.5% N, 1.1% P, 1% K). Conventional land-spreading methods pose environmental concerns, but nutrigation through drip irrigation emerges as a solution for precise nutrient application, minimizing nitrogen losses and environmental impact. To address these issues the present study was focused on the development of a filter for drip nutrigation with biogas digestate with the objectives (i) characterization of biogas slurry and development of its protocol for its use in drip nutrigation (ii) designing the filter for biogas digestate fed drip system to reduce clogging and (iii) Techno-economic evaluation of filtration system in a drip outrighted vegetable crop. The study characterized biogas slurry, noting spatial and temporal variations in macro-nutrients, with nitrogen levels varying by over 3-6% pre- and post-monsoon. Positive correlations existed between nitrogen content and phosphorous, organic carbon, pH, and electrical conductivity. A settling behavior protocol indicated that higher solid concentrations slowed particle settling (average size: 2.07 mm). In filter design, a lab study determined optimal filtration layers (3:1:1.5 P: G:S) with a dilution ratio of 1:2. The cascade filter showed superior performance with 61.8% slurry storage, 5.1 L m^2 h^{-1} filtration rate, 79.4% effluent efficiency, and reductions in turbidity (198 NTU) and total solids (51.2 g/L). Incorporating biogas slurry into drip irrigation enhanced spinach growth, reducing synthetic nitrogen needs. Combining biogas slurry nutrigation (BSN) with 80% RDF yielded 5.52 tons/ha, comparable to 100% RDF. BSN promoted balanced enzymatic soil profiles, contributing to improved agricultural outcomes. The filter system's clogging ratio ranged from 6.91% to 29.11%, with an acceptable CV for all parameters, making it economically viable with a payback period of 1.33 years and a benefit-cost ratio of 2.29. Biogas slurry nutrigation holds promise for sustainable agriculture, aligning with closed-loop economy principles and sustainable development goals.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	M. Keerthana Maveril (21726)	M.Sc.	Impact of drip fertigation on GHG emission and crop productivity of tomato	Dr. Manoj Khanna	ICAR-IARI, New Delhi
2.	Vishal Sangwan (21727)	M.Sc.	Impact of heavy metals spiked wastewater irrigation on metal phytoremediation, soil health, and productivity of Gaillardia (*Gaillardia pulchella* Foug.)	Dr. D. S. Gurjar	ICAR-IARI, New Delhi
3.	S. Naveen Kumar (21728)	M.Sc.	Impacts of maize residue incorporation on nickel translocation in Ni-spiked wastewater irrigated wheat	Dr. Khajanchi Lal	ICAR-IARI, New Delhi
4.	Krishna Patidar (21729)	M.Sc.	Soil matric potential-based irrigation scheduling in drip fertigated Pakchoi (*Brassica rapa* subsp. chinensis L.) crop	Dr. Manoj Khanna	ICAR-IARI, New Delhi
5.	Pavan Prabhakar Panzade (21744)	M.Sc.	Eco Hydrological analysis of water bodies in NCT of Delhi	Dr. Susama Sudhishri	ICAR-IARI, New Delhi
6.	Jitendra Rajput (10708)	Ph.D.	Modeling soil water and nutrient dynamics under drip irrigation in broccoli (*Brassica oleracea* L. var. italica Planck)	Dr. Man Singh	ICAR-IARI, New Delhi
7.	Richa Pandey (10914)	Ph.D.	Irrigation system performance assessment of Narmada Canal project in Rajasthan using surface energy balance modelling approaches	Dr. Ravinder Kaur	ICAR-IARI, New Delhi
8.	Shiv Shanker Chaudhari (11139)	Ph.D.	Irrigation water security index for district Bahraich, Uttar Pradesh, India	Dr. Susama Sudhishri	ICAR-IARI, New Delhi

9.	Neha Singhal (11357)	Ph.D.	Drought vulnerability assessment using composite drought index	Dr. Manoj Khanna	ICAR-IARI, New Delhi
10.	Smita Jaiswal (11360)	Ph.D.	Design optimization of water harvesting structures for their efficient utilization in watersheds, Haryana	Dr. Susama Sudhishri	ICAR-IARI, New Delhi
11.	Arockia Anusty J (11635)	Ph.D.	Application of soil and water assessment tool in simulating water balance and assessing crop water productivity in the Chittar basin of Thamirabarani river	Dr. Man Singh	ICAR-IARI, New Delhi
12.	Diana Dhayal (11636)	Ph.D.	Water and nutrient dynamics in drip fertigated maize-wheat-moong bean system”	Dr. Khajanchi Lal	ICAR-IARI, New Delhi
13.	B. Kiruthiga (11638)	Ph.D.	Simulating water productivity of purple broccoli under different water regimes and nitrogen levels using the Aqua Crop model	Dr. Man Singh	ICAR-IARI, New Delhi
14.	Rashmi Yadav (11641)	Ph.D.	Development of filter for drip nutrigation with biogas digestate	Dr. Susama Sudhishri	ICAR-IARI, New Delhi

Session IV: School of Basic Sciences

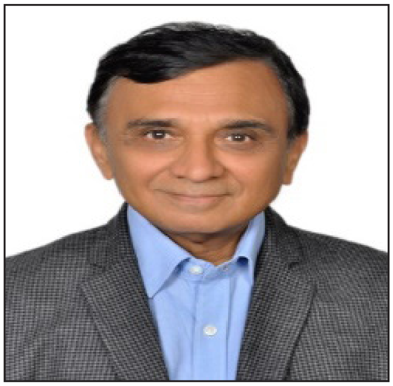
Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Biochemistry	03	08
Molecular Biology and Biotechnology	20	10
Plant Physiology	09	11
Total	**32**	**29**

SCHOOL OF BASIC SCIENCES

Convenor: Dr. Monika A. Joshi, Professor, Division of Seed Science & Technology
Co-convenor: Dr. Shruti Sethi, Principal Scientist, Division of Food Science & Post harvest Technology

Chairperson: Dr. Anil Grover, Senior Professor, Department of Plant Molecular Biology, University of Delhi (South Campus)



Dr. Grover is currently INSA Senior Scientist, Department of Plant Molecular Biology, University of Delhi South Campus. He completed his B.Sc. (Hons.) and M.Sc. (Botany) from Delhi University in 1977 and 1979; respectively. In 1984, he did his PhD in Plant Physiology from ICAR- IARI, New Delhi. He has also served as Head, Department of Plant Molecular Biology, University of Delhi South Campus (2007-2010; 2019-2022). Dr Grover is a Fellow of various societies viz. Indian Academy of Sciences, Bangalore; Indian National Science Academy, New Delhi; National Academy of Agricultural Sciences, New Delhi and National Academy of Sciences, Allahabad. He has been conferred with numerous awards; notable among them being Sir J.C. Bose National Fellow, Department of Science and Technology, Govt. of India; National Bioscience award, Department of Biotechnology (DBT), Government of India; B.M. Birla Science Prize in Biology, B.M. Birla Science Centre, India; Indian National Science Academy Young Scientist Medal, New Delhi and many more. Dr Grover has taught Advanced Plant Molecular Biology and Biotechnology to M.Sc. Plant Molecular students for 34 years. He has a vast research experience of 39 years post Ph.D.; and has supervised 19 Ph.D. thesis; published nearly 140 research papers including original research papers, reviews and book chapters in various International and National journals.

Biochemistry

15

Prof. Anil Dahuja

The mandate of the Division of Biochemistry is to undertake fundamental and applied biochemical, molecular biological and nutritional research related to the current problems in the field of agriculture and to conduct teaching and training programmes to develop skilled human resource in the area of plant biochemistry and molecular biology. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Evaluation and Enhancement of the Nutrition, Functionality, Bioavailability and Processability of Nutritive/Bioactive Components of Food Crops

Formulation and validation of oil blends for enhanced nutritional quality and stability

Blending two or more oils is an effective and economical method to get optimized fatty acid composition and physicochemical properties. In this study, the blending ratio for rice bran oil and algal oil was optimized to get superior physicochemical characteristics and omega-3 fatty acid content. Microalgal cultures producing EPA and DHA were selected, blending ratios of RBO and algal oil were optimized for improved nutritional quality and stability followed by *in-vivo* validation of health benefits of the oil blend. Among the seven microalgal cultures *viz.Chlorella minutissima, Chlorella sorokiniana, Haematococcus* sp., *Coelastrella* sp., *Nannochloropsis* sp., *Dunaliella* sp., and *Spirulina platensis,* EPA and DHA were detected in *Nannochloropsis* sp. and *Spirulina platensis* (0.46 % and 0.50%, respectively). The algal oils *viz.* oil extracted from *Nannochloropsis* sp. (NAO) and *Spirulina platensis* (SPO) and purified algal oil from *Schizochytrium* sp (SCO) were used for blending with RBO. Binary oil blends (RBO: SCO, RBO: NAO, RBO: SPO) were formed in six ratios *viz.* 90:10, 85:15, 80:20, 75:25, 70:30, and 65:35 and ternary oil blends (RBO: NAO: SPO) were formed in four ratios *viz.* 80:10:10, 80:05:15, 70:10:20 and 65:10:25. Among the formulated oil blends, RBO: SCO (80:20) was found superior as it had the lowest peroxide value (2.5 meq O_2/kg), acid value (4.2 mg KOH/g), iodine value (118 g/100g) and a significant amount of total tocopherol (426 mg/kg) and total oryzanol (1.19 %). SFA: MUFA: PUFA (saturated: monounsaturated: polyunsaturated fatty acid) was 1.09: 1: 1.29 which is very near to the ideal fatty acid composition (1:1.5:1) as given by WHO. The total omega-3 fatty acids content was 20.71% compared to 0.79 % in RBO. The hypocholesterolemic, hepatoprotective and non-allergic properties of RBO: SCO (80:20) were validated in the hypercholesterolemic rats. This revealed that the formulated oil blends have promising applications in the fields of neutraceuticals, oil industry, feed and food industry.

Enhancing the nutritional quality, sensory properties, and bioavailability of soy-isoflavones in soymilk using probiotic fermentation approach

Soy foods, considered exemplary delivery vehicles for probiotics, have enormous potential to improve the nutritional characteristics of the diet. The principle of our study is to implement a detailed *in vitro* comparison between the physico-biochemical characteristics of probiotic *Lactobacillus* and novel probiotic *Weissella* strains for their efficiency in enhancing the nutraceutical potential of fermented soymilk. The study indicates an increase in total antioxidant activity, a reduction in phytic acid and increased free mineral content for both iron and zinc. Moreover, isoflavone glucoside hydrolysis into aglycones, a reduction in hexanal and an increase in the viable count of bacteria was observed. The novel *Weissella* isolates performed in a fashion similar to well-established *Lactobacillus* type strains. Two strains identified in each group, i.e., *Lacticaseibacillus rhamnosus* JCM1136 and *Weissella confusa* 30082b were used for mixed fermentation and examined for their possible techno-functional features. We have also implemented a detailed comparison between the synbiotic effect of Fructooligosaccharides (FOS) and Raffinose Oligosaccharides (RFOs) on the viable count of bacteria, hydrolysis into monosaccharides for the biosynthesis of postbiotic Short Chain Fatty Acids and sensory attributes of soymilk fermented with 1% (v/v) mixed cultures of *Lacticaseibacillus rhamnosus* JCM 1136 and *Weissella confusa* 30082b. Synbiotic soymilk with 3% RFOs showed a 99-fold increase in methyl propionate, while the one supplemented with 3% FOS showed an increase in methyl butyrate which can promote cancer cell apoptosis. The highest acceptability was for soymilk fermented with 2% RFOs + 2% FOS + 2% table sugar + 1% vanillin (7.87 ± 0.52) with high mouth feel, product consistency, taste, and flavour. Overall, our study demonstrates that the dietary combination of soy with probiotics and prebiotics seems to increase the synergistic interaction between probiotic bacteria and soy-components, which resulted in the up-gradation of nutritional quality rather than being solely attributable to individual components.

Characterization of hulless barley grains and fractions for nutritionally relevant traits for food purpose

Hulless barley *(Hordeum vulgare L.)* is gaining attention for its potential in food applications due to its elevated levels soluble dietary fibre *β*-glucan, and polyphenolic compounds. *β*-glucan has been proved in reducing the blood cholesterol levels, controlling sugar levels and also as a prebiotic in reducing the risk of colon cancer. This study evaluated 52 hulless barley genotypes for nutritionally relevant traits. Around two-fold variability was observed for all the traits except protein content. The range observed for starch content, amylose content, protein content, *β*-glucan content, DPPH radical scavenging activity, Ferric reducing antioxidant power, total phenolic content, iron content, zinc content and phytic acid content were in the range of 49.5-77.0%, 19.3-27.9% 12.3-18.6%, 3.1-7.2% 26.3-59.4%, 6.4-14.0 mmol/g. 0.66-1.77 mgGAE/g, 32.7-70.2 ppm, 26.3-49.3 ppm and 0.68-1.16%, respectively. The genotypes were classified into low, medium, and high categories, marks were given to different categories and a total score was calculated for each genotype. DWRNB17 had highest score of 22 followed by DWRB18, DWRFB40, INBON-HI-(2015)-19, INBON-HI-(2016)-11 and INBON-HI-(2015)-78 with a score of 21. All these genotypes have better combination of nutritional traits and can be promoted for food uses. Moreover, genotypes with highest values for each trait were also identified which can be used as donors for food barley improvement programmes. The study extended to employ dry fractionation techniques including milling followed by sieving. Three different milling techniques *viz*. roller, cyclone and stone milling were used to prepare different types of flours which were subjected to fractionation using BSS sieves (44-170 mesh size). The coarse grain fractions showed around two-fold increase in beta-glucan, total phenolic content, and antioxidant activity. These fractions can be further characterized for functional properties. These enriched hulless barley fractions align with consumer demands for natural, economical, and sustainable sources of health-promoting traits, meeting the rising interest in healthier foods.

Isolation, structural characterization and hypoglycemic effects of functional polysaccharides from Shiitake (*Lentinula edodes*)

Niche crops are our unique heritage and GoI emphasizes the 'One District One Product (ODOP)' initiative to promote fostering balanced regional development across the country. Medicinal mushrooms have received the attention of international communities for their nutraceutical potential benefitting type II Diabetes Mellitus (TIIDM). Among the components owing therapeutic value in mushrooms, lentinans (LNTs) which are β-glucans are the most important. LNT has a β-(1–3)-glucose backbone with two β-(1–6)- glucose branches of five glucose units each. As the promising role of β-glucan to lower hyperglycemia has been validated, mushrooms hold the idea of a future free from diabetes if in-depth characterized. But Indian Shiitake genotypes have not yet been screened for LNT nor validated for their anti-diabetic potential. Understanding the complex structure (single, double, or triple helical) contributes to the ultimate functionality. A study was conducted to optimize the extraction of LNTs and screened 12 indigenous Shiitake mushroom strains collected and maintained at ICAR-NEH Manipur. Among the extraction methods selected for optimization, acid-alkali-based method was suitable. Single helical and triple helical LNTs were estimated using exoglycanase and Congo Red (CR) methods respectively. A maximum LNT content of 47% (37% triple helical and 9% single helical) was obtained in DMRO-623. Further purification was carried out through de-proteination (by dialysis) and polysaccharide grading (Chromatography) prior to characterization. The biophysical characterization to confirm the unique fingerprint of LNT was carried out using Fourier transform infrared spectroscopy (FT-IR), MALDI-MS, XRD, C13 and ^{1}H NMR. Further *in vitro* anti-diabetic assay of the purified extracts validated an inhibition percentage of 25%. This study characterized LNT from Indian Shiitake and validated its anti-diabetic potential for the first time. Future research should focus on science-based evidence of LNT to support our immune system, especially on food product like whole Shiitake mushrooms or food supplemented with isolated lentinan.

Developing biochemical intervention(s) for enhancing the bio-accessibility of lutein and provitamin A carotenoids in carrot chips

Carrot chips, a popular snack, can be enhanced in nutritional value through the optimization of processing parameters and pre-treatments. This study aimed to enhance the nutritional value of carrot chips through optimized processing parameters and pre-treatments, focusing on improving the stability and bio-accessibility of lutein and provitamin A carotenoids. Carrot genotypes were screened for chip production based on amounts of provitamin A carotenoids and lutein, total phenolics, total carbohydrates, reducing sugars, antioxidant potential, and dry matter content. Nantes exhibited the highest carotenoid content (251 mg/100 g CP), with beta-carotene reaching 164 mg/100 g CP. Air frying (AF) at 120°C for 30 minutes and deep-fat frying (DF) at 160°C for 15 minutes showed the highest carotenoid retention. Various pre-treatments, including potassium metabisulphite (KMS), fructose, and citric acid (CA), were tested to improve carotenoid retention. AF-KMS displayed the highest carotenoids retention (156.7 mg/100g). Vacuum frying (VF) consistently retained the most carotenoids, with VF-KMS at 238 mg/100g. Antioxidant potential was highest in VF-KMS (56.3% DPPH inhibition). Vacuum-fried chips were the crispiest, with VF-Fructose having the least breaking force (959g). VF-KMS exhibited the highest bioaccessibility (77.3%). TBARS values for vacuum frying were the lowest (0.57µM/g). Sensory analysis favored VF-KMS, indicating superior consumer acceptability. Volatile compound analysis highlighted distinctive profiles for VF-0.2%KMS and IR-0.2%KMS, with propanoic acid ethyl ester and pent-4-enal contributing to VF-0.2%KMS aroma. Overall, pre-treatment and frying methods significantly influenced carotenoid retention, antioxidant potential, sensory attributes, and volatile compound profiles in carrot chips. Vacuum frying with KMS pre-treatment emerged as the most effective approach, providing valuable insights for optimizing the nutritional and sensory attributes of carrot chips and contributing to the development of healthier and more appealing snack options.

Unravelling the nutritional diversity contributing towards starch quality and its physico-chemical traits during ageing of rice (*Oryza sativa* L.)

Ageing is a complex and useful method of post-harvest improvement in rice grain quality. This study provides an optimum period of rice ageing based on the dynamics of nutritional, cooking, sensory properties of basmati (PB-1121, PB-1509) and non-basmati (BPT-5204, Swarna) rice. No significant differences in starch, protein, and lipid contents were observed, but amylose content (AC) and resistant starch (RS) showed an increasing trend during ageing. Hardness and stickiness showed a negative correlation with R^2 of -0.73, -0.74, -0.71 and -0.54 for PB-1121, PB-1509, BPT-5204 and Swarna respectively. *In vitro* digestibility revealed 30% reduction in rapidly digestible starch (RDS) and 60% increase in slowly digestible starch (SDS) during ageing process. Fatty acid profiling revealed palmitic and linoleic acids as the most dominant fatty acids, while myristic and stearic acids were found at the lower levels. Amino acid profiling revealed increased concentrations of essential amino acids such as Thr, Met, Phe, His and Lys and semi essential amino acid Arg during ageing. Analysis of matrix components (Starch, lipid and protein) revealed that starch and protein interaction was prominent after 12 months of storage, while starch and lipid interaction was noticeable after 18 months of storage. Free thiol content in basmati and non-basmati varieties were reduced at the maximum by 0.45 fold and 0.5 fold respectively after 24 months of storage. The evaluation of sensory parameters by human panelist showed that 12-18 months of storage had good overall acceptability score ~8 and above. 12-18 months aged basmati rice is recommended for rice eaters and 18-24 months aged non-basmati rice for food industries. The indicators identified through this study may be useful in determining the age of rice and finding will also help in understanding the mechanism of rice ageing to mimic accelerated process of rice ageing with reduced time span and cost.

Deciphering physio-biochemical and molecular mechanisms involved in enhanced drought tolerance and nutritive value of rice through seed-priming

Drought is a major limiting factor for rice (*Oryza sativa* L.) production globally and a cost-effective seed priming technique using bio elicitors have found to have stress mitigating effects. Till the date, mostly phytohormones have been preferred as bio elicitors but the present study is a novel attempt to demonstrate the favorable role of micronutrients-phytohormone (iron; I, zinc; Z, methyl jasmonate; MJ) and their cocktail via seed priming method in mitigating the deleterious effects of drought stress and enhancement of grain quality through physio-biochemical and molecular manifestations. The expressions of drought-responsive genes *OsZn-SOD*, *OsFe-SOD*, and *Nox1* were found modulated under drought stress in contrasting rice genotypes -N-22 (Nagina-22, drought tolerant) and PS-5 (Pusa Sugandh-5, drought sensitive). A progressive rise in carotenoids (10-19 %), ABA (18-50 %), proline (60-80%), activities of SOD (27-62%), APX (46-61%), CAT (50-80%), Nox (16-30 %), and upregulated (0.9-1.6 fold) expressions of *OsZn-SOD*, *OsFe-SOD*, and *Nox1* genes were found in the plants raised from treated seeds under drought condition. Enzyme activity assays revealed that pullulanase enzyme (Pull) increased significantly with priming and was found highest in MJIZ primed samples. Stach synthase (SS) and Branching enzyme (BE) activity increased significantly in both genotypes with priming compared to unprimed controls. Gene expression analyses revealed upregulation of *SS-I*, *SS-IIa*, and *Pull-2* genes in primed samples, indicating enhanced starch biosynthesis. Scanning electron microscopy (SEM) based starch granule morphology revealed differences in shape, size, and packing across the treatments and genotypes. Priming, especially MJIZ, led to larger granules and modified endosperm cell structure. Thus, the findings of this study illuminate how plants, when subjected to stress, initiate a complex cascade of biomolecular mechanisms. These mechanisms are triggered by the seed priming process, ultimately equipping the plant with the capacity to adapt to and thrive under stressful conditions.

Theme 2: Biochemical and Molecular Characterization of Food Crops for Enhanced Yield, Nutrition, Nutrient Use Efficiency and Abiotic Stress Tolerance

Deciphering miRNome modulation at reproductive stage drought in rice genotypes

Drought tolerance is a complex/multigenic trait controlled by a network of genes, which is fine-tuned by subtle coding/non-coding regulatory mechanisms to mitigate the deleterious effects of drought stress. Reproductive stage drought stress occurs at panicle initiation stage which results in reduced seed-set/grain filling, deteriorated grain quality, and lower yield. MicroRNAs (miRNAs) are one of the non-coding regulators that control gene expression at post-transcriptional level by suppressing the translation process or cleaving the mRNA. Thus, to identify the reproductive stage drought-responsive novel as well as known miRNAs in contrasting rice genotypes, comparative miRNome and transcriptome analyses were performed. SmallRNA libraries for panicle and root tissues of drought-tolerant [Nagina 22 (N-22)] and -sensitive (IR-64) rice genotypes grown under control and reproductive stage drought stress were sequenced using Illumina SE50 bp chemistry. A total of 128 known and 121 novel miRNAs expressed in panicle, while 270 known and 91 novel miRNAs expressed in root of contrasting rice genotypes were identified as differentially expressed miRNAs. Significant alterations in expression level as well as the number of known and novel miRNAs were observed in drought-tolerant (N-22) genotype compared to that in the drought-sensitive (IR-64) genotype. The target of novel miRNA included 409 and 237 genes in panicle and root tissues, respectively, with majority of them belonging to drought-responsive transcription factors involved in metabolic/developmental processes, photosynthesis, panicle and grain development, phytohormonal-crosstalk, root system development via auxin signaling. Validation of the differentially expressed miRNAs as well as their target genes, performed using an independent set of samples, confirmed their expression pattern. Based on the gathered information, the functions of miRNAs in controlling gene expression at reproductive stage drought in rice has been proposed, which might be useful in the genetic manipulation of rice towards the development of climate-smart crops for sustainable food production.

Molecular and biochemical characterization of rice for phosphorus use efficiency

Phosphorus (P) deficiency poses a significant challenge to rice production, necessitating a thorough understanding of the molecular mechanisms underlying low P tolerance. The Pup1 QTL has been identified as a crucial contributor to P starvation tolerance in rice genotypes; however, its molecular mechanism remains elusive. In this study, we investigated the physiological, biochemical, epigenetic, transcriptional, and proteomic changes in response to P starvation stress in two contrasting rice genotypes: Pusa-44 and NIL-23, which contains the Pup1 QTL. Whole-genome bisulfite sequencing unveiled a notable increase in cytosine methylation levels, particularly under stress conditions. Hypomethylation in the CHH context correlated with the upregulation of numerous genes in both shoot and root tissues. We also identified key genes associated with DNA methylation, demethylation, and RNA-directed DNA methylation that were upregulated in the roots under stress. Conversely, hypermethylation in gene bodies influenced the expression of transcription factors, P transporters, phosphoesterases, retrotransposon proteins, and other proteins. Global transcriptome analysis revealed extensive transcriptional reprogramming, involving transcription factors, signaling pathways, and regulatory genes. Notably, the roots of NIL-23 exhibited significant upregulation of genes under P starvation stress, indicating their contribution to P starvation tolerance. Furthermore, comparative proteome profiling of shoot and root tissues identified differentially expressed proteins associated with photosynthesis, carbohydrate metabolism, energy production, transcription factors, and phytohormone signaling under P starvation stress. Thus, the study emphasized the significant role of post-transcriptional regulation mediated by the Pup1 QTL as a mechanism in response to P starvation stress. Overall, this integrated omics study, coupled with physio-biochemical investigations, provides valuable insights into the molecular aspects of Pup1 QTL-mediated P starvation responses in rice. The findings underscore the importance of epigenetic DNA modification, gene regulation, and protein-level adaptations in P starvation tolerance, offering potential strategies for improving phosphorus-use efficiency and productivity in rice cultivars grown in P-deficient soil.

Deciphering the nutrient uptake, translocation, remobilization and nutritional quality of wheat grain under elevated CO_2 and heat stress

Heat stress (HS) is a major constraint on wheat production globally, impacting physiological and biochemical processes, ultimately leading to yield reduction. Furthermore, the rising atmospheric carbon dioxide (eCO_2) levels have complex effects, including potential reductions in nitrogen content and grain protein concentration, on C3 plant species like wheat. A study was carried to assess the effect of eCO_2, HS and differential nitrogen dose on nitrogen, carbon metabolism and grain quality in HD2967, HD2329, HI1500 and GW322. Putative NRT1, NiR and AGPase were identified by data mining and cloned from HD2967 genotype with amplicon size of 0.8 kb, 1.8 kb and 1.9 kb, respectively. Real time quantitative expression analysis of NR, NiR, and HSP17 gene showed maximum of 3.8-fold, 3.9-fold and 18-fold increase in expression respectively under nitrogen supplement in HD2967. Result showed highest percentage increase in NR (19%), NiR (26%), GS (24%) and GDH activity (33%) in selected genotypes under N-supplement subjected to eCO_2 and HS. Higher nitrogen dose further enhanced the photosynthetic rate in HD2967 under eCO_2 condition. eCO_2 treatment (650 ± 50 ppm) enhanced the AGPase and SSS activity activity in HD2967 as compared to control, while both enzymes exhibited lower activity under HS treatment. A positive impact of eCO_2 on starch content, maximum in HD2967 (74%), whereas HS led to a decrease in starch content with minimum starch content HD2329 (57%). eCO_2 enhanced the accumulation of total soluble sugar and reducing sugar. Zinc concentration in all genotypes increased under heat stress conditions, with the highest values observed in HD2967 (38 mg/kg) and HI1500 (31 mg/kg). Conversely, iron concentration decreased with eCO_2 and HS treatment, with HD2329 (29.79 mg/kg) showed the lowest concentration. These findings have practical implications for selecting wheat germplasms capable of enduring eCO_2 and HS while maintaining optimal nutrient uptake.

Characterizing the effect of terminal heat and drought stresses on tolerance and grain quality of wheat (*Triticum aestivum* L.)

Drought stress (DS) and heat stress (HS) play negative roles in wheat growth and are the two most important factors limiting grain yield. In the present study, we have studied the effect of drought stress and heat stress on C306 (Heat tolerant), HI1500 (Drought tolerant), HD3226 (Drought susceptible), and HD3271 (Heat susceptible) on carbon metabolism, tolerance and grain quality parameters. Putative DREB 30, mtHSP and cpHSP were identified by data mining and cloned from C306 genotype with amplicon size of 858bp, 1058bp and 985bp respectively. BLASTn search analysis of the putative DREB 30, mtHSP and cpHSP showed the highest similarity with *Aegilops tauschii*. Real-time quantitative expression analysis of the DREB 30 and cpHSP genes revealed a maximum of 6 and 21 fold increases in expression in leaves under combined stress treatment during the grain filling stage respectively. Our study found that combined stress has severe effects on the relative water content (RWC) and photosynthetic parameters compared to individual stress. The maximum reduction in photosynthetic rate (7.0 $\mu mol\ CO_2/m^2/sec$), stomatal conductance (0.31$\mu mol\ H_2O/m^2/sec$) and transpiration rate (0.8 $\mu mol\ H_2O/m^{-2}/s^{-1}$) was observed in HD3271. Grain weight per spike was reduced by 30 % in C306 and 47.3% in HD 3271 under combined stress treatment. The activity of different antioxidant enzymes such as SOD (10.7 U/mg), GPx (27.38 U/mg), and catalase (32.48 U/mg) were increased significantly in C306 under combined stress treatment. Combined stress also resulted in higher accumulation of proline (40.56%) and TAC (30%) with compare to control. Combined stress showed higher reduction in starch (49.70%), amylose (12.28%), amylopectin (37.41%), AGPase (1.08 U/mg) and Soluble starch synthase (1.66 U/mg) activity in HD3226. Among genotypes HD3226 was severely affected, C306 was least affected by combined stress. Overall results, suggest that combined effect of drought and heat stress has more detrimental effects than the individual stress.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the Student & Roll No.	M.Sc/ Ph.D	Title of the Thesis	Chairperson	Institute
1.	Shuvarghya Chakraborty (21615)	M.Sc.	Isolation, structural characterization and hypoglycemic effects of functional polysaccharides from Shiitake (*Lentinula edodes)*	Dr. Veda Krishnan	ICAR-IARI, New Delhi
2.	Vivek Kumar (21616)	M.Sc.	Developing biochemical intervention(s) for enhancing the bio-accessibility of lutein and provitamin A carotenoids in carrot chips	Dr. Sweta Kumari	ICAR-IARI, New Delhi
3.	Sanjay Behera (21618)	M.Sc.	Characterization of hulless barley grains and fractions for nutritionally relevant traits for food purpose	Dr. Sneh Narwal	ICAR-IARI, New Delhi
4.	Mahesh Kumar Samota (10777)	Ph.D.	Deciphering physio-biochemical and molecular mechanisms involved in enhanced drought tolerance and nutritive value of rice through seed-priming	Dr. Archana Singh	ICAR-IARI, New Delhi
5.	Minnu Sasi (11002)	Ph.D.	Enhancing the nutritional quality, sensory properties and bioavailability of soy-isoflavones in soymilk using probiotic fermentation approach	Dr. Anil Dahuja	ICAR-IARI, New Delhi
6.	Prathap V (11222)	Ph.D.	Molecular and biochemical characterization of rice for phosphorus use efficiency	Dr. Aruna Tyagi	ICAR-IARI, New Delhi
7.	Swapnil Sharadrao Thakare (11224)	Ph.D.	Unravelling the nutritional diversity contributing towards starch quality and its physico-chemical traits during ageing of rice (*Oryza sativa* L.)	Dr. Archana Singh	ICAR-IARI, New Delhi
8.	Arti Kumari (11459)	Ph.D.	Formulation and validation of oil blends for enhanced nutritional quality and stability	Dr. Aruna Tyagi	ICAR-IARI, New Delhi
9.	Abhishek Chitranashi (11463)	Ph.D.	Deciphering the nutrient uptake, translocation, remobilization and nutritional quality of wheat grain under elevated CO_2 and heat stress	Dr. Ranjeet Ranjan Kumar	ICAR-IARI, New Delhi
10.	Simardeep Kaur (11464)	Ph.D.	Deciphering miRNome modulation at reproductive stage drought in rice genotypes	Dr. Suresh Kumar	ICAR-IARI, New Delhi
11.	Nandini G A (11736)	Ph.D.	Characterizing the effect of terminal heat and drought stresses on tolerance and grain quality of wheat (*Triticum aestivum* L.)	Dr. Ranjeet Ranjan Kumar	ICAR-IARI, New Delhi

Molecular Biology and Biotechnology

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Prof. Debasis Pattanayak

ICAR-National Institute for Plant Biotechnology (ICAR-NIPB) is the premiere research institution of the Indian Council of Agricultural research (ICAR), engaged in molecular biology and biotechnology research. The Biotechnology Centre, established in 1985, as the Molecular Biology & Biotechnology Division of the Indian Agricultural Research Institute (IARI), was upgraded to a National Research Centre on Plant Biotechnology (NRCPB) in the year 1993, with a vision to impart the biotechnology advantage to the National Agricultural Research System (NARS). NRCPB had been upgraded to full-fledged institute as NIPB in 2019. Since its inception in 1985 the centre is contributing significantly to competent human resource development by way of offering regular M.Sc. and Ph.D. programmes by partnering with The Graduate School, ICAR-IARI as the Discipline of Molecular Biology & Biotechnology (MBB). Significant research findings of post graduate students are enlisted under the following themes:

Theme 1. Abiotic Stress Tolerance

RNAi mediated silencing of UDP-glucose pyrophosphorylase gene (*UGPase*) for the amelioration of cold-induced sweetening in potato

Low temperatures storage of potato (*Solanum tuberosum*) at 4°C prevents post-harvest losses but is also associated with reducing sugars (RS) accumulation, a phenomenon commonly known as cold-induced sweetening (CIS). High RS content makes potato commercially undesirable for processing due to an unacceptable brown color in the chips and the production of acrylamide (a potential carcinogen). UDP-glucose pyrophosphorylase (UGPase) is a key enzyme involved in the regulation of CIS in potato. RNAi-mediated silencing was used to down-regulate the expression level of the *UGPase* in potato to reduce the accumulation of RS in cold-stored potato tubers and improve the chipping quality. The transformation of internodal explants of the Kufri Chipsona-4 cultivar by *Agrobacterium* led to the production of 22 positive PCR-screened lines. Assessment of cold chipping attribute after cold storage at 4°C for 30 days and reconditioning for 21 days identified four lines with a considerable decrease in RS content and improved cold chipping quality. The selected transgenic lines were found to possess two to five copies of the transgene. Moreover, the production of siRNA and the corresponding decrease in the target gene expression was confirmed through molecular analysis of transgenic plants. The present work effectively demonstrates the efficacy of RNAi:*StUGPase* lines in controlling CIS in transgenic potato and adds to the existing strategy to deal with CIS.

Elevated temperature effect on grain chalkiness and meta-analysis of underlying QTLs in rice

Understanding the genetic determinants of grain chalkiness in rice is important. Hence, a comprehensive meta-analysis, amalgamating data from 21 multiple QTL studies for grain chalkiness and QTLs mapped for grain chalkiness under high-temperature stress to enhance detection accuracy and provide precise genetic effect estimations. Using the BioMercator software, an integrated genetic map was derived from these studies, constructing a consensus map using 4,000 markers that span a genetic distance of 1832.37cM. From studies, identified 236 chalkiness-associated QTLs, 182 (69.63%) were projected onto this map. A total of 18 metaQTLs were identified on chromosomes 1, 3, 6, and 8. Based on the lowest AIC values, the best-fit model and qtls having clusters at least from 2 or more different studies were taken for further studies. Thus, four significant meta QTLs, MQTL 1.3 with 9 QTL clusters covered 2.15 Mb region, MQTL 3.3 with 6 QTL clusters spanned 2.63Mb region, while MQTL 6.1 with 7 QTL clusters having 2.07 Mb in length were taken and these metaqtls were further chosen for candidate genes identification involved in starch metabolism, resulted in the identification of eight genes. To examine the influence of these eight genes under temperature stress on rice, twelve distinct rice varieties were exposed to temperatures 2-3°C higher in a greenhouse (regulated from 9 AM to 3 PM with diurnal variation) than the prevailing atmospheric temperature at the flowering time. Gene expression analyses of the identified candidate gene were studied at two-time point intervals, 8 DAF and 16 DAF. LOC_Os03g56460 showed overall downregulation, LOC_Os06g28194 showed increased expression, while LOC_Os03g52460 peaked at 8 DAF and then declined by 16DAF under heat stress. LOC_Os06g04200 expression declined in all varieties, showing reduced amylose synthesis. Gene LOC_Os06g06560, LOC_Os01g52250, LOC_Os01g5175, and LOC_Os03g52560 displayed varied patterns across rice varieties, highlighting the genetic complexities in grain maturation.

Understanding epigenetic regulatory mechanisms influencing drought tolerance pathways for identification of key genes in chickpea

Modifications within the epigenome of an organism in response to external environmental conditions allows it to withstand the hostile stress factors. Drought in chickpea is a severely limiting abiotic stress factor which is known to cause huge yield loss. The methylomes of two chickpea varieties, ICC 4958 and ICC 1882, which contrast for drought tolerance, were analysed in response to drought stress conditions. It was observed that the mCHH was most variable under drought stress, and the drought tolerant (DT) genotype exhibited substantial genome-wide hypomethylation as compared to the drought sensitive (DS) genotype. Important genes were identified as potential targets of epigenetic regulation in response to drought stress. This included the genes encoding the ribosomal proteins (RPs) and the SPL (Squamosa Promoter Binding Protein-Like) transcription factor (TF) genes. Specifically, the gene *RPS6* (ribosomal protein small subunit) was found to be downregulated in the DS genotype which leads to reduced ribosome biogenesis. An important class of drought-responsive transcription factors, the GRAS (gibberellic acid insensitive, repressor of GAI and scarecrow) TFs was identified. Proteins belonging to the RNA helicase gene family were identified which are involved in the *de novo* methylation in chickpea. Based on homology, it was inferred that the protein encoded by the *CaDExD/H66* gene shares a high degree of homology with one of the CLSY (CLASSY) proteins of *A. thaliana*. The CLASSY proteins are involved in regulation of tissue-specific methylation pattern, both at the genome-wide level as well as in a locus-specific manner. This gene therefore could possibly be involved in regulation of DNA methylation levels in chickpea by regulating siRNA production, in conjunction with other proteins.

Identification and expression profiling of genes involved in aluminum tolerance in chickpea (*Cicer arietinum* L.)

Nearly 1.5 Gha soil of the world soil is acidic (pH 5.5), which affects 40% of agricultural cultivated land. Roughly, 49 million hectares of land in India is acidic (pH5.5), in which 24 million hectares are very much acidic (pH4.5). About 95% of the soil in the Northeastern (NE) states is acidic, and 65% of the soil is severely acidic with a pH of 4.5. The chickpea (*Cicerarietinum*) is a prominent pulse crop, and India is the world's largest producer of chickpeas, accounting for 77% of total acreage and production. Aluminum is toxic in its trivalent ion in acidic soil and impairs plant growth, damages root tip, generates signal transduction disorders and as a result crop yield is reduced. Aluminium exclusion and tolerance mechanisms are used by plants to minimise the ill effects of aluminium toxicity. The genes involved in aluminium tolerance have been studied in a variety of crop plants. But in chickpea, the physiological mechanism of Al-tolerance has not been studied, so far. In addition, no efforts have been made to understand the effect of Al-toxicity on the genes involved in organic acid biosynthesis and transport. Thus, identification of the genes involved in aluminium tolerance in Chickpea was undertaken. Screening of reference collection genotypes was done to find tolerant and succeptible genotype. Identified tolerant and susceptible genotypes were used for further experiments. Expression analysis of genes involved in organic acid biosynthesis and transport was performed which showed that only STOP 1 was upregulated in response to Al treatment, but the expression of ALMT, MATE and PEP carboxylase genes was found to be either downregulated or unchanged than the respective controls. It appears that the transcription of these genes might be induced in response to higher concentration of Al or at the delayed time points than the ones used in the present study. Organic acid estimation in the root exudate through HPLC clearly showed that citrate is the major organic acid secreted by chickpea under aluminum toxicity.

Validation of anaerobic germination tolerance QTL, *QAG7.1*, in a RIL population

The fragrance or aroma present in rice is regarded as a distinct attribute of significant economic importance. Utilizing molecular maps and genome sequences, a key fragrance-related gene (*badh2*) is located on chromosome 8. A deletion of 8 base pairs within exon 7 of this gene was discovered to cause the truncation of the betaine aldehyde dehydrogenase enzyme. This loss of function subsequently leads to the buildup of a significant aromatic compound known as 2-acetyl 1-pyrroline (2AP) in fragrant rice. While Basmati and Jasmine rice varieties have been extensively studied, Indian short-grain aromatic cultivars have not received as much attention. Therefore, the present study investigates the genetic basis and environmental influences on aroma in Indian short-grain aromatic rice cultivars. A panel of genotypes including aromatic and non-aromatic rice accessions, wild rice species, and cultivated varieties was analyzed. The 8-bp deletion and aroma-associated determinants in the *BADH2* gene were present in aromatic non-basmati and basmati rice, except Bishnu Bhog. Unexpectedly, Bhishnu Bhog exhibited a non-aromatic gene sequence. Notably, wild rice accessions displayed the aroma allele, suggesting recent hybridization events. Phylogenetic analysis clustered accessions into distinct groups, supporting the heritability of the aroma trait. Additionally, investigation of the *BADH1* gene revealed protein haplotypes associated with aroma, including one linked to the characteristic *BADH2* allele. A multi-location trial was done to understand the impact of the environment on grain attributes. Tukey's tests indicated significant variation in 1000-grain weight across locations, while grain length and diameter showed relative uniformity; notably, short-grain aromatic rice exhibited stability in specific environments. The influence of the environment on gene expression was investigated through analysis of seven aroma-associated genes across different locations, with *pro*DH, linked to proline metabolism, found to be exclusively expressed in non-aromatic rice. Overall, this study sheds light on the intricate genetic, molecular, and environmental factors shaping rice aroma.

Understanding the effect of auxin, cytokinin and their cross talk on root growth under Al^{3+} stress in chickpea (*Cicer arietinum*)

In plants, auxin and cytokinin homeostasis is crucial for regulating various growth and developmental processes. However, under aluminum stress, the synergistic effect of auxin and cytokinin can lead to root growth inhibition. The present study was undertaken to understand the effect of auxin and cytokinin and their cross talk on root growth and development under Al-stress conditions in chickpea (*Cicer arietinum*). Aluminum stress can interfere with hormone signaling pathways, including those of auxin and cytokinin. Aluminum can disrupt the transport and distribution of these hormones within the plant, affecting their proper functioning. This disruption can lead to imbalances in auxin-cytokinin ratios, which may contribute to root growth inhibition. Aluminum stress was found to alter root architecture, such as reduced root length and increased lateral root number. Aluminum stress suppresses primary root growth by inhibiting cell division and elongation in the root apical meristem. Both auxin and cytokinin play important roles in regulating these processes. However, under aluminum stress, the auxin-cytokinin balance can be disrupted. High levels of cytokinin relative to auxin can lead to reduced primary root growth and elongation. Aluminum stress often inhibits lateral root development. Auxin promotes lateral root initiation and emergence, while cytokinin has an inhibitory effect on lateral root formation. Gene expression analysis indicated that STOP1 transcription factor is induced in response to Al, but downregulated by IAA and BAP treatments. Similar expression pattern of ALMTs and MATE suggest that STOP1 directly regulates expression of these genes. Taken together, auxin and cytokinin play important role in root growth inhibition under Al-toxicity in chickpea, by influencing the expression of Al-tolerance related genes.

Identification and characterization of salt-stress-related lncRNAs in Indian mustard (*Brassica juncea* L.)

Indian mustard is one of the world's most important oilseed crops, ranking third in terms of vegetable oil after soybean and palm. The production and productivity of this important oil seed crop are greatly affected by various biotic and abiotic stresses. In India, major mustard growing area is salt-affected, causing huge yield losses. LncRNAs are a diverse class of RNAs with more than 200 nucleotides (nt) in length, that have a significant role in plant adaptation to a range of abiotic stresses. A transcriptome analysis of CS-52 salt stress and shock revealed a total of 391 lncRNAs by in-silico characterization. Of these 391 lncRNAs, 5 lncRNAs formed eTMs with 4 miRNAs. The eTM prediction analysis revealed that BJUN_LNC169, BJUN_LNC122, and BJUN_LNC122 act as eTM for *Br*Mir-172b, *Br*Mir-1886, and Novel-011, respectively, whereas BJUN_LNC133 and BJUN_LNC026 both act as eTM for *Br*Mir-854a. The target prediction of eTM revealed that *Br*Mir-172b, *Br*Mir-1886, Novel-011, and *Br*Mir-854a target mRNAs of BjuVB08G26110 (ethylene-responsive transcription factor RAP2-7), BjuVB08G09130 (serine carboxypeptidase-like 47), BjuVB06G56570 (methyl transferase ptaI), and BjuVB08G16350 (xyloglucan galactosyl transferase GT15), respectively. All four targeted genes were involved in salt stress tolerance in *Brassica juncea*. The qRT-PCR based expression validation revealed that the lncRNAs BJUN_LNC133 and BJUN_lNC169 its target BjuVB08G16350 and BjuVB08G26110 significantly upregulated in the leaf tissues under salt stress conditions. Similarly, lncRNAs BJUN_LNC035, BJUN_LNC122, and its target BjuVB06G56570, BjuVB08G09130 showed upregulated expression in both root and leaf tissues under salt stress conditions, respectively. The expression analysis of lncRNAs and their targets confirmed that lncRNAs BJUN_LNC133, BJUN_lNC169, BJUN_LNC035 and BJUN_LNC122 express under salt stress and regulate the expression of salt stress-responsive genes in *Brassica juncea*.

Theme 2: Biotic Stress Resistance

Genome-wide identification and characterization of microRNAs and their target genes in response to chickpea-*Fusarium oxysporum* interaction

Fusarium wilt (FW) of chickpea caused by *Fusarium oxysporum* f. sp. *ciceris* (*Foc*) is a destructive soil-borne disease that severely decreases chickpea yield. MicroRNAs and the microRNA/target gene crosstalk involved in chickpea resistance to FW were investigated. Firstly, various morphological, physiological, biochemical and molecular studies were carried out for a better understanding of the disease resistance and susceptibility in different genotypes of chickpea. The study was carried out at two time points, early (2 days post inoculation) and late (10 days post inoculation) in four genotypes, JG 62 and ILC 482 (FW-susceptible), WR 315 and Pusa Green 112 (FW-resistant). Based on the results obtained from a fore mentioned studies, control and stress samples from two genotypes, JG 62 (FW-susceptible) and WR 315 (FW-resistant) collected at 10 days post inoculation, were selected for small RNA sequencing. The sequencing and bioinformatics analyses of twelve libraries resulted in identification of 544 miRNAs which included 406 known and 138 novel miRNAs. A total of 115 miRNAs showed differential expression in both genotypes in different combinations. Prediction and functional annotation of miRNA targets revealed their role in transcription regulation (transcription factors), disease resistance, defense response, metabolism etc. Sixteen miRNAs and their targets were validated using poly(A) based qRT-PCR in four genotypes grown in lab and field conditions. A high correlation in expression patterns of miRNAs and their targets in lab and field grown plant samples was observed. Interestingly, Car-miR398 targeted copper chaperone for superoxide dismutase (CCS) that, in turn, regulated SOD activity during chickpea-*Foc* interaction. The cleavage site in targets were mapped for 6 miRNAs by analyzing publicly available degradome data for chickpea. The study, for the first time, provides novel insights into microRNA-mediated regulation of resistance and susceptibility mechanisms in chickpea against Fusarium wilt and opens up avenues for development of the wilt resistant varieties in chickpea.

Identification of vital genes of aphid infestation and pyramiding genes for aphid tolerance in *Brassica juncea*

Brassica juncea is an important oilseed crop contributing for Indian economy. The huge yield loss caused by *Lipaphiserysimi* (Mustard aphid) infestation drew the attention of researchers to mine its vital gene targets and develop aphid resistant Brassica. This is the first report of *L. erysimi* draft genome sequence (67.9 Gb data, 225018571 total sequences, and 22825 unique predicted genes) and their functional annotation. The vital target genes of *L. erysimi* (203 genes) were identified by subtractive genomics and screened the conserved domains to design the knockdown/ knockout targets. The *L. erysimi* genome sequence gene ontology (GO) report and vital targets represented the high frequency of macromolecule metabolic process sequences under biological process (21 and 16 respectively). The plant based insecticidal genes chickpea lectin (CHPL, Accession: HM235917.1) and urdbean protease inhibitor (UPI, Accession: KU382735.1) affect the macromolecule metabolic process of *L. erysimi*. The *B. juncea*, *B. rapa*, and *B. nigra* genome were mined for the presence of candidate gene containing CHPL and UPI. Only one CHPL ortho-group was present in Brassica species but in different clade. The UPI orthologs was not found in Brassica species. With this confirmation, both the transgenic parental lines were crossed and advanced to F2 population. The F2 plants containing both the transgenes were analyzed for gene expression analysis and in-planta aphid bioassay. Transgenes were expressing constitutively and showed good efficacy in terms of mortality (95% on the 9th day after *L. erysimi* infestation) and natality (66.3X less birth rate than on control plants).

Understanding the defence mechanisms of *Brassica juncea* L., *Sinapis alba* L. and *Camelina sativa* L. against infection by *Alternaria brassicae*

Brassica juncea (L.) is susceptible to Alternaria blight caused by *A. brassicae*. Wild genotypes possess degree of resistance against *A. brassicae*. *S. alba* has moderate resistance and *C. sativa* has high degree of resistance against *A. brassicae*. Disease severity in three species after *A. brassicae* infection was studied. It was found that in infected *B. juncea*, chlorosis started after 3 dpi and disease symptoms appeared after 6 dpi. Clear necrotic lesions developed after 8 dpi and 9 dpi in *S. alba* and *C. Sativa*, respectively. After 9 dpi the diameter size of lesion was 1.4 cm in *B. juncea*, 9 mm in *S. alba* and 7 mm in *C. sativa*. In tryphan blue stained leaves, necrosis was observed after 24 hpi in *B. juncea*. In *S. alba* it was observed after 48 hpi while in *C. sativa* it appeared after 72 hpi. Highest level of necrosis was observed in *B. juncea* after 8dpi. RT-PCR showed the differential expression of *PR1* and *PR12* gene at different time point intervals in *B. Juncea* and *C. sativa*. In *B. junceaPR 1* was induced but in *C. Sativa PR1* was not expressed significantly. *PR 12* was not induced significantly in *B. juncea* but higher levels of expression were seen in *C. sativa*. In infected *C. sativa*, PR proteins like pathogenesis-related protein 5, endochitinase At2g43590-like, thionin, defensin, thaumatin-like protein 1, endo-1,3;1,4-beta-D-glucanase were upregulated compared to infected *B. juncea* and infected *S. alba*. In infected *C. sativa* transcription factors bZIP transcription factor 28-like, WRKY transcription factor 70, WRKY transcription factor 2, WRKY transcription factor 19 were upregulated as compared to *B. juncea* and *S. alba*. Transcription factor MYB32 was upregulated in *C. sativa* as compared to *S. alba*. Upregulation of defense genes at high level in *C. sativa* has provided resistance against *A. brassicae*.

Prevalence of lepidopteran-toxic genes in *Bacillus thuringiensis* isolates recovered from different agro-ecological regions in India and determination of toxicity towards different developmental stages of *Spodoptera frugiperda* (fall army worm)

Seventy-two *Bt* isolates recovered from different habitats in various agro-ecological regions of India were screened for presence of relatively unexplored and less abundant lepidopteran-toxic *cry15Aa, cry30Fa, cry30Ga, cry54Aa and cry79Aa*-type genes. PCR amplification was observed in 15 native *Bt* isolates namely, SK-110, SK-213, SK-21, SK-223, SK-700, SK-714, SK-727, SK-768, SK-935, SK-949, SK-976, SK-979, SK-996, SK-1100 and SK-1322 and four *Bt* strains, BGSC HD1, 4F3, 4A6 and 4K1. The *cry30*-type genes were found to be more prevalent, with *cry30Fa1* and *cry30Ga1 genes (*13.88 and 8.33% respectively); followed by *cry15Aa1* (6.94%) and *cry79Aa1* (2.77%) genes. Amplification of *cry54Aa1* gene was not observed in any *Bt* isolate. Variant bands observed in some isolates require further investigation. Among different agro-climatic regions, *Bt* isolates from Trans-Gangetic Plain Region and Gujarat Plains and Hills Regions harbored three types of novel *cry* gene alleles. Among different sources of isolates, those from phyllosphere were observed to be most prevalent in novel *cry* gene alleles (42.85%). Furthermore, *Bt* isolates from phyllosphere and soil displayed diversity in prevalence of novel *cry* genes by harboring four types of novel *cry* genes in each source. The full-length *cry15Aa1* gene and partial *cry79Aa1* gene amplified from *Bt* isolates SK-1100 and SK-768 isolated from mustard seeds, Rajasthan and jowar grain dust, Andhra Pradesh, respectively, were cloned in pGEMT-Easy vector. Toxicity of previously cloned *vip* genes, *vip3Aa44, vip3Aa67 and vip3Aa69* in pET29a vector and expressed in *E. coli* BL21(DE3) cells, was examined against *S. frugiperda*.Vip3Aa69 was most found to be most toxic (LC_{50} 1.38 μg/g). Sub-lethal effects at different developmental stages in whole life cycle of *S. frugiperda, viz.* reduction in larval growth, malformation of pupae and adults, delay in pupal and adult formation were also observed. Thus, these Vip toxins are potential candidates for deploying in crop protection for biological insect pest control.

Frequency distribution of coleopteran and hemipteran-toxic genes in *Bacillus thuringiensis* isolates recovered from diverse habitats in India and evaluation of toxicity of *vip3Aa68*, *vip3Aa72* and *cry1Ib7* genes towards *Spodoptera frugiperda* (fall army worm)

Bt (*Bacillus thuringiensis*) is a sustainable option for insect pest control. However, it is necessary to identify new types of insecticidal genes from *Bt* to combat development of resistance in insect pests. Native *Bt* isolates have been recovered from diverse sources and agro-climatic regions in our laboratory. These isolates were screened for presence of coleopteran- and hemipteran-toxic genes in this study. Coleopteran-toxic *cry7/8* type genes were more prevalent (20.25%) among native *Bt* isolates, as compared with hemipteran-toxic genes *cry64Ca* (5.06%), *cry78Aa* (2.53%), and *cry78Ba* (2.53%). Presence of *xpp37Aa* and *cry75Aa* genes was not observed in any *Bt* isolate. Three *Bt* isolates, with two or more *cry*-type genes toxic to both coleopteran and hemipteran insects, were SK-768 from jowar grain dust in Guntur, Andhra Pradesh, containing *cry7/8* and *cry78Ba* genes; SK-942 from Desert soil in Khyaliwala, Sriganganagar, Rajasthan, containing *cry7/8* and *cry64Ca* genes; and SK-979 from Cotton field soil in Khyaliwala, Sriganganagar, Rajasthan, containing *cry7/8, cry64Ca*, and *cry78Aa* genes, are promising candidates for deployment for broad-spectrum biocontrol. Additionally, isolates, SK-979 and SK-768, were found to possess lepidopteran-toxic genes (*cry30Fa* and *cry79Aa*) in another study in our laboratory, indicating biopesticidal potential of these isolates towards different insect orders. Full-length *cry64Ca* and *cry78Ba* genes from *Bt* isolates SK-979 and SK-768 respectively, were cloned for further analysis. Toxicity of *vip3Aa68, vip3Aa72*, and *cry1Ib7* genes cloned previously from *Bt* isolates in our laboratory, towards *S. frugiperda*in laboratory bioassays, showed that Vip3Aa toxins were more toxic to *S. frugiperda* than Cry1Ib7. The toxins caused 100% larval mortality with no pupation or adult emergence, at higher concentrations (50 and 100 ppm). Cry1Ib7+Vip3Aa toxins in combination(100 ppm), caused reduction in larval growth and survival, indicating efficacy of these toxins, both individually and in combination. These findings suggest potential of these toxins for deployment in biological pest control.

Expression and developing CRISPR/CAS9 constructs of flavanone-3-hydroxylase (*F3H*) and flavone synthase (*FNS*) genes in contrasting lines of soybean to yellow mosaic disease

Soybean (*Glycine max*) is a globally significant legume crop, recognized for its diverse nutritional composition and potential health benefits derived from flavonoid compounds. Flavonoids, a class of secondary metabolites predominantly found in leguminous plants, play a crucial role in plant defense against both abiotic and biotic stresses. In soybean, flavonoids such as isoflavones exhibited antiviral and antibacterial properties, highlighting their potential in mitigating Yellow Mosaic Disease (YMD) caused by mung bean yellow mosaic India virus (MYMIV). The present study investigated the expression profiles of key genes (*F3H* and *FNS* isoforms) involved in the phenylpropanoid pathway responsible for flavonoid biosynthesis. Analysis of soybean varieties susceptible (JS335) and resistant (DS9712) to YMD revealed distinct gene expression patterns, with *F3H1* and *F3H4* exhibited elevated expression in the susceptible variety, while *F3H2, F3H3, FNS1*, and *FNS2* showed high expression in the resistant variety. Notably, *F3H1* emerged as a potential candidate for gene manipulation in the susceptible variety to redirect naringenin flux towards isoflavone synthesis, for enhancing resistance. The leaf discs of JS335 were vacuum infiltrated with the *Agrobacterium* culture harboring the Cas9 construct specific to the *F3H1* gene. The sgRNA integration was confirmed in the infiltrated leaf discs using sgRNA-specific primers. Therefore, vacuum infiltration can also be a rapid screening for validation of sgRNA integration. This research offers insights into the potential of genome editing to improve plant resistance to viral pathogens while addressing biosafety concerns associated with genetically engineered crops.

Molecular characterization of begomoviruses infecting okra in the eastern region of India

Bhendi yellow vein mosaic (BYVMD) and enation leaf curl disease (OELCD) are important diseases of bhendi. In the Chhattisgarh region, the BYVMD and OELCD were reported but the causal agent has not been identified yet. In the present study, three BYVMD samples from three different places in Chhattisgarh (Raipur, Kanker,andKawardha) and two OELCD samples (Raipur and Kawardha) were collected and characterized viral gemonic components. Okra enation leaf curl virus (OELCV) is found to be associated with all the samples BYBMD and OELCD. Three betasatellites; Ludwigia leaf distortion betasatellite (LLDB) with BYVMD from Kanker, bhendi yellow vein mosaic betasatellite (BYVB) associated with BYVMD from Raipur, okra enation leaf curl betasatellite(OLCB) associated with OELCD from Kawardha found associated with the samples. Phylogeny tree analysis revealed that four OELCV clustering together with the other strains of OELCV and all four betasatellites clustering with their respective host from which they were isolated. The recombination analysis revealed that OELCV from Raipur, Kanker, and Kawardha were recombinant. This study also suggests that BYVMD and OELCD are caused by monopartitebegomovirus associated with betasatellite.

Isolation and characterization of bacterial endophytes having antimicrobial potential against *Sclerotium rolfsii* in chickpea

Collor rot, caused by fungal pathogen*, Sclerotium rolfsii,* is causing huge economic loss to chickpea (*Cicer arietinum* L.). Bacterial endophytes have emerged as eco-friendly alternative approach to chemical management for mitigation of such diseases. In this study, total 108 bacterial endophytes were isolated from five plant tissues of chickpea namely root (20), stem (39), leaf (35), flower (6) and nodule (8). Morpho-biochemical tests and 16s rDNA sequencing was employed for identification of isolates. Gram's staining showed 77 isolates as Gram's positive and 31 as Gram's negative. The isolates were evaluated for Plant growth-promoting (PGP) traits *viz.,* phosphate solubilization, production of siderophore, IAA, urease, cellulose, nitrate reduction activity, citrate utilization and protease production in which 7, 35, 36, 22, 29, 35, 30 and 76 were positive, respectively. In dual culture assay, 21 isolates showed antagonistic activities against *Sclerotium* with fungal growth inhibition ranging from 25 to 60%. These isolates were found to harbor genes for lipopeptides *viz.,* iturin, surfactin, fengycin, and bacillomycin D. Based on PGP and *in-vitro* antagonistic activities, five isolates namely NIBSM_CpR8, R20, NIBSM_CpS5, S25 and NIBSM_CpL12 were selected for *in-planta* validation. Chickpea plants bio-primed with selected endophytes showed better survival rate against *Sclerotium* pathogen with protection of 25-75% over control. Isolate NIBSM_CpS5 was found best in imparting protection against *Sclerotium.* During differential expression of genes in tri-partite interaction (Chickpea- *Sclerotium*- Endophyte) study, there was increased expression of genes *viz.,* NAC transcription factor, CDPK, linoleate 9S-lipoxygenase (LOX) and chitinase in endophyte bio-primed and pathogen-inoculated plants during the early stages (24-48 h) of pathogen infection indicating role endophyte-mediated resistance through enhanced plant's immunity through modulating phytohormone, signalling pathways and secondary metabolite production. The findings suggest that bacterial endophytes identified to have antimicrobial could be integrated into disease control strategies.

Molecular detection and *in-silico* analysis of broadspectrum resistance genes for bacterial leaf blight in wild and cultivated *Oryza* species

Bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv. *Oryzae* (*Xoo*), negatively impact rice growth and yield. Out of 50 phenotypically evaluated rice germplasms, 16 lines were selected for phenotypic and genotypic evaluation which may proffer the potential candidate donor for Broad Spectrum Resistance (BSR) genes in rice breeding programs. In this study, 16 selected rice germplasms were phenotypically evaluated using four distinctive *Xoo* isolates; and results showed that diverse degrees of resistance in rice line to at least three distinct *Xoo* isolates. Among them *Xoo* isolates BBR-18 was found to be more virulent. PCR based screening of BLB-resistant genes using respective gene linked markers showed that out of five genes screened, four genes *Xa21, Xa13, Xa4* and *Xa7* were frequently present in the tested rice lines with a combination of any one of their homologous genes except *xa5*, which was often not amplified in the screened lines. In addition, 11 positive/negative gene regulators having potential BSR activity against Xoo and various rice diseases were investigated. The enlisted BSR genes includes *Xa21*, *OsGLP2-1, OsLYP4, OsPAD4, OsSWEET11 (Xa13), OsWAK25, SPL33, OsSWEET14,* *OsPAL4, 6* and *2.* Comparative sequence analysis of 9 BSR genes using *in-silico* approach showed variability and homology across the *Oryza* species by the differentiated sites of the structural variations (Indels/ SNPs) in the nucleotide sequences. Gene based primers were developed and used for PCR based detection of presence of genes. Major *Oryza* species includes *Oryza longistaminata, O. rufipogon, O. glaberrima* and *O. minuta,* were evinced with possible amplification of 6, 8, 8, and 8 combinations of selected BSR genes, respectively. This study showed the presence of *R* genes in *O. sativa* and identified structural nucleotide variations tend to be holding the salient functional features that could possibly regulate the BSR mechanism across the *Oryza* species.

Molecular insight into the protective role of green copper nanoparticle against *Fusarium oxysporum* in chickpea

Nanotechnology has emerged as a promising technique for crop improvement. The present study acesses the effectiveness of green copper oxide nanoparticles, synthesized from copper sulphate pentahydrate, ascorbic acid and sodium hydroxide, to decipher the molecular mechanism behind the dose dependent impacts of copper against fungi *Fusarium oxysporum* causing wilt in chickpea. FTIR, DLS,and UV-VIS were used in the characterization of the nanoparticle. Chickpea seeds were planted, infected and after treatment with various doses of CuO NPs, various morphological and physiological indices were documented, and molecular study were done. Histological and FACS data were gathered. All the results were compared to the negative and positive control. A 500 ppm dose of CuO NPs was found superior to 2500 ppm treatment of $CuSO_4$ for morphological parameters. These results were validated using Realtime PCR where effect of CuO NPs were evaluated. The expression of defence genes- SOD, GATA, CAO CHI F, and LAC increased many folds in the plants with 500 ppm of CuO NPs compared to the plants where copper sulphate of 2500 ppm. Therefore, it is possible to suggest that nano-copper at a concentration of just 500 ppm, can serve as a suitable replacement for copper sulphate of 2500 ppm against Fusarium wilt in chickpea.

Theme 3. Basic Research

Fine mapping of *qPH5.1QTL* region for dwarfness in pigeon pea (*Cajanus cajan* L. Milsp. cv Pusa Dwarf)

Pusa Dwarf (PD) is a dwarf breeding line used in breeding programmes to introduce dwarfness. The BC6F1 population, developed from PD and a CMS line GT288, was used for fine mapping the QTL *qPH5.1*, in which the dwarfness was provided by PD. Since the QTL flanking markers were not polymorphic, alternate SNPs were identified using BSA using a 62K *Cc*SNPnksAxiom^{TM}Affymetrix array chip. SNPs (1115) identified were mapped in QTL- specific pseudo-molecule sequences, and two SNPs, Ax46 and Ax01, flanking the QTL region were used to design the KASP assay. KASP was used to genotype the BC6F1 population, and 5.9% recombination was obtained. The KASP assays of SNPs Ax46 and Ax01 were validated in PD-derived dwarf (PDDD) breeding lines. Gibberellin (GA) application induced internode length in both parents indicating both biosynthesis and signalling of GA are normal in both parents. Auxin application delayed branching in PD; the quantity of auxin was almost similar in the leaf, stem, and bud of both parents, indicating a change in mediators in auxinsignalling or transporters. Strigolactone (Sl) GR24 application increased internode length in GT and did not inhibit branching in PD, indicating PD is behaving like strigolactone response mutants. The sucrose content in the PD stem was double that of GT288 while the leaf tissue of both parents had an almost equal concentration. Transcriptome data revealed four times more expression of sucrose synthase in the sink tissue of PD. Sucrose is known to prevent the perception of strigolactone and induce lateral branching. The SNPs Ax46 and Ax01 could be used as molecular markers in the PDDD population, along with early branching as a naked eye molecular marker, and second internode length in seedlings could be followed to confirm the inheritance of dwarfism.

Carbon partitioning and its genetic regulation during grain filling in wheat (*Triticum aestivum* L.) under nitrogen stress

Nitrogen nutrition plays a crucial role in improving grain filling and dry matter accumulation. In this study, four genotypes were selected based on the effect of N stress on their yield attributes. Despite similar N uptake, biomass and grain yield under N stress conditions, the genotypes exhibited variations in their response to N stress on grain yield attributes. The contrasting genotypes, Chotilerma (CL) and HD-2967 (HD), experienced a reduction in grain number per plant, while the genotypes HB-208 (HB) and VL-829 (VL) showed a decrease in grain weight, volume and size in addition to grain number, and hence grain filling was affected under N stress. These genotypes were grown under N control and stress N condition, and studied for partitioning of carbon using 14C labelled sucrose. The study revealed partitioning of carbon into different metabolites among the genotypes under N stress. Poor grain filling genotypes under N stress exhibited a significant reduction in 14C partitioning towards starch, which correlated with decreased grain weight and volume. Transcriptome study of contrasting genotypes revealed predominance of AP2/ERF transcription factor family, involved in hormone signalling among upregulated DEGs in both the genotypes in response to N stress. GO analysis revealed low activity of ammonium transporters, suggesting a reduced ability to transport nitrogen in HB. A potential candidate gene, APG (TraesCS1B02G100400), was identified as differentially expressed under nitrogen stress in HB and differences in promoter sequences among the genotypes were potentially influencing the gene expression. *In silico* protein-protein interaction showed its interaction with phytochrome, and corroborating that, cis-regulatory elements showed the presence of various light regulatory elements where aggregation of these elements was highest in HB. Overall, this study provides insights into the complex genetic regulation and metabolic pathways involved in wheat grain filling under nitrogen stress.

Identification of genes and markers associated with flowering trait in diverse pigeonpea genotypes

The current study was designed to identify the markers and genomic regions associated with flowering in pigeonpea using advanced genomics approaches. Association mapping was conducted on 142 lines using both traits and PC scores as phenotypes through seven models, and a non-redundant set of 22 MTAs to either DOF, DFF or PC1 were identified. The PC based GWAS was found to be more robust in delineating the pleiotropic genes, whereas FarmCPU was found as better choice compared to other models. The F2 population indicates the presence of linkage between days to flowering (DTF) and determinacy. In total 8 and 4 novel QTLs were identified for days to flowering and determinacy. QTL-seq identified a linked QTL for DTF and determinacy on chromosome 3, which harbors a 10bp deletion in the first exon of *TFL1* gene. Two QTLs at chromosome 3 and 10 were common for DTF and determinacy traits when inspected in QTL mapping and QTL-seq results. These QTL regions were found to posses 18 MTAs in the core collection. In total 78 genes were shortlisted from these QTL regions which were clustered into three groups representing autonomous pathway, photo-periodic pathway and epigenetic regulators. Fine mapping narrowed the linked QTL from ~6 Mb to 0.24Mb, flanked by Primer46-*TFL1* with 36.47% of PVE. Cumulatively, 30 genes were shortlisted for expression profiling, where it was evident that their expression was in congruence to their role except few such as LD and FWA. It is evident that there is no alteration in the expression of *TFL1* and *LFY* genes, supporting that deletion in *TFL1* gene renders this interaction, ultimately leading to determinate phenotype. In conclusion, TFL1 gene specific deletion is found to be a major player for days to flower as well as determinant phenotype and could be used a functional marker in breeding program.

Inactivation of amylase-trypsin inhibitors through genome editing for development of low immunogenic wheat

Amylase/Trypsin inhibitor (ATI) present in wheat can trigger immunogenic reactions either by restricting α-amylase and trypsin enzyme activities resulting in food indigestion or stimulate innate immune cells by interacting with Toll-like receptors (TLR). ATIs is known to be associated with many diseases; Bakers' asthma onset of celiac disease (CD), Non-celiac wheat sensitivity (NCWS) and other intestinal inflammatory disorders of the gastrointestinal tract. The need of the hour is to develop wheat varieties with low ATI concentrations. To address this problem, attempt has been made to develop ATI inactivated wheat through genome editing technology. Multiplex CRISPR/Cas9 genome editing technology was adopted to target ten ATI genes through single transformation. An improved wheat regeneration protocol for Bobwhite and HD2967 wheat varieties was optimized and developed with regeneration efficiency of 93.13% and 96.40%. To knockout ten ATIs, a total of twelve targets were selected, two targets for each ATI gene to increase the chances of gene disruption. Two CRISPR/Cas9 constructs namely pSP2.1 and pSP2.2 were developed, each having six targets each. The two CRISPR/Cas9 constructs were co-bombarded at immature scutella using a biolistic gun. Transformed scutella were raised to plants through callusing using the optimized protocol. Two edited plants of each variety were obtained having mutations in a minimum of six ATI genes. Edited plants were characterized at the molecular level to understand the type of mutations in targeted ATI genes. Eight ATI gene mutations in both Bobwhite and six in HD2967 genotypes were observed. Most of the mutations resulted in 1-4 bp deletion within the editing window. Compared with the wild type, the concentration of ATIs was reduced by 30.61% and 20%, α-amylase enzyme inhibition activity reduced to 50.74% and 37.84%, and trypsin enzyme inhibition activity reduced to 44.90% and 34.41% for edited Bobwhite and edited HD2967 respectively.

Identification and characterization of the yield-responsive cytokinin oxidase/dehydrogenase (CKX) gene in *Brassica juncea* (L.) Czern

Cytokinin oxidase/dehydrogenase (*CKX*) is an important enzyme regulating cytokinin homeostasis, and genetic manipulation of *CKX* in several crops has increased yield and stress tolerance. This study identified the *CKX* gene family in elite cultivars of *B. juncea*, and found that *CKX3.4* and *CKX5.2* are the yield-responsive genes. For this, the whole genome sequence of the *B. juncea* cv. Varuna (AABB, 2n = 36) was explored and a total of 24 *CKX* members were identified distributed over the A and B set chromosomes of *B. Juncea*cv. Varuna. The phylogenetic analysis has classified these 24 *BjCKX*s into 7 groups. The 20 motifs analyzed in *Bj*CKX were found majorly conserved and two functional domains (FAD-binding and Cytokinin binding domains) required for CKX activity were conserved in all the predicted members and two members (*Bj*CKX1.6 and *Bj*CKX3.3) were found having additional domains. The *Bj*CKXs were predicted to be localized to vacuoles, endoplasmic reticulum, or extracellular regions, and the upstream region of each *BjCKX* showed presence of various *cis*-regulatory elements. The two-contrasting low-yielding (RLM 198) and high-yielding (PJK) genotypes of *B. juncea* showed morphological variations in yield-attributing traits and the comparative expression profiling in leaf, stem junction, flower buds, and silique tissues showed differential expression of all the 24 *BjCKX*. Based on the differential expression in flower buds and silique tissues and phylogenetic relationship with functionally characterized *CKXs* influencing yield in *A. thaliana*, and *B. napus, BjCKX3.4* and *BjCKX5.2* were putatively selected as the yield-responsive in *B. juncea.* The gene sequence information generated showed no difference in the *BjCKX3.4* sequence between the two genotypes whereas two base pair substitution from thymine to cytosine were found in the 4th intron of *BjCKX5.2*. The putative yield-responsive *BjCKXs* will further be utilized to increase the production and productivity of Indian mustard (*B. juncea*) through genome editing.

Designing prime edit guide RNA and construct development for base editing of rice *Osbri1*

Prime editing, also referred to as 'Search and replace' genome editing methodology, is a modification of the conventional CRISPR-Cas system. This technique utilizes a modified Cas9 enzyme, functioning as a nickase, coupled with an engineered reverse transcriptase (RT). Additionally, designing an extended guide RNA equipped with a primer binding site along with template sequences containing the desired edits increases the efficiency of editing. These modifications collectively facilitate the insertion, deletion, or substitution of genetic material at targeted loci within the DNA using the RNA template as a guide. The present research delved into the utilization of this technology to create prime editing constructs aimed at inducing nucleotide substitution. This was specifically designed to alter the amino acid composition of the *Osbri1* coding region, converting Alanine at the 467th position into Valine. Working towards this endeavour, a prime edit guide RNA (pegRNA) was designed. The pegRNA expression assembly for the A467V edit was cloned into binary vector (pH-ePPE) expressing nickase and RT, codon optimized for monocot and another for dicot, thus generating constructs ready for transformation in rice. Furthermore, this work established that PCR approach is not a reliable technique for confirming Gibson assembly.

Haplotype diversity of *BADH1* and *BADH2* genes and its relation to the aroma in Indian short-grain aromatic rice cultivars

The fragrance or aroma present in rice is regarded as a distinct attribute of significant economic importance. Utilizing molecular maps and genome sequences, a key fragrance-related gene (*badh2*) is located on chromosome 8. A deletion of 8 base pairs within exon 7 of this gene was discovered to cause the truncation of the betaine aldehyde dehydrogenase enzyme. This loss of function subsequently leads to the buildup of a significant aromatic compound known as 2-acetyl 1-pyrroline (2AP) in fragrant rice. While Basmati and Jasmine rice varieties have been extensively studied, Indian short-grain aromatic cultivars have not received as much attention. Therefore, the present study investigates the genetic basis and environmental influences on aroma in Indian short-grain aromatic rice cultivars. A panel of genotypes including aromatic and non-aromatic rice accessions, wild rice species, and cultivated varieties was analyzed. The 8-bp deletion and aroma-associated determinants in the *BADH2* gene were present in aromatic non-basmati and basmati rice, except Bishnu Bhog. Unexpectedly, Bhishnu Bhog exhibited a non-aromatic gene sequence. Notably, wild rice accessions displayed the aroma allele, suggesting recent hybridization events. Phylogenetic analysis clustered accessions into distinct groups, supporting the heritability of the aroma trait. Additionally, investigation of the *BADH1* gene revealed protein haplotypes associated with aroma, including one linked to the characteristic *BADH2* allele. A multi-location trial was done to understand the impact of the environment on grain attributes. Tukey's tests indicated significant variation in 1000-grain weight across locations, while grain length and diameter showed relative uniformity; notably, short-grain aromatic rice exhibited stability in specific environments. The influence of the environment on gene expression was investigated through analysis of seven aroma-associated genes across different locations, with *pro*DH, linked to proline metabolism, found to be exclusively expressed in non-aromatic rice. Overall, this study sheds light on the intricate genetic, molecular, and environmental factors shaping rice aroma.

Development of CRISPR-CAS vector for haploid induction in maize

Maize is a vital cereal grain with global significance, playing a crucial role in food security, economic development, and industrial applications. The development of hybrid maize through haploid production has revolutionized agriculture by enhancing yield, uniformity, disease resistance. The genes *ZmMTL/ZmPLA1/ZmNLD* & *ZmDMP* has a pivotal role in haploid induction. Genetic natural variation in *ZmMTL/ZmPLA1/ZmNLD* having

4 bp insertion in the gene have been identified, possibly contributing to haploid embryo induction. So, we targeted to knockout a specific target region of *ZmPLA1/ZmNLD/ZmMTL,* and *ZmDMP*, using the CRISPR/Cas9 genome editing system. We constructed two gRNA for *ZmPLA1/ZmNLD/ZmMTL* and one gRNA for *ZmDMP* cloned into Cas9 vector using Golden Gate cloning technology in three level. A construct was developed consisting three gRNAs, driven by OsU3 promoter; Cas9 gene expressed under ubiquitin promoter and hygromycin as plant selection marker. Immature embryo was transformed using *Agrobacterium,* and the hygromycin resistance of the transformants were checked. *In vitro* method for haploid production through anther, was systematically investigated to optimize culture conditions and assess genotypic responses. The YP basal medium was supplemented with 2mg/l 2,4 D & 1mg/l Kinetin, pretreatment conditions and environmental factors. Twelve different hybrid maize genotypes were evaluated, and among them, three genotypes i.e., Pusa HM8 Improved, Pusa HQPM1 Improved, APCH-2 which demonstrated favourable outcomes in another culture. The induction frequency of calli and embryoids ranged in 4% in Pusa HM8 Improved, 8% in Pusa HQPM1 Improved, 5% in APCH-2 anthers plated among the three responsive genotypes. Overall, these findings contribute to advancing haploid induction methods in maize breeding, offering potential for accelerated development of pure-breeding lines with desirable traits.

Understanding the dose-dependent impact of zinc oxide nanoparticles on the physiology and molecular response in chickpea

The current study focuses on efficacious delivery and fortification of zinc in chickpea (*Cicer arietinum L.*). To evaluate this, an *in vitro* and *in vivo* study was conducted with nano zinc coated with a polymeric material i.e., carboxymethyl cellulose (CMC). The dose impact of the nanoparticles was assessed on the morphological, enzymatic and molecular end-points of zinc-responsive genes in chickpea. Nanozinc synthesized by the co-precipitation method and further characterized by FTIR, UV-Vis, and DLS was delivered at different concentrations (25 ppm, 100 ppm and 150 ppm) in a dose-dependent study. The results revealed the maximum efficacy of nanoparticle supplementation at 25 ppm in enhancing the physiological status, seed germination percentage and other antioxidant activities of the plant. The dosage also showed an upregulation of the zinc responsive genes such as ZIP 1, ZIP 19, SOD and ZIF 1. Moreover, the bioaccumulation of zinc and its impact on the rhizospheric microorganisms exhibited a positive response in the treatment groups. Thus, the study suggests that the supplementation of nano zinc as a possible alternative to zinc sulphate in the chickpeas.

Genome-wide identification and characterization of PEBP family genes in winged bean (*Psophocarpus tetragonolobus* L.)

Winged bean is a potential underutilized photoperiod sensitive legume usually grown under short-day conditions. It is comparable to soybean in terms of yield and nutritional composition, making it a valuable substitute for soybean in tropical areas. The transition from vegetative stage to reproductive stage in flowering plants is regulated by various plant internal and external environmental factors. In plants, PEBP proteins regulate flowering time, plant architecture, and seed dormancy. Understanding the molecular mechanism of photosensitivity in winged bean help to figure out the flowering mechanism and also to expand its cultivating area. In this study, genome-wide analysis revealed 12 PEBP genes in the winged bean genome which are probably responsible for flowering. Expression of the twelve PEBP genes were analyzed using the quantitative Real-Time PCR (qRT-PCR) in the photosensitive (AKWB-1) and photo-insensitive (IIABPIS-1) genotypes. Based on expression analysis, the *PEBP6* (*FT3*), and *PEBP8* (*FT4*) genes showed increased expression at reproductive stage in the photoperiod-insensitive genotype i.e., IIABPIS-1 under the long day condition compared to the vegetative stage. While *PEBP5* (*FT2*) shows lower expression than *PEBP6* (*FT3*) and *PEBP8* (*FT4*). In the photoperiod sensitive AKWB-1 genotype, there is no expression of any PEBP genes under long-day conditions therefore it remained in its vegetative stage. Taken together, overall results indicate that the PEBP family genes responsible for flowering and *PEBP5* (*FT2*), *PEBP6* (*FT3*), and *PEBP8* (*FT4*) are the probable FT genes involved in photoperiodic flowering in winged bean.

Investigating the molecular role of seed-coated nanoscale iron in chickpea

The current study explores the application of iron-oxide nanoparticles (IONPs) in enhancing chickpea growth and iron biofortification. Iron oxide nanoparticles were synthesized using the co-precipitation approach and characterized using UV-Vis, DLS, & FTIR techniques. To deliver nanoparticles effectively into the plant system, seed coating with CMC was employed. The study was conducted in two phases: first, germination sheets were used to determine optimal nanoparticle doses for the pot experiment. Second, the pot experiment evaluated various morpho-physiological parameters, including plant height, branching, flowering, pod formation and chlorophyll content. Chickpea plants supplemented with 75 ppm IONPs showed higher growth in all parameters compared to other treatments. Microbial analysis of rhizosphere soil revealed no adverse effects of nanoparticles on soil microbes. Using FTIR analysis, biochemical differences between treatments were observed. ICP analysis confirmed significantly increased iron biofortification in chickpeas treated with 75 ppm nanoparticles. Furthermore, the expression levels of selected iron-regulated genes were upregulated, particularly at a dose of 75 ppm iron oxide nanoparticles, leading to positive plant growth responses. Molecular docking demonstrated interactions between antioxidant enzymes and heme, highlighting potential mechanisms underlying the observed effects. Hence, application of seed coated nano iron-oxide at concentration of 75 ppm is effective for chickpea cultivation.

Understanding the biochemical and molecular basis of L-DOPA biosynthesis in faba bean (*Vicia faba* L.)

Faba bean (*Vicia faba* L.) is a cool season grain legume and is a rich source of the anti-parkinson drug, L-3,4-dihydroxyphenylalanine (L-DOPA). The biosynthesis of L-DOPA in plants is not uniform and remains unexplored. While, the hydroxylase activity of tyrosine hydroxylase (TH), cytochrome P450 (CYP450) class of enzymes and polyphenol oxidases (PPOs) are reported in plants, only the roles of PPOs in L-DOPA biosynthesis have been recently established in velvet bean. To understand the role of PPOs in the differential accumulation of L-DOPA in contrasting tissues of faba bean, contents of L-tyrosine, L-DOPA, tyramine, and dopamine in leaf, flower and other tissues were measured. It was found that the amount of L-DOPA is dependent on the types and growth stages of the tissues. Further, dopamine biosynthesis is majorly mediated through L-DOPA from L-Tyr. Gene-specific expression analysis in leaf and flower tissues revealed the selective induction of only four out of ten members of the PPOs gene family, namely *Vf*5g680, *Vf*1g760, *Vf*240, and *Vf*440. Higher expression of L-DOPA in young leaves and flower buds than in mature leaves and flowers was correlated with significantly higher expression of *Vf*5g680 and *Vf*1g760, respectively. The functional validation of these identified genes is required in future.

Identification and characterization of long non-coding RNAS (lncRNAs) related to pod and seed development in winged bean (*Psophocarpus tetragonolobus* L.)

The winged bean is a nutritionally rich, under-utilized legume crop widely cultivated for its immature pod, tubers and seeds. The winged bean plant parts, like tender pods, leaves, stems, flowers, and tubers, are nutritionally valuable and consumed as food. Its seeds are rich in protein (34.3–40.7%), oil (16.4–21.3%) and carbohydrates (23–40%). Hence, this crop has huge potential to provide nutritional security to a rapidly growing population. lncRNAs play a crucial role in regulating the gene expression profile at various developmental stages as well as combating biotic and abiotic stresses. In the present study, 9453 unique full-length transcripts were generated through Isoseq sequencing of RNAs isolated from the pod and seeds of winged bean. A total of 137 lncRNAs were identified using seed- and pod-specific full-length transcripts. *In-silico* interaction studies between lncRNAs, miRNAs and mRNAs identified three sets of endogenous target mimics (eTMs) involved in seed and pod development. The co-expression analysis of lncRNA and its eTM targets suggests that lncRNAs 16036, lncRNA_10137, and their target transcript_469 (Nuclear transcription factor Y) and transcript_3190 (Phosphate Transporter PHO1), respectively, are regulated through lncRNA-mediated eTMs. Our study concluded that lncRNA plays an important role in seed development and maturation.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Tharun Kumar C. J. (21673)	M.Sc.	Prevalence of lepidopteran-toxic genes in *Bacillus thuringiensis* isolates recovered from different agro-ecological regions in India and determination of toxicity towards different developmental stages of *Spodoptera frugiperda* (fall army worm)	Dr. Sarvjeet Kaur	*ICAR-NIPB, New Delhi
2.	Ashutosh Dilliprao Thakare (21674)	M.Sc.	Identification and expression profiling of genes involved in aluminum tolerance in chickpea (*Cicer arietinum* L.)	Dr. Anil Kumar Singh	*ICAR-NIPB, New Delhi
3.	Soumya Chakraborty (21675)	M.Sc.	Validation of anaerobic germination tolerance QTL, *QAG7, 1* in a RIL population	Dr. Deepak Singh Bisht	*ICAR-NIPB, New Delhi
4.	Balaji B. (21676)	M.Sc.	Identification and characterization of the yield-responsive cytokinin oxidase/ dehydrogenase (*CKX*) gene in *Brassica juncea* (L.) Czern	Dr. N. C. Gupta	*ICAR-NIPB, New Delhi
5.	Sanjay T. D. (21677)	M.Sc.	Designing prime edit guide RNA and construct development for base editing of rice *Osbri1*	Dr. P. K. Dash	*ICAR-NIPB, New Delhi
6.	Sonam Brijlal Ingle (21678)	M.Sc.	Understanding the effect of auxin, cytokinin and their cross talk on root growth under Al^{3+} stress in chickpea (*Cicerarietinum*)	Dr. Anil Kumar Singh	*ICAR-NIPB, New Delhi
7.	Subhash A. (21679)	M.Sc.	Frequency distribution of coleopteran and hemipteran-toxic genes in *Bacillus thuringiensis* isolates recovered from diverse habitats in India and evaluation of toxicity of *vip3Aa68*, *vip3Aa72* and *cry1Ib7* genes towards *Spodoptera frugiperda* (fall army worm)	Dr. Sarvjeet Kaur	*ICAR-NIPB, New Delhi
8.	Bhanu Kumar Tiwari (21680)	M.Sc.	Haplotype diversity of *BADH1* and *BADH2* genes and its relation to the aroma in Indian short-grain aromatic rice cultivars.	Dr. Deepak Singh Bisht	*ICAR-NIPB, New Delhi
9.	Kiran Mahavir Magdum (21681)	M.Sc.	Development of CRISPR-CAS vector for haploid induction in maize	Dr. Jayanti M.	*ICAR-NIPB, New Delhi
10.	Pallavi S. (80020)	M.Sc.	Expression and developing CRISPR/CAS9 constructs of flavanone-3-hydroxylase (*F3H*) and flavone synthase (*FNS*) genes in contrasting lines of soybean to yellow mosaic disease	Dr. Palaiyur Nanjappan Sivalingam	**ICAR-NIBSM, Raipur

11.	Ajay Kumar (80021)	M.Sc.	Molecular characterization of begomoviruses infecting okra in the eastern region of India	Dr. Palaiyur Nanjappan Sivalingam	**ICAR-NIBSM, Raipur
12.	Usha M S. (80022)	M.Sc.	Isolation and characterization of bacterial endophytes having antimicrobial potential against *Sclerotium rolfsii* in chickpea	Dr. Vinay Kumar	**ICAR-NIBSM, Raipur
13.	Shakespear S. (80023)	M.Sc.	Molecular detection and *in-silico* analysis of broad spectrum resistance genes for bacterial leaf blight in wild and cultivated *Oryza* species	Dr. Vinay Kumar	**ICAR-NIBSM, Raipur
14.	Olivia Nianglunhoih (90008)	M.Sc.	Understanding the dose-dependent impact of zinc oxide nanoparticles on the physiology and molecular response in chickpea	Dr. Biplab Sarkar	**ICAR-IIAB, Ranchi
15.	Shivakumaraswamy M. (90015)	M.Sc.	Identification and characterization of salt-stress-related lncRNAs in Indian mustard (*Brassica juncea* L.)	Dr. Binay Kumar Singh	**ICAR-IIAB, Ranchi
16.	Mustafa N. (90016)	M.Sc.	Genome-wide identification and characterization of PEBP family genes in winged bean (*Psophocarpus tetragonolobus* L.)	Dr. Binay Kumar Singh	**ICAR-IIAB, Ranchi
17.	Sudheer Bishnoi (90017)	M.Sc.	Investigating the molecular role of seed-coated nanoscale iron in chickpea	Dr. Biplab Sarkar	**ICAR-IIAB, Ranchi
18.	Pratik Prasad Singh (90018)	M.Sc.	Molecular insight into the protective role of green copper nanoparticle against *Fusarium oxysporum* in chickpea	Dr. Biplab Sarkar	**ICAR-IIAB, Ranchi
19.	Sradhanjali Jena (90019)	M.Sc.	Understanding the biochemical and molecular basis of L-DOPA biosynthesis in faba bean (*Vicia faba* L.)	Dr. Biplab Sarkar	**ICAR-IIAB, Ranchi
20.	Ankit Raj (90020)	M.Sc.	Identification and characterization of long non-coding RNAs (lncRNAs) related to pod and seed development in winged bean (*Psophocarpus tetragonolobus* L.)	Dr. Kishor Uttamrao Tribhuvan	**ICAR-IIAB, Ranchi
21.	Sandeep Jaiswal (10639)	Ph.D.	RNAi mediated silencing of UDP-glucose pyrophosphorylase gene (*UGPase*) for the amelioration of cold-induced sweetening in potato	Dr. Debasis Pattanayak	ICAR-IARI, New Delhi
22.	Priyanka Singh (10697)	Ph.D.	Elevated temperature effect on grain chalkiness and meta-analysis of underlying QTLs in rice	Prof. N. K. Singh	*ICAR-NIPB, New Delhi
23.	Parichita Priyadarshini (10837)	Ph.D.	Genome-wide identification and characterization of microRNAs and their target genes in response to chickpea-*Fusarium oxysporum* interaction	Dr. P. K. Jain	*ICAR-NIPB, New Delhi
24.	Sreeshma N. (10839)	Ph.D.	Fine mapping of *qPH5.1* QTL region for dwarfness in pigeon pea (*Cajanus cajan* L. Milsp. cv Pusa Dwarf)	Prof. N. K. Singh	*ICAR-NIPB, New Delhi
25.	Alka Bharati (10840)	Ph.D.	Carbon partitioning and its genetic regulation during grain filling in wheat (*Triticum aestivum* L.) under nitrogen stress	Dr. P. K. Mandal	*ICAR-NIPB, New Delhi
26.	Kuldeep Kumar (10842)	Ph.D.	Identification of genes and markers associated with flowering trait in diverse pigeonpea genotypes	Dr. Kishor Gaikwad	*ICAR-NIPB, New Delhi

27.	Deepanshu Jayaswal (10843)	Ph.D.	Identification of vital genes of aphid infestation and pyramiding genes for aphid tolerance in *Brassica juncea*	Dr. Rekha Kansal	*ICAR-NIPB, New Delhi
28.	Sachin (11074)	Ph.D.	Inactivation of amylase-trypsin inhibitors through genome editing for development of low immunogenic wheat	Dr. P. K. Mandal	*ICAR-NIPB, New Delhi
29.	Sheel Yadav (11291)	Ph.D.	Understanding epigenetic regulatory mechanisms influencing drought tolerance pathways for identification of key genes in chickpea	Dr. P. K. Jain	*ICAR-NIPB, New Delhi
30.	Waghmare Sandesh Tulshiram (11370)	Ph.D.	Understanding the defence mechanisms of *Brassica juncea* L., *Sinapis alba* L. and *Camelina sativa* L. against infection by *Alternaria brassicae*	Dr. Anita Grover	*ICAR-NIPB, New Delhi

*Sister Institute

**Outreach Institute

Plant Physiology

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Prof. Anjali Anand

Division of Plant Physiology focuses on basic and strategic research for enhancing physiological efficiencies under abiotic stress conditions and resource use efficiency for better productivity. To achieve these targets, studies related to high throughput phenotyping for identification of superior donors and breeding lines, functional validation of genes and mapping QTLs for abiotic stress tolerance are conducted. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Resource Use Efficiency of Crop Plants

Physiological characterization of component traits associated with nitrogen use efficiency in contrast rice genotypes

The influence of nitrogen (N) availability on rice grain yield and quality is significant. However, excessive N usage results in higher costs and negative environmental impacts. To enhance nitrogen use efficiency (NUE) in rice genotypes and understand the mechanisms behind N stress tolerance, a pot culture experiment was conducted at Nanaji Deshmukh Plant Phenomics Centre (NDPPC), ICAR – IARI, New Delhi during the 2022 *kharif* season. Fifteen rice genotypes were evaluated in controlled greenhouses under two nitrogen conditions: controlled (120 Kg/ha) and without additional nitrogen (N0: 0 Kg/ha). Data was collected at five growth stages. Through an analysis of 140 traits among the genotypes, standout performers in terms of NUE were identified as Cauvery and BAM3690, while Moroberekan and BAM8315 showed lower NUE using the Multi-Trait Genotype-Ideotype Distance Index (MGIDI). Additionally, two novel indicators, namely rCCI (relative chlorophyll content index) and QY (Quantum yield) at 30 days after transplanting (DAT), were discovered. These indicators could predict early N stress and qualitative discrimination of N stress levels using machine learning-based multivariate linear discriminant analysis (ML-LDA). The connection between nitrogen uptake efficiency (NUpE) and grain weight per plant (GWPP) was found to be contrasting in high NUE (R=0.94) and low NUE (R=0.32) groups, emphasizing NUpE role in enhancing overall NUE. Comparative analysis of nitrogen assimilatory enzyme activity (NR, NiR, GS, GOGAT & GDH) and gene expression patterns (*OsNLP4, OsNRT1.1b*, and *OsGS1.1*) confirmed that the Cauvery genotype exhibited efficient nitrogen sensing, uptake, transport, and assimilation.

Evaluation of *Triticum dicoccum* genotypes for nitrogen response and identification of associated genomic regions

Wheat (*Triticum dicoccum L*) is a global staple food crop accounting for nearly 20% of calories and protein consumed by human population. The nitrogen use efficiency (NUE) of cereal crops including wheat is approximately 33%. It is well known that a large number of genes regulate the quantitative traits such as NUE. However, compared to other traits, in crops, including wheat, have had fewer studies on QTL analysis for NUE. It is possible to identify the genetic elements mediating high NUE and N deficiency tolerance (NDT) using natural genetic variation. The present study was conducted to identify *Triticum dicoccum* lines with contrasting response to three different nitrogen doses. A standardization experiment was carried out using the bread wheat variety HD 3298. In the main experiment, study 170 *Triticum dicoccum* lines and 2 bread wheat varieties as checks were included. The variation in chlorophyll content index (CCI), biomass (fresh weight and dry weight), root system architecture and chlorate resistance score under different nitrogen doses were significant with respect to the three N treatments. The collected data was then used for genome-wide association study (GWAS) for nitrogen response. For the six traits analyzed under three nitrogen treatments a total of 40 SNPs with significant marker trait association were identified. Principal component analysis (PCA) of phenotypic data identified promising genotypes. Seven lines performed better in at least two comparisons. Selected genotypes were re-evaluated and physiological and molecular analysis of two genotypes were conducted. The variation in N metabolism was partially explained by changes in gene expression, suggesting the equally important role of post-translational regulation. Our findings suggest that the newly identified genomic regions and associated the candidate genes may serve as resources for genetic advancement and increase the effectiveness of N utilisation in wheat.

Association between haplotype and phenotype for *NRT1.1* gene in *Oryza sativa*

An attempt was made to identify the haplotypes of nitrate transporter, *NRT1.1*, that can be used as a "donor" for haplotype-based breeding. Twenty-five days old seedlings of 272 rice accessions (3KRG panel) were phenotyped under low and sufficient N. Principal component analysis resulted in 9 most contributing traits governing genotypic variability in response to low N. Based on relative values, hierarchical cluster analysis resulted in three clusters, N-efficient, N-inefficient, and intermediate. The haplotype analysis for OsNRT1.1 classified the rice accessions into two haplogroups for *OsNRT1.1A*, three for *OsNRT1.1B*, and five for *OsNRT1.1C*. Based on haplo-pheno association, by comparing the mean trait values of haplotypes, the superior haplotypes (SH) were H2 and H3 in *OsNRT1.1A*, and *OsNRT1.1B* respectively, while for *OsNRT1.1C*, SH were H3 and H1 among the efficient cluster. However, the inferior haplotypes (IH) were H1 in *OsNRT1.1A*, H3 in *OsNRT1.1B*, and H3, H2 in *OsNRT1.1C* among the N-inefficient cluster. The haplo-pheno association reveals five accessions (ARC 7091, ADT 12, ARC 11571, SIMUL KHURI, ARC 12920) as N-efficient, while three accessions (BK 26, ARC 13591, KARAHANI) were N-inefficient, that were common in all three *NRT1.1* efficient and inefficient haplotypes of paralogs. The qRT-PCR data showed expression of *OsNRT1.1A* and *OsNRT1.1B* was significantly higher in SIMUL KHURI in both shoots and roots under low N compared to the sufficient N. Most of the inferior accession's expression was higher in root and lower in shoot resulting in N-inefficiency of the genotype. Protein alignment of the contrasting accessions revealed an amino acid change in OsNRT1.1C at 403rd position (I/V) in the inferior accessions which affects the active site of protein, accounting for the N-inefficiency of those accessions. In conclusion, our haplotype research on the *NRT1.1* gene sheds light on its genetic diversity and potential implications for nitrate uptake efficiency.

Physiological assessment of nano-urea application on rice crop

Present scenario indicates for continuous efforts in enhancing rice productivity and that too with effective use of resources. Among diverse strategies, effective use of nitrogen (N) fertilizers is crucial. In this context, introduction of nano-urea is an important development. There are reports pointing out benefits as well as concerns on the use of nano-urea. Therefore, a study was taken up on physiological assessment of nano-urea application on rice crop (variety, Pusa Basmati 1692). Normal sown rice crop (under flooded condition) was subjected to five treatments. Control (T_1) with recommended doses of fertilizers. Other four treatments consist of application of 50

% N (T_2 and T_4) and 75 % N (T_3 and T_5) to the soil. To these, N was supplemented through foliar applications, either as normal-urea (2 % w/v) (T_2 and T_3) or nano-urea (0.016 % w/v) (T_4 and T_5) at 30 days after transplanting (DAT) and at 50 DAT. The results revealed that foliar applications had no impact on photosynthetic pigments. Photosynthesis related parameters at 50 % N were lower and at 75 % N were comparable with control. T_5 was found to be statistically at par with control for many physiological and shoot, root, leaf growth and dry matter partitioned to panicle. N and protein % in leaf, shoot, root and grain showed no difference across treatments. T_5 showed lower N uptake for leaf at tillering stage than the control, but later at anthesis and post-anthesis stages, it matched with control. Control achieved highest grain yield and it was statistically comparable to T_5 and higher than other treatments. Overall, based on this short-term (one year) study, T_5 was at par with control, indicating for saving of about 25 % of urea. However, there exists strong possibility for mining of N from the soil itself. In future, it is important to monitor for sustenance in long-term (with continuous use of nano-urea) not only on specific crop and cropping systems but broadly in terms of agriculture, ecosystem and environment. Issues like; safety and impact on health also need to be answered before reaching to any final conclusion with respect to large-scale use of nano-urea in India.

Phenomics and genetic analysis of nitrogen use efficiency in wheat (*Triticum aestivum* L.)

High throughput automated sensor and computer vision-aided phenotyping, semi-automated phenotyping and manual phenotyping were used to evaluate the nitrogen deficiency response and NUE in a wheat RIL population derived from RAJ 3765 × HD 2329. Plants grown in control and N-deficiency were phenotyped during 60, 70, 80, 90 and 100 days after sowing (DAS) by using Visual, IR thermal and Near Infra-Red sensors using LemnaTec Scanalyzer3D system at NDPPC, IARI, New Delhi. A novel colour class related traits classification, and multimodal RGB and NIR based machine learning model for biomass estimation identified. Whole plant transpiration estimations showed that nitrogen deficiency increased the transpiration requirement of wheat 15%. Superior RILs with high yield, NUE and grain N concentration were identified by using the MGIDI. A high-density linkage map was constructed for 355 RILs with 1749 binned markers spanned over a total of 5,468 cM with marker density of 2.84 (marker/cM). A total of 554 significant QTLs (>3 LOD) were mapped (349 QTLs for phenomics traits and 205 QTLs for manual and semi-manual traits). QTLs for NUE, NUpE, NUtE, UI and Grain N content under both nitrogen sufficient and deficient conditions namely *QUi.iari-5A* (LOD: 3.32 & PVE: 8.95), *QUi.iari-7D* (LOD: 3.43 & PVE: 8.67), *QNUtE.iari-7A* (LOD: 3.76 & PVE: 9.59) and *QGrainN.iari-1A* (LOD: 3.35 & PVE: 8.45) were mapped. A major stable pleiotropic QTL namely *QSp.N.iari-7A* was mapped chromosome 7A for spikelet number and spikelet density under both control and N-deficiency conditions. By performing the *in silico* analysis of the QTL region, novel candidate genes coding for Cytokinin riboside 5'-monophosphate phosphoribohydrolase (LONELY GUY), glutathione metabolism, auxin signaling were identified. The superior RILs identified and QTLs mapped in this study will be useful in genetic improvement of NUpE and NutE in wheat.

Genome-wide analysis of calcium signalling network genes and their role in nitrogen response of bread wheat (*Triticum aestivum*)

The current in-practice semi-dwarf wheat genotypes (*Rht-1*) exhibit low nitrogen use efficiency (NUE) contributing to fertiliser N loss, environmental pollution and global climate change. Recent evidence suggests calcium (Ca^{2+}) as crucial mediator of nitrate (NO_3^-) signaling and metabolism. Using the near-complete genome of *Triticum aestivum* and its three progenitor species, we identified different Ca^{2+} signalling genes; 7 CBLs, 24 CIPKs, 17 CPKs, and 6 NLPs exhibiting distinctive expression patterns across tissue, genotype, and NO_3^- treatment. Sequence characterisation of CBL6 supports the possibility of NO_3 responsive post-translational modification.

We discern that optimum cytosolic Ca^{2+} levels ($[Ca^{2+}]_{cyt}$) up-regulate the NO_3^--responsive genes potentially by emulating NO_3^- signal. While high/low $[Ca^{2+}]_{cyt}$ hinder nitrate starvation response (NSR). Time-course analysis revealed peak expression of Primary nitrate responsive (PNR) sentinel genes at 30 min post NO_3^- treatment. EGTA, a Ca^{2+} chelator, validated Ca^{2+}'s involvement in PNR gene regulation and NO_3^- uptake. We unveiled tissue-specific, NO_3^--dose-dependent regulation of nitrate reductase, with Ca^{2+} as a crucial mediator. Elevated NO_3^- levels, with exogenous auxin and Ca^{2+}, inhibit root growth, possibly mediated by ethylene downstream of $[Ca^{2+}]$ cyt. We uncovered a synergistic interaction between nitric oxide (NO) and native auxin in lateral roots (LRs), with auxin elevating $[Ca^{2+}]$cyt, while NO acting downstream, affecting NO_3^--responsive LR hair growth. High NO_3^- levels hinder root hair development by importing shoot-derived auxin, validated by polar auxin transport inhibitor. Wheat leaf protoplast experiments confirmed NO_3^--induced $[Ca^{2+}]$cyt changes rely on extracellular Ca^{2+} influx and intracellular Ca^{2+} release. Further field experiment has shown that external calcium supplement will improve the NUE which is mainly due to improved N remobilisation and post anthesis N uptake. This comprehensive evidence underscores Ca^{2+}'s vital role in wheat's NO_3^- responses, simplifying NO_3^- signalling comprehension and offering potential solutions to enhance plant growth, yield and NUE through Ca^{2+} supplementation.

Physiological and molecular characterization of rice for nitrogen remobilization efficiency and nitrogen use efficiency

The primary requirement for nitrogen (N), a vital mineral ingredient needed to sustain the growth, development, and productivity of major cereal crops, is met by exogenous N sources. Roughly 60% of the nitrogen input for rice is thought to be wasted or lost to the environment. While nitrogen utilization efficiency (NUE) is greatly influenced by nitrogen remobilization efficiency (NRE) and microRNA (miRNA) driven regulatory processes, rice lacks characterization of NRE donors and NRE linked genes/miRNAs. Finding and characterizing donors for NRE, other NUE component qualities, and NRE-associated miRNAs/genes is the goal of the current work. Thirty different rice genotypes were subjected to field phenotyping in sufficient and deficient N circumstances over the course of two seasons (*Kharif*-2019 and *Kharif*-2020). Four distinct genotypes were chosen from these tests for additional physiological assessment, miRNA sequencing, and expression profiling in the *Kharif* season of 2021. The rice genotypes that performed well for more than one NUE component traits under both N sufficient (N120) and N deficient (N0) circumstances were IR-83929-B-B-291-3-1-1, Kalinga-1, APO, Pusa Basmati-1, and Nerica-L-44. A total of 26 miRNAs were found to express differently in response to N deficiency based on miRNA sequencing data. Of the 26, one (osa-miRNA2907) was a known miRNA, while the other twenty-five were new to rice. Of the 25 new miRNAs found in rice, 11 were up-regulated and 14 were down-regulated. It is clear that miRNA-mediated gene reprogramming is occurring based on the miRNAseq data and the qPCR validation of new and reported miRNAs. The differentially expressed miRNAs and the target genes they bind to are valuable tools for enhancing NRE and NUE in rice.

Marker-trait association studies for identification of genes governing nitrogen use efficiency in bread wheat

Field experiment for two seasons and hydroponics were conducted to phenotype a diverse set of wheat genotypes (351) for nitrogen use efficiency (NUE) under low and optimum N levels to identify the donors and QTLs/genes associated with NUE traits through genome-wide association studies (GWAS). Genotypes and N treatment significantly influenced all the traits. Genotypes were categorized into three major clusters in both field and hydroponics. From field experiment, N-efficient genotypes with high values for NUE-related traits were identified (BWL 5487, DBW 14, DBW 88, Halna, HD 2891, HD 2285, HD 2687, HD 2987, KAUZ_AA_KAUZ, and KLP 415). In hydroponics, genotypes were evaluated under low and optimum N conditions for root traits. Based on PCA, genotypes GUTHA, GW 322, HD 2987, NANJING 8611, and HD 2891 belonged to N-efficient as they exhibited robust root growth in hydroponic conditions. Both panels (field, panel 1 and hydroponics, panel 2) were subjected to genotypic evaluation with a total of 8,941 and 8,788 SNPs. Population structure analysis of both GWAS panels revealed three subpopulations; whereas, LD decay was observed at 4.26 Mb and 4.35 Mb region for panel 1 and panel 2, respectively. GWAS analysis of Panel-1 revealed a total of 22 MTAs among them three were pleiotropic. The SNP AX-94476859 was linked to primary root length and root tips under optimum N. Additionally, two markers (AX-94823242 and AX-94407400) were identified for root biomass and root-shoot-ratio under optimum and low N respectively. GWAS analysis of Panel-2 revealed a total of 78 MTAs, including two stable and eight pleiotropic MTAs. Notably, marker AX-95159335 and AX-94778143 associated with grain N uptake and total grain weight, respectively were expressed in both seasons under low N supply. These SNPs associated with important candidate genes governing NUE has the potential to improve N-efficiency in wheat through marker assisted breeding.

Phenotyping and characterization of radiation use efficiency in basmati rice accessions

Radiation use efficiency (RUE) is a potential target for improving biomass productivity and yield in Basmati rice. Initial field evaluation of RUE related traits in Basmati rice at anthesis (biomass production, leaf area and biomass accumulation per leaf area per day) was used to select 24 contrasting Basmati genotypes and two non-Basmati HYVs (PRH-10 and IR-64). Further detailed investigation of RUE related traits in selected genotypes, such as - radiation interception, RUE, photosynthesis, biomass, yield and yield components showed that biomass production was significantly correlated with the total intercepted PAR (TIPAR) and RUE. The genotypes with higher TIPAR also showed the ability of the canopy to intercept higher fraction of incident PAR (fIPAR). The fIPAR was associated with the leaf architecture in terms of leaf angle, leaf size and leaf area index (LAI). RUE was correlated with the higher net assimilation rate; however, the correlation of RUE could not be scaled down to the leaf photosynthesis rate and stomatal conductance. Nevertheless, higher RUE was associated with the absolute growth rate (AGR) and crop growth rate (CGR) through the influence of higher NAR and LAI. Higher biomass production was also associated with plant height. In terms of yield parameters, partitioning was associated with the reduced plant height and higher grain numbers per m2 through production of more spikelets per panicle. High biomass Basmati genotypes showed higher LAI, smaller erect leaves indicated by its lower extinction coefficient (k) and flag leaf area, higher CGR, RUE and Pn rate compared to the low biomass genotypes. The present study led to the understanding that yield improvement in Basmati rice will require higher radiation interception, RUE and improved harvest index and there will be need to reduce plant height and increase the sink capacity in terms of higher grain numbers per m^2.

Theme 2: Abiotic Stress Tolerance of Crop Plants

Phenotyping of wheat genotypes for heat stress

Wheat (*Triticum aestivum*) is widely cultivated on a global scale and plays a crucial role as a staple food for a substantial proportion of the world's population. Due to its sensitivity to high temperatures, wheat is susceptible to heat stress, which is a key environmental factor that exerts an adverse effect on global wheat production. In order to effectively address the increasing constraints caused by increased temperature, it is important to identify wheat genotypes that exhibit more resistance to heat stress. In light of these stated issues, our study aimed to assess the impact of heat stress on a sample of 300 distinct wheat genotypes, with four checks (HD-3271, HD-3086, HD-

3237, HD-2967). The study was carried out in controlled greenhouse conditions during the rabi season of 2022 at the Nanaji Deshmukh Plant Phenomics Centre, ICAR - IARI, New Delhi. Two distinct sets of experiments were conducted, one under normal temperature and the other under elevated temperature condition. Heat stress was given after the plants attained booting stage. The experiment was carried out using pots and followed a completely randomized block design (CRD) statistical approach. Morphological, physiological and yield data were collected after heat stress implementation which provided insights into plant characteristics and physiological processes. A total of 25 stable promising genotypes were identified that exhibited superior performance across many characteristics in both controlled and heat stress conditions. Biomass, HI and many other traits were found to be effective for the selection of heat-tolerant genotypes. The Multi-trait genotype-ideotype distance index (MGIDI) analysis aided the identification of 29 superior heat tolerant donor genotypes. The genotypes that have been identified as heat-tolerant hold potential for additional research and integration into breeding programme aimed at enhancing wheat resilience to heat stress.

Genome wide association studies on seedling high night temperature tolerance in wheat

Early sowing of wheat is undertaken in north western and central parts of India to capitalize on the residual soil moisture after the paddy harvest. This may lead to establishment of a poor crop stand due to high temperature exposure to the emerging seedlings. The dissection of high temperature into maximum and minimum temperature show that over the past there is a greater increment in night- (0.28 °C/decade) than *day-time* (0.19°C/decade) temperatures. This emphasizes the need of developing seedling stage high night temperature (HNT) tolerant lines in wheat for which phenotyping of the germplasm is necessary for selection of donors for introgression of the trait in breeding programs. We phenotyped 290 diverse wheat germplasm for tolerance to high night temperature (HNT) of ~ 4.9 ^{O}C over ambient, to identify associated SNP markers and candidate genes for heat tolerance using genome-wide association studies. Phenotypic variability was observed amongst the germplasm for vigor indices, root and shoot dry weight, root architecture, length of first emergent leaf, specific leaf area, chl a/b and total soluble protein. The mean shoot dry weight reduced significantly by 49.26% under HNT in comparison to control which was positively correlated with Vigor index- II, length of first emergent leaf, specific leaf area and root dry weight and surface area. The HNT tolerant donors were identified based on heat susceptibility index (< 0.5). The putative genes controlling HNT tolerance in wheat genotypes at seedling stage were found to be *Traes CS3A02G022600, TraesCS6A02G296700, TraesCS2A02G474300, TraesCS4A02G333800* and *TraesCS6A02G339100*. Candidate gene analysis unveiled substantial sequence resemblances between certain significant loci and candidate genes implicated in plant stress responses, encompassing heat, drought, and salt stress. Thus, our study provides the genetic basis of heat tolerance to high night temperatures at the seedling stage which will be useful for developing climate smart varieties.

Regulation of stay green trait by cytokinins and γ-aminobutyric acid (GABA) under heat stress in wheat (*Triticum aestivum* L.)

Wheat crop is often challenged by terminal heat stress resulting in premature leaf senescence, forced maturity and finally yield loss. One of the strategies for minimizing the yield loss is to maintain 'stay green trait'. Thus, in order to improve the stay green trait two experiments were conducted and heat stress was imposed by delaying the sowing date i.e. normal sown (11th Nov, 2022) and late sown (4th Jan, 2023). During 1st experiment, out of 32 genotypes Chirya 3 and HD 2851 were emerged out to be stay green types. 2nd experiment was conducted using contrasting genotypes viz. Chirya 3 (stay green) and HD 2329 (non-stay green) to dissect the cytokinins and GABA-modulated stay green trait for the heat tolerance and yield. Experiment comprised of main temperature treatments (normal and late sown heat stress) and sub-treatments had applications of bioregulatory molecules i.e. BA (50 ppm), TDZ (10 ppm), GABA (100 ppm), BA+GABA (50+100 ppm) and TDZ+GABA (10+100 ppm) and water spray as control at anthesis. Observations were recorded after anthesis at 0, 7, 21 & 28 days. Heat stress enhanced the leaf senescence, lipid peroxidation, hydrogen peroxide, membrane injury, TSS, proline, antioxidant enzymes activity, chlorophyllase activity, zeaxanthin, expression of *Ta*VDE, *Ta*WRKY42 and *Ta*SAG12 and reduced SPAD value, NDVI, leaf area, LAD, photosynthetic pigments, photosynthesis, *Ta*RbcL expression, TR, gs, Fv/Fm, YII, GFR, biomass, yield and its components. Response to heat stress was higher in HD 2329. However, foliar application of cytokinins based treatments enhanced the stay green trait, yield and thermotolerance by improving photosynthetic pigments, photosynthesis, Fv/Fm ratio, NPQ, expression of RbcL, antioxidant enzymes activity, osmolytes, zeaxanthin, expression of VDE and restricting lipid peroxidation, ROS production, membrane injury, chlorophyllase enzyme activity, expression of WRKY42 & SAG12 and leaf senescenceunder normal and stress conditions. The maximum efficacy in terms of stay green trait, thermotolerance and yield was obtained with the foliar treatment of BA+GABA.

Analyzing growth and physiological response of Brassica genotypes under moisture deficit stress

Drought, affecting over 40% of the world's land, poses a significant threat to global food production. It impacts mustard's development and seed yield in India's arid and semi-arid regions. To address climate change challenges, crops must thrive in challenging environments and enhance quality and output. Understanding plant responses and physiological mechanisms can help breeders create stress-tolerant varieties. An experiment conducted during 2022-23 at ICAR-IARI examined the impact of drought stress on 30 elite mustard genotypes. Results showed that drought significantly affected plant traits such as relative water content, SPAD value, photosynthetic parameters, total chlorophyll content, quantum yield, canopy temperature, proline content, and yield parameters. The study found that drought stress decreased RWC, SPAD value, photosynthetic parameters, total chlorophyll content, and quantum yield, while increasing canopy temperature and proline content. The siliqua number, siliqua weight and seed yield are decrease significantly due to drought stress. Genotype IM-39, PM-25, PDZM-31 and DJ-26 was found promising for drought tolerance traits. The study analyzed 30 mustard genotypes under control and drought stress conditions using ImageJ software. The analysis used parameters like area, height, perimeter, roundness, width, feret's diameter, Feret's angle, solidity, and aspect ratio to interpret shoot and silique features. All genotypes were assessed, with DJ-26, IM-39, LES-54, DRMRCI-116, PM-25, and RE-8 being found to be promising. IM-22, PM-25, DRMRCI-116, and PM-30 were also found promising under drought conditions. Therefore, our findings indicate that image-based methods can be employed to screen mustard genotypes based on shoot and the siliqua features.

Optimization of phenotyping protocol to assess waterlogging induced roots in cowpea (*Vigna unguiculata* (L.) Walp.)

Cowpea is a favoured crop for intercropping and crop rotation due to its short growth duration and resilience to drought and high temperatures. However, the absence of waterlogging tolerance traits in improved cultivars, primarily bred for yield, quality, and pest resistance, poses a threat to cowpea production. To address this, efficient non-invasive phenotyping tools are crucial for evaluation of cowpea genotypes for waterlogging tolerance traits. Hence, this study was aimed to optimize an affordable and non-invasive phenotyping protocol for assessing waterlogging-induced roots (WIR). The methods optimized for stress imposition, image acquisition, and image analysis could effectively differentiate waterlogging stress-response of cowpea genotypes. Significant genotype variations in WIR architecture and growth rate were revealed by image derived Total Root Length (TRL), Network

Area (NA), Convex Area (CA), Volume (Vol) and Median number of roots (MeN) etc. The efficacy of these traits in distinguishing waterlogging-tolerant and intolerant genotypes was validated with conventional parameters. A strong positive correlation between conventional and WIR image features indicated that WIR, playing a role in waterlogging tolerance, can be reliably measured noninvasively. The phenotyping protocol, along with traditional parameters, could help in identification of promising genotypes viz., CG221 and CG121, showcasing enhanced WIR and superior performance under waterlogging conditions. These genotypes also exhibited remarkable recovery from waterlogging. The affordable phenotyping protocol developed in this study promises to serve as an effective phenotyping tool for assessing waterlogging-induced roots in cowpea and promising genotypes like CG221 and CG121 may serve as donors for waterlogging tolerance.

Phenomics and molecular analysis of water use efficiency (WUE) and drought tolerance in rice (*Oryza sativa* L.)

A study with 152 RILs of BVD109 x IR20 under well-irrigated and drought stress conditions was conducted to utilize phenomics to bridge the phenotype-genotype gap in WUE in rice. Two experiments were conducted at NDPPC, ICAR-IARI, New Delhi. Sixteen machine learning models were tested for predicting biomass and found that the Bayesian regularized neural network (BRNN) model is the best with $R^2 = 0.96$ and 0.95 for FW and DW of biomass, respectively. Mean day time transpiration and mean night time transpiration among RILs varied from 533-944 and 162-222 g $H_2O.m^2PSA.day^{-1}$, respectively. Among RILs WUE varied from 0.003 - 0.307 with a mean of 0.093 cm^2 PSA.g^{-1} H_2O water used. The estimated broad sense heritability (h^2) of transpiration efficiency and WUE traits were ranged from 44-95%, and 65-86%, respectively. We used 1859 good quality markers for construction of genetic linkage map. A total of 112 QTLs were detected for 240 traits. Three stable QTLs associated with transpiration efficiency (qT2_TTEswpsa 6.1 qT2_TTEbm 6.1 and qT2_DTEbm6.1) were identified across two years in 2018 and 2019. Four most significant major effect QTLs for total WUE (tWUE) namely *qT1-T5_tWUE 6.1, qT2-T5_tWUE 6.2, qT3-T5_tWUE 6.1 and qT3-T4_tWUE 6.1* were identified to possess very high LOD (>4) and PVE values (>26). Stable QTLs for night-time WUE viz., *qT3-T5_ntWUE 6.1, qT3-T4_ntWUE 6.1, qT1-T2_ntWUE 6.1*, which present in same loci (Chromosome 6 position 82cM) were identified with very high LOD (>4) and PVE values (>21) across years. Candidate gene analysis led to the identification of several novel genes and most of the known genes for stomatal development (*OsERECTA2, OsEPF1, OsEPFL7, STOMOGEN,MAPK3/6 ,OsSPCH1/2,OsICE1/2*) and stomatal opening and closing (ABA receptor PYL1, PP2Cs, SnRK2s, BAK2). The superior RILs identified and QRLs mapped will be useful in development of water-wise climate resilient rice crop.

Temporal changes in sink carbon metabolism in developing rice grains under high night temperature

Increase in night temperature can disrupt the carbon flux in plants by targeting the intricate physiological processes of photosynthesis and respiration. The crop yields are penalized due to limitation of the photosynthates towards the development of grains. The present study was conducted to evaluate the adjustment in the carbon pool at the source and sink terminus and its influence on grain filling dynamics of spatially differentiated sinks (superior and inferior spikelets) in two genotypes of varying high night temperature (HNT) sensitivity viz. Vandana (HNT sensitive) and Nagina 22 (HNT tolerant) under HNT (+4°C above control) from anthesis to physiological maturity. Both genotypes showed notably elevated night respiration rates but the high respiration rates in Nagina 22 were balanced by an augmented photosynthesis rate, ensuring consistent total dry matter production under HNT. The photosynthetic to respiratory rate ratio (Pn/Rn) was highly correlated with the number of grains per plant (r =0.86***) and negatively with spikelet sterility (r = -0.93***) resulting in higher grain number and grain weight per plant, particularly of inferior grains in Nagina 22. Nagina 22 recorded a higher grain filling rate at 5 and 10 days after anthesis (DAA) along with 1.5- and 4-fold increase in translocation of ^{14}C sugars towards superior and inferior spikelets, respectively. Increased sucrose breakdown at peduncle combined with lower sucrose synthase activity in both the spikelets of Vandana limits starch synthesis and grain weight. However, reconfigured sugar allocation to inferior spikelets, as well as increased sucrose synthase activity and starch synthesis, helped Nagina 22 to maintain grain weight under HNT. An increase in the rheological properties of rice flour of Nagina 22 under HNT indicated the stability of starch. Thus, source and sink adjustments under HNT helped in maintaining the yield and quality of the tolerant genotype (Nagina 22).

Understanding physiological and molecular mechanism regulating yield and quality during combined drought and heat stress in wheat (*Triticum aestivum L.*)

Climate change poses a severe threat to global wheat production, with rising temperatures and increased heat waves exacerbating heat and drought stress. This study investigated the combined effects of these stressors on four wheat genotypes—drought-tolerant (C306), drought-susceptible (HD2967), heat-tolerant (Raj3765), and heat-susceptible (WL711). Examining various stress conditions during critical anthesis and post-anthesis stages, the study found that the simultaneous occurrence of heat and drought stress significantly reduced chlorophyll content, photosynthetic rate, stomatal conductance, Fv/Fm ratio, and SPAD value across all genotypes. Conversely, levels of hydrogen peroxide, malondialdehyde, abscisic acid, and transpiration rate increased under combined stress. The impact extended to physiological and biochemical aspects, affecting pollen viability, relative water content, membrane stability, proline content, soluble sugars, proteins, total antioxidant capacity, and antioxidative defense mechanisms. Among genotypes, Raj3765 exhibited the most robust tolerance to combined stress, with elevated expression of genes related to chlorophyll and proline biosynthesis during anthesis. Correlation analysis highlighted significant associations between biochemical/physiological characteristics and agronomic productivity. Analysis of yield-related parameters and nutritional elements revealed that the combined stress had a more pronounced effect on yield, yield components, and grain quality compared to drought stress alone. Notably, under heat stress conditions, there were increases in protein, zinc, iron, and nitrogen concentrations. However, grain yield per plant was higher under non-stress conditions, emphasizing the severe consequences of simultaneous drought and heat stress. In conclusion, this study underscores the urgency of developing wheat varieties resilient to combined heat and drought stress to ensure global food security. Raj3765 emerged as a top performer, maintaining crucial physiological processes even under challenging conditions. The findings highlight the complexity of plant responses to stress and emphasize the need for comprehensive research on combined stress conditions in wheat crop productivity studies.

Identification of donors and evaluation of component traits for salinity tolerance in wheat (*Triticum aestivum*)

Soil salinity (EC of ≥4 dS m^{-1}) is a major abiotic stress leading to decreased crop production due to osmotic, ionic, and cellular ionic imbalance balance effects. The comprehensive study comprising four experiments aims to identify salinity-tolerant wheat landraces by thoroughly assessing component traits through physio-biochemical and molecular analyses. Due to the osmotic effect, the growth of the plants was compromised, and the associated decrease in stomatal conductance increased the canopy temperature. Thermal images could differentiate salt-tolerant and sensitive genotypes. Three hundred fifty wheat landraces and check lines were evaluated for salt stress (15 dS m^{-1}) tolerance in a hydroponic set-up. The clustering analysis categorized 350 genotypes into four control and 15 dS m^{-1} conditions clusters. Across the multi-trait genotype-ideotype distance index (MGIDI), Smith Hazel Index (SHI), and Stress Susceptibility Index (SSI), seven genotypes were consistently identified as tolerant among the top 150. In comparison, 12 genotypes were consistently classified as least tolerant. The selected tolerant and least tolerant lines were evaluated in pot and field experiments (at ICAR-CSSRI, Karnal). Salt stress accelerated shoot growth, reducing spikelet primordia quantity, leading to premature development of the terminal spikelet stage and anthesis. This decreased spike length and the number of spikelets per spike, ultimately reducing overall wheat yield. The most tolerant and minor tolerant genotypes with other tolerant lines, showed upregulation of tissue tolerance-associated genes. In the pot experiment, the TaSST gene was downregulated in all the sensitive genotypes, suggesting it to be a crucial regulator of salt sensitivity. Crosses were made with the salt-tolerant cultivars and Kharchia-65 to explore the tolerance traits of selected genotypes. The molecular regulators correlated with tolerance and the mapping populations generated in the present study can aid in exploring natural variation for developing sustainable strategies for salt tolerance in wheat.

Genetic dissection of salinity tolerance in chickpea

Salinity is a major abiotic stress that causes substantial yield loss in agriculture worldwide. Chickpea (*Cicer arietinum* L.) is an important legume crop but it is salt-sensitive. Genetic studies have revealed that salinity tolerance in chickpea is a complex trait governed by multiple genetic factors. Genome-wide association studies (GWAS) are now widely used to identify key candidate genes and regulatory pathways associated with salinity tolerance. In our study, to understand the complex physiological and molecular regulation of salt tolerance mechanisms in chickpea reference set, along with the positive check (CSG 8962) we examined how these genotypes respond to salinity at the seedling stage under hydroponic condition for two seasons (2021-22 and 2022-23) and selected two tolerant genotypes and least tolerant genotypes based on 20 different traits using selection indices such as SSI, MGIDI, and SHI. The selected contrasting genotypes were re-evaluated in a pot experiment for different component traits such as physiological traits, stress-associated traits, photosynthesis-related traits, tissue ionic contents, yield, and expression pattern of candidate genes. Higher transcript abundance was seen in genes such as *CaCLCb, CaNHX2, CaAGP14, CaP5CS like, CaEXPA2, and CaHSC70-2* under salinity in tolerant genotypes.Tolerant genotypes had higher yield than other genotypes and was on par with the check. The two seasons of hydroponic study data were used to conduct GWAS with 5 different models using GAPIT 5.0. Seven significant and stable SNPs were identified for five different traits and the candidate genes associated with these SNPs were identified. The expression pattern of these genes gave clear insights into how salinity-related genes are regulated in contrasting genotypes, especially in genes such as *CaROS1L, CaCYP450, CaOPR11, CaCCX4, CaAKT2/3, and CaCML11*.

Physiological and molecular dissection of melatonin signalling in development and stress responses of rice

Melatonin plays crucial role in plant growth, development and stress responses. Melatonin receptors have been identified in Arabidopsis, maize, tobacco, and cassava, but no *bona fide* receptor has been confirmed in rice. In this study, *OsPMTR*, was identified as a homolog of *AtCAND2* in rice and molecular docking revealed interaction between the OsPMTR and melatonin.OsPMTR is predicted as a plasma membrane localized, seven transmembrane domain containing protein resembling G-protein coupled receptor and has gene structure and physiochemical properties similar to that of *AtCAND2*. OsRGA1, a signaling protein in G-protein pathways, was confirmed as an interacting partner with OsPMTR via protein-protein docking. Gene expression analysis revealed that two OsPMTR interacting partners *(OsRGA1, OsCOLD1)* and four co-expressed genes(*OsrTGA2.1*, *OsWRKY90*, *OsDREB6/OsERF60* and *OsTCP5*) were significantly induced by exogenous melatonin treatment in rice, suggesting their role in melatonin signaling. For functional validation, transgenic rice cv. MTU1010 overexpressing *OsPMTR* and CRISPR-Cas9 mediated gene edited mutant lines were developed and confirmed by molecular analysis. *OsPMTR* overexpression results in increased plant biomass, higher stomatal density, productive tiller number and grain yield. Under drought stress it helps in maintaining transpiration-cooling, water balance, photosynthesis, and reducing reactive oxygen species levels. In contrast, *OsPMTR* mutants showed significant reduction in biomass, productive tiller and yield. Thus, OsPMTR is a positive regulator of plant growth and development, drought stress tolerance ability and grain yield. The growth impairments and drought susceptibility of *OsPMTR* mutants showed that the intracellular C-terminal region of OsPMTR is necessary for signaling for normal plant growth and development and drought stress tolerance. Our findings lay the foundation for future plant system experiments to explore OsPMTR's role as a melatonin receptor and it's signaling pathway in rice.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Pradeep K (21696)	M.Sc.	Genome wide association studies on seedling high night temperature tolerance in wheat	Dr. Anjali Anand	ICAR-IARI, New Delhi
2.	Kunkala Rahul Karthik (21697)	M.Sc.	Evaluation of *Triticum dicoccum* genotypes for nitrogen response and identification of associated genomic regions	Dr. Lekshmy Sathee	ICAR-IARI, New Delhi
3.	Sivapragasam (21698)	M.Sc.	Phenotyping of wheat genotypes for heat stress	Dr. Sudhir Kumar	ICAR-IARI, New Delhi
4.	K. Bharath Chandra (21699)	M.Sc.	Physiological assessment of nano-urea application on rice crop	Dr. Vijay Paul	ICAR-IARI, New Delhi
5.	Amooru Harika (21700)	M.Sc.	Physiological characterization of component traits associated with nitrogen use efficiency in contrast rice genotypes	Dr. Dhandapani R	ICAR-IARI, New Delhi
6.	Subrata Debnath (21701)	M.Sc.	Analyzing growth and physiological response of Brassica genotypes under moisture deficit stress	Dr. Mahesh Kumar	**ICAR-NIASM, Baramati
7.	Shricharan S (70014)	M.Sc.	Regulation of stay green trait by cytokinins and γ-aminobutyric acid (GABA) under heat stress in wheat (*Triticum aestivum* L.)	Dr. Pramod Kumar	**ICAR-NIASM, Baramati
8.	Dharani E (70015)	M.Sc.	Association between haplotype and phenotype for *NRT1.1* gene in *Oryza sativa*	Dr. Renu Pandey	**ICAR-NIASM, Baramati
9.	Chanumolu Hari Gopala Krishna (70016)	M.Sc.	Optimization of phenotyping protocol to assess waterlogging induced roots in cowpea (*Vigna unguiculata* (L.) Walp.)	Dr. Jagdish Rane	**ICAR-NIASM, Baramati
10.	Nitin Sharma (10869)	Ph.D.	Temporal changes in sink carbon metabolism in developing rice grains under high night temperature	Dr. Anjali Anand	ICAR-IARI, New Delhi
11.	Sandeep B Adavi (11095)	Ph.D.	Genome-wide analysis of calcium signalling network genes and their role in nitrogen response of bread wheat (*Triticum aestivum*)	Dr. Lekshmy Sathee	ICAR-IARI, New Delhi
12.	Biswabiplab Singh (11097)	Ph.D.	Phenomics and genetic analysis of nitrogen use efficiency in wheat (*Triticum aestivum* L.)	Dr. Viswanathan Chinnusamy	ICAR-IARI, New Delhi

13.	Elangovan A (11098)	Ph.D.	Phenomics and molecular analysis of water use efficiency (WUE) and drought tolerance in rice (*Oryza sativa* L.)	Dr. Viswanathan Chinnusamy	ICAR-IARI, New Delhi
14.	Payal Priyadarsini (11101)	Ph.D.	Phenotyping and characterization of radiation use efficiency in basmati rice accessions	Dr. Madan Pal Singh	ICAR-IARI, New Delhi
15.	Birendra Kumar Padhan (11318)	Ph.D.	Physiological and molecular characterization of rice for nitrogen remobilization efficiency and nitrogen use efficiency	Dr. Lekshmy Sathee	ICAR-IARI, New Delhi
16.	Dipankar Barman (11320)	Ph.D.	Physiological and molecular dissection of melatonin signalling in development and stress responses of rice	Dr. Viswanathan Chinnusamy	ICAR-IARI, New Delhi
17.	Shashi Meena (11322)	Ph.D.	Understanding physiological and molecular mechanism regulating yield and quality during combined drought and heat stress in wheat (*Triticum aestivum* L.)	Dr. Ajay Arora	ICAR-IARI, New Delhi
18.	Jagadhesan B (11582)	Ph.D.	Identification of donors and evaluation of component traits for salinity tolerance in wheat (*Triticum aestivum*)	Dr. Lekshmy Sathee	ICAR-IARI, New Delhi
19.	Suriyaprakash R (11586)	Ph.D.	Genetic dissection of salinity tolerance in chickpea	Dr. Lekshmy Sathee	ICAR-IARI, New Delhi
20.	Deepti Tiwari (11587)	Ph.D.	Marker-trait association studies for identification of genes governing nitrogen use efficiency in bread wheat	Dr. Renu Pandey	ICAR-IARI, New Delhi

**Outreach Institute

Session V: School of Horticultural Sciences

Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Floriculture and Landscape Architecture	06	09
Fruit Science	07	09
Post Harvest Technology	04	10
Vegetable Science	14	14
Total	**31**	**42**

SCHOOL OF HORTICULTURAL SCIENCE

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Co-convenor: Dr. Shruti Sethi, Principal Scientist, Division of Food Science & Post harvest Technology

Chairperson: Dr. Major Singh, Member (Plant Sciences), ASRB, KAB 1, Pusa, New Delhi

Dr. Major Singh has served in Agricultural Research and Management for 36 years under various capacities (Scientist – 13 years, Sr Scientist – 8 years, Principal Scientist/Professor – 15 years); Administrative experience- (Director – 5.3 years, Project Coordinator - 1.5 years, Head of Division - 5 years). He is the Fellow, National Academy of Agricultural Sciences, New Delhi. He has been bestowed with several awards, namely, ICAR Team Award for outstanding contributions in the field of vegetable breeding 2005, Rajiv Gandhi National Award from Ministry of Home Affairs 2010, Dr. Harbhajan Singh Award for outstanding research 2003, 2004 and 2015, Certificate of merit by Seed Research 2005 and CHAI Appreciation award 2021. He has served as Vice-president, Indian Society of Alliums, Pune; Secretary, APIV, Varanasi; Chief editor, Vegetable Science and Journal of Alliums. Mobilization of external funding. Dr. Singh was Leader/Principle Investigator in 13 externally funded projects which had inter-disciplinary, inter-institutional and even international participation. He has published more than 200 research articles in various reputed national and international journals and has authored three books ‘Heterosis in crop plants’, ‘Legume vegetables’ and ‘Biotechnology in crop improvement: concepts and manual’. He has guided 5 M.Sc. and 13 Ph.D students. Dr Singh has developed two hybrids ‘Kashi Sandesh’ and ‘Kashi Komal’, two varieties ‘Kashi Taru’ and ‘Kashi Prakash’ in brinjal; three hybrids ‘Kashi Surkh’, ‘Kashi sinduri’, ‘Kashi gaurav’ and one variety ‘Kashi Anmole’ in chilli; two varieties ‘Kashi Shakti’ and ‘Kashi Mukti’ in pea; one hybrid ‘Kashi Abhiman’ and one variety ‘Kashi Aman’ in tomato and one variety ‘Kashi Param’ in french bean. He has also developed Bt brinjal and Bt tomato using Cry 1Ac gene construct for resistance to shoot and fruit borer and has coordinated biosafety evaluation of Bt brinjal lines in the country. Dr. Singh has also developed transgenic lines in tomato using AtDREB1A and BcZAT12 gene constructs for water-deficit and multiple abiotic stress tolerance. He started marker assisted breeding in tomato and pyramiding of genes Ty1, Ty2 and Ty3 to develop durable resistant varieties against TyLCV. He initiated research on climate resilience and developed two tomato lines and two onion lines for high temperature tolerance. In onion two lines were identified for drought and excess water tolerance. Under the tribal support project, Nandurbar district of Maharashtra was taken up for technology transfer and promotion of onion cultivation. Due to continuous efforts of 5 years, the area under onion has increased 4 times in the district and farmers have benefited a lot by getting good price. Kharif onion, which is confined to Maharashtra and Karnataka, was extended to non-traditional regions such as eastern Uttar Pradesh and north eastern region of India. During the last three years, more than 400 farmers have started production of Kharif onions in Mirzapur, with the help of the state government, the production of Kharif onions is being increased to 2000 hectares.

Floriculture and Landscape Architecture

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Prof. K.P. Singh

Division of Floriculture and Landscaping heralds articulated and comprehensive research programmes in important flower crops on various aspects such as crop improvement using conventional and biotechnology tools, production in open and protected environments, micropropagation for mass multiplication, landscape gardening etc. Division is also imparting Under Graduate and Post Graduate teaching and human resource development as well as involved in dissemination of information and transfer of technology through outreach programmesfor the benefit of farming fraternity. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: *In vivo* and *In vitro* Evaluation of Germplasm of Ornamental Crops for Abiotic Stress

Studies on *in vitro* response of French marigold (*Tagetes patula* L.) genotypes to salt stress

This study was carried out on *in vitro* response of marigold genotypes to salt stress involving five marigold genotypes: Gulzafri Orange, Dainty Marietta, Pusa Arpita, Pusa Deep and Sel.Fr./R-5. Morphological traits, including shoot diameter and length, exhibited a decline with increasing NaCl level. Sel. Fr./R-5 displayed the maximum shoot diameter (1.03 mm) at 200mM NaCl, while 'Dainty Marietta' showed the minimum (0.72 mm). Shoot length peaked in 'Sel. Fr./R-5' (4.43 cm) and 'Gulzafri Orange' at 200mM NaCl, contrasting with 'Dainty Marietta' (1.90 cm). No significant difference was observed in internodal length and number of shoots. Root characteristics varied, with 'Sel. Fr./R-5' displaying the maximum number and length of roots. Survival percentage declined with increased NaCl, with 'Sel. Fr./R-5' showed the highest survival (66.67%) at 200mM NaCl. Chlorophyll and carotenoid content decreased with higher NaCl level. 'Sel. Fr./R-5' showed the highest chlorophyll a (5.09 mg/g FW), chlorophyll b (1.4 mg/g FW), and carotenoid (1.4 mg/g FW) at 200mM NaCl. Relative water content (RWC) was highest in 'Sel. Fr./R-5' (72.78%) and lowest in 'Pusa Arpita' (55.27%) at 200mM NaCl. Salt injury index increased, reaching a maximum in 'Pusa Arpita' (3.98) and a minimum in 'Sel. Fr./R-5' (3.00) at 200mM NaCl. Proline and MDA content, along with SOD, catalase, and GPX activity, increased with salt concentration. 'Sel. Fr.R/5' accumulated the highest proline (12.22 µmol/g FW) and exhibited the highest antioxidant enzyme activities. Nutrient parameters showed an increase in Na^+ content and Na:K ratio, while K^+, Ca^{2+}, and Mg^{2+} content decreased with higher NaCl. 'Pusa Arpita' displayed the highest Na^+ content and Na:K ratio, whereas 'Sel. Fr./R-5' showed the lowest Na^+ content and ratio. 'Sel. Fr.R/5' exhibited higher K^+, Ca^{2+}, and Mg^{2+} content. In conclusion, 'Sel. Fr./R-5' showed superior performance up to 200mM NaCl, suggesting its potential utilization in marigold breeding programs for salt tolerance.

Study on drought tolerance in chrysanthemum (*Chrysanthemum morifolium* Ramat.)

Chrysanthemum is one of the most beautiful ornamental crops grown for cut stems, loose flowers, as a pot and bedding plant. It is well known globally as a commercial crop and exhibition flower. It occupies a major place in the world market next to rose, but most chrysanthemum cultivars are very vulnerable to drought stress. To understand its resilience, a study on drought tolerance in chrysanthemum (*Chrysanthemum morifolium* Ramat.) was carried out. For this study, fifty genotypes were subjected to drought stress in pot, with assessments using traditional and modern image-based methods. Two drought phases were imposed: first, during the vegetative phase (30 days after planting), and second, during the flowering stage. Observations were recorded on morphological, physiological and biochemical parameters. Along with these parameters, plant responses were also captured through different imaging systems by employing plant phenomics facility. Results showed that drought stress imposed at vegetative and flowering stage; adversely affected growth and physiological processes in all genotypes which resulted in decreased commercial yield. Most of the genotypes showed early flowering as a drought escape mechanism. Physiological parameters like relative water content (RWC), chlorophyll levels, and photosystem II fluorescence were notably lower under stress, while canopy temperature was comparatively higher. Reduced chlorophyll and carotenoid content limited photosynthesis, impacting primary production. However, increased accumulation of total soluble sugars and proline correlated positively with stress tolerance. Among the genotypes, Gulmohar demonstrated superior resilience to drought stress. It maintained better physiological status, and exhibited desirable traits for drought tolerance, including greater plant height, biomass, and extensive root features. Overall, Gulmohar emerged as the most promising genotype, followed by Himjyoti, New Man, and Daity Med, showcasing commendable performance under drought stress.

Studies on performance of warm-season turf grasses under treated wastewater

Turf, composed of narrow-leaved grass species, serves both aesthetic and recreational purposes and is essential in various settings such as airports, sports fields, residential lawns, and more. However, urban water scarcity poses a challenge for maintaining green spaces. In 2023, a study entitled "Studies on performance of warm-season turf grasses under treated wastewater" at ICAR-Indian Agricultural Research Institute evaluated seven turf grass species under different treated wastewater irrigation levels (0%, 100%, 75%, 50%, 25%). Among the species, Seashore paspalum (*Paspalum vaginatum*) (S_6) demonstrated superior morphological characteristics when irrigated with 50% treated wastewater. Bermuda grass (*Cynodon dactylon* var. Tif dwarf - 419) (S_1) exhibited the highest nodes per inch, while Zoysia grass (*Zoysia japonica*) (S_1) displayed the longest internode and highest leaf count per shoot under the same irrigation level. Physiologically, Bermuda grass (*Cynodon dactylon* var. Tif dwarf - 419) (S_2) excelled in relative water content, membrane stability index, and chlorophyll content under 50% treated wastewater. *Paspalum vaginatum* (S_6) showed the highest leaf area index. In nutrient accumulation, Zoysia grass (*Zoysia japonica*) (S_1) had the highest nitrogen and potassium content, while Bermuda grass (*Cynodon dactylon* var. Tif dwarf - 419) (S_2) exhibited the highest phosphorus content under 50% treated wastewater. For heavy metals, Bermuda grass (S_2) accumulated higher levels of Ni, Pb, and Cu in its root region, while Zoysia grass (S_1) had elevated Cr levels. Overall, Seashore paspalum (S_6) demonstrated the most favorable performance with 50% treated wastewater, followed by Bermuda grass (S_2) and Zoysia grass (S_1). St. Augustine grass (S_7) exhibited the least favorable response. Warm-season turfgrass species showed promising results at 50% treated wastewater, followed by 25%, and the control group, while 100% and 75% treated wastewater conditions yielded the least favorable responses.

Studies on *in-vitro* response for salt stress tolerance in rose (*Rosa* spp.)

Roses, revered globally as the ‘Queen of Flowers’ for their enchanting beauty and profound symbolism, serve various purposes, including as cut flowers, loose flowers, hedges, and essential oil sources. Despite their versatility, the impact of salinity on different rose species and varieties remains inadequately explored. This study delves into the *in-vitro* response of five rose genotypes - 'Rose Sherbet,' '*Rosa chinensis* strain (FLS-RC-1),' 'Pusa Alpana,' 'Pink Parfait seedling,' and 'Pusa Lakshmi' - to salt stress. Under *in-vitro* conditions, the experiment involved inoculating explants on MS media supplemented with growth regulators and varying NaCl concentrations (0, 50, 100, 150, 200 mM). Results indicated that 'Pusa Lakshmi' exhibited the maximum shoot length (2cm), while '*Rosa chinensis* strain (FLS-RC-1)' displayed the minimum (1.27 cm) at 200 mM NaCl. 'Rose Sherbet' excelled in the number of shoots (0.67) and internodal length (0.43 cm) at the same concentration. 'Pusa Lakshmi' also outperformed in root-related parameters at 200 mM. As salinity increased, fresh and dry weight of plantlets decreased, with 'Rose Sherbet' and 'Pusa Alpana' registering the lowest values. Chlorophyll a, b, and total chlorophyll content varied among genotypes, with '*Rosa chinensis* strain (FLS-RC-1)' and 'Pusa Lakshmi' exhibiting maximum values. Carotenoid and relative water content peaked in '*Rosa chinensis* strain (FLS-RC-1)' and 'Pusa Alpana,' respectively, at 200 mM NaCl. Salt injury index increased with NaCl concentration. Proline content was highest in '*Rosa chinensis* strain (FLS-RC-1),' while SOD and GPX activity showed variability among genotypes. MDA content, an oxidative stress indicator, reached maximum levels in 'Pusa Alpana.' Catalase activity varied, with '*Rosa chinensis* strain (FLS-RC-1)' displaying the highest value. Na^+ and Na:K ratio were highest in 'Pusa Alpana,' while K^+ concentration peaked in '*Rosa chinensis* strain (FLS-RC-1).' Ca^{2+} and Mg^{2+} values were highest in 'Pusa Lakshmi' at 200 mM NaCl. Na^+ exhibited negative correlations with essential elements in leaf tissue and adversely affected various growth parameters. Conclusively, '*Rosa chinensis* strain (FLS-RC-1)' demonstrated superior performance up to 200 mM NaCl, suggesting its potential application in rose breeding programs for salt stress tolerance.

Theme 2: Improvement of Flower Crops Using Tissue Culture Techniques

Induction of doubled haploids in marigold through androgenesis

The present investigation was conducted with the goal of standardizing the *in vitro* androgenesis protocol for inducing doubled haploids in African and French marigolds, considering its significance to obtain a homogeneous population for crop improvement. Five genotypes representing the African and French marigolds were chosen in order to determine the correlation between the size of disc florets and buds, the microspore developmental stage, and the effect of genotypes on androgenic responses. Partially open buds of 1.5-1.9 cm to 2.0-2.4 cm sizes containing disc florets of 3.0-3.9 mm to 4.0-4.9 mm sizes were ideal for African marigold. Fully closed buds of sizes ranging from 1.0-1.4 cm to 1.5-1.9 cm containing disc florets of 1.0-1.9 mm to 2.0-2.9 mm were appropriate for French marigold. Genotypes "Af/w-4" and "Fr/R-5-2" exhibited superior androgenic response among African and French marigold genotypes under the study. Cold pre-treatment at $4^{o}C$ for 8 days, followed by heat pre-treatment at $30^{o}C$ for 48 hours and $4^{o}C$ for 8 days, followed by $32^{o}C$ for 24 hours, enhanced androgenic efficiency in Af/w-4 and Fr/R-5-2, respectively. Indirect regeneration as well as direct regeneration medium for anther culture was standardized using EMS medium, sucrose, and PGRs such as 2,4-D, TDZ, NAA, Kinetin, and BAP at various concentrations. Microspores isolated and cultured in liquid medium showed cell division and growth up to a few weeks; however, it failed to develop embryos. Proliferation, shoot elongation, and rooting medium were standardized using MS medium and PGRs such as Kinetin, NAA, GA_3, and IBA. The ploidy level of regenerants was assessed using cytological techniques, stomatal observations, and flow cytometry with equal reliability. Doubled haploid (DHs) plants were achieved through genome duplication of androgenesis-derived haploid plants using two chromosome doubling agents, *viz*., colchicine and oryzalin. The Doubled haploids were *in vitro* hardened using different strategies, and plastic pots covered with polyethene were found to be the best amongst all. Thus, the *in vitro* technique for haploid induction, maintenance, and conversion into doubled haploids in African and French marigold species was successfully standardized.

Induction of doubled haploids in marigold (*Tagetes erecta* L.) for thermotolerance

The study focuses on optimizing the protocol for doubled haploid production through anther culture in African marigold (*Tagetes erecta*), in the summer-flowering genotypes Desi Orange and Desi Yellow. Heat shock pretreatment at 32°C for 24 hours resulted in maximum callus and shoot bud induction. Enriched MS medium with meta topolin (0.5 mg/L) and NAA (0.25 mg/l) showed the best response for callus initiation and direct shoot bud induction. Different media were tested for shoot proliferation and rooting, with MS medium containing meta topolin (0.5mg/L) and NAA (0.1 mg/L) for proliferation and half-strength MS medium with Indole Butyric acid (0.5 mg/L) for rooting proving most effective. The regenerants were characterized for ploidy levels through stomatal and cytological analysis. Doubled haploids were produced by treating shoot tips of confirmed haploids with 5 µM oryzalin for 48 hours. Thermotolerance was enhanced using elicitors (salicylic acid and epibrassinosteroid) at specific concentrations under different temperature regimes (40, 42, and 45°C for 24 and 48 hours). Salicylic acid (0.2 mM) and epibrassinosteroid (1.0 mM) at 40-42°C for 12 hours resulted in the maximum survival and actively growing shoots. Physiological and biochemical parameters were analysed, including chlorophyll content, relative water content, carotenoid levels, electrolyte leakage, osmolyte accumulation, enzymatic activities, malondialdehyde content, and protein levels. The optimal conditions for enhanced thermotolerance were identified as 0.2 mM salicylic acid and 1.0 mM epibrassinosteroid at 40-42°C for 12 and 24 hours in both genotypes.In conclusion, the study recommends specific conditions for anther culture and doubled haploid production in African marigold, along with strategies to enhance thermotolerance using salicylic acid and epibrassinosteroid under *in vitro* conditions.

Induction of doubled haploids through androgenesis and characterization of doubled haploid based hybrids for qualitative and quantitative traits in marigold (*Tagetes erecta* L.)

This study involves *in vitro* regeneration of haploids in *Tagetes erecta* L., their doubling to produce doubled haploids, their *in vitro* multiplication and maintenance and subsequent use as parents in hybridization programme and finally hybridity testing using SSR markers. Anthers of *Tagetes erecta* L. (Genotype Af/R/L-1) were used for haploid production. Anthers were given a pre-treatment, to increase the regeneration percentage. Among pre-treatments, best response was recorded from chilling of anthers at 4°C for 9 days. In case of anther starvation with mannitol, best response was recorded when anthers were starved in 0.3M mannitol solution for 4 days. Afterwards, the basal MS media was modified by adding copper sulphate and best regeneration response was recorded when copper sulphate was added in the concentration of 20 µM. After using direct and indirect methods of ploidy determination, 6 haploids were obtained in total which were further used for chromosome doubling. Maximum diploidisation was obtained when colchicine was used in the concentration of 100 mg/L for 38 hours while in case of oryzalin maximum diploidisation was observed at the concentration of 50 mg/L for 38 hours. Further the doubled haploid plants were multiplied and proliferated using various growth regulators showing different results. Afterwards, the Doubled Haploids were characterised for various qualitative and quantitative traits and it was observed that different doubled haploids showed different results in various characters. Further, all the doubled haploids were used as pollen parents and crossed with three male sterile lines (MS-5, MS-7 and MS-8), the obtained doubled haploid based hybrids were characterised for various qualitative and quantitative traits and it was observed that hybrids showed varying results in various characters assessed. Finally, the hybridity of doubled haploid based hybrids was tested successfully using SSR markers. All 18 promising interspecific hybrids exhibited markers present in both male and female parents, confirming their hybridity. The protocol generated in this study can be used to produce doubled haploids which can be further used in hybridisation programmes. Further the knowledge of various qualitative and quantitative traits as characterised in this study will help in strengthening breeding programs involving doubled haploids.

In-vitro and *in-vivo* mutagenesis for commercial traits in rose (*Rosa* × *hybrida* L.)

The present investigation was undertaken to develop *in-vitro* protocol for rapid mass multiplication of rose (*Rosa* × *hybrida* L.) and induced variation by gamma rays under *in-vitro* and *in-vivo* mutagenesis in cv. ‘Pusa Virangana’ and cv. ‘Rose Sherbet’. Highest explant survival (73.82 and 76.41 %) was obtained with treatment T_1 (0.2% carbendazim + 200 mg/l 8-HQC) for 3 hours, respectively. Explants surface sterilized with 0.1 % $HgCl_2$ for 6 minutes exhibited maximum survival percentage (73.09%) in ‘Pusa Virangana’, while in ‘Rose Sherbet’ maximum survival percentage (74.46%) was observed with treatment 0.1% $HgCl_2$ for 5 minutes. MS medium supplemented with BAP (3mg/L) + NAA (0.1mg/L) +GA_3 (0.5mg/L) gave the better culture establishment in ‘Pusa Virangana’ however, in ‘Rose Sherbet’ best results were observed in treatment T_7 (5.0 mg/ L BAP + 0.1 mg/L NAA + 0.5 mg/L $GA_{3)}$. MS medium comprising 4.0 mg/L BAP + 0.1mg/L NAA+ 0.2 mg/L kinetin+0.5 mg/L GA_3 along with 40 mg/L adenine sulphate was found better for shoot proliferation with maximum micro-shoots (4.33 and 4.96 shoots/ explant) in both cultivars, respectively. Elongation of plantlets and maximum internode length was recorded in treatment T_2 (MS + GA_3 1.0 mg/L) in ‘Pusa Virangana’, whereas, it was maximum in treatment T_4 (MS + GA_3 2.0 mg/L) for ‘Rose Sherbet’. Rooting of micro shoots was induced on MS basal medium supplemented with IBA (1.0 mg/L) in ‘Pusa Virangana’ and IBA (0.5 mg/L) in ‘Rose Sherbet’. The regenerated plantlets of both cultivars were efficiently hardened in plastic pots (4″) filled with cocopeat + vermiculite + perlite (2:1:1). ‘Pusa Virangana’ and ‘Rose Sherbet’ axillary bud and semi hard wood cuttings were exposed to different gamma rays doses (20, 30, 40, 50, 60, 70, 80, 90 and 100 Gy). Higher dose of gamma rays after 50 Gy in cv. ‘Pusa Virangana’ and 70 Gy in cv. ‘Rose Sherbet’ exhibited 100 % explant mortality. The maximum plant growth and flower characters variation in 20, 30 and 40 Gy doses of gamma rays in both the cultivars. Two *in-vitro* induced mutants were isolated from ‘Pusa Virangana’ (PVM-3 and PVM4) and three from ‘Rose Sherbet’ (RSM-2, RSM-3 and RSM-4). Two mutants were isolated from *in-vivo* mutagenesis in ‘Pusa Virangana’ (PVM-1 and PVM-2) and one in ‘Rose Sherbet’ (RSM-1).

Theme 3: Production Technology of Ornamental Plants and their Uses in Landscaping

Effect of 5-azacytidine and plant growth regulators on dormancy and flowering in lilium (*Lilium x hybrida* L.)

The Lilium (X=12) genus contains most of the species that undergo a dormancy period during unfavorable environmental conditions for growth. Many species, frequently hybrids, are produced for the production of cut flowers. Asian, Oriental, Longiflorum x Asian, and OT-hybrid are the groups that are commonly developed for commercial purposes. Its dormancy and flowering are influenced by various factors. Plant growth regulators are essential in modern agriculture, enabling precise control over various plant development stages. The key technology used in commercial production is to break and prolong dormancy, which is a trait shared by the majority of lily bulbs. The present experiment was conducted under protected conditions to explore the dormancy and flowering behavior of Lilium (*Lilium x hybrida*) in response to different pre-treatments. For this purpose, the non-vernalised bulbs of the ‘Eyeliner’ cultivar were taken. These bulbs were subjected to different concentrations of GA_{4+7} (150, 300 and 400ppm), CPPU (100, 150, and 200 ppm), 5-azaC (50, 75, and 100 ppm), and meta-topolin (50, 75 and 100 ppm) with different duration of soaking of bulbs in different treatment (12, 18 and 24 hours) prior to the cultivation. Most of the bulbs were able to break the dormancy earlier than the control (T_1). The shortest period for the sprouting of bulbs (14.06 days earlier than T_1) belonged to CPPU pre-treatment. In addition, the 5-azaC treatment accelerated the flowering time (about 4.76 days earlier) and many other parameters. Most of the morphological characteristics were significantly affected by pre-treatment duration of soaking especially D_1 (12 hours) shown the most effective. Our results indicated a positive correlation between different parameters and pre-treatment conditions. The study demonstrated that different pre-treatments can able to reduce the dormancy period of Lilium bulbs with high ornamental value.

Studies on mitigation of cold stress in marigold (*Tagetes erecta* L.)

An experiment was carried out to explore various strategies aimed at mitigating cold stress in marigold. The experiment was designed in Factorial Randomized Block Design (FRBD) with three replications, comprising of four factors *viz*. two varieties (Pusa Narangi Gainda and Pusa Bahar), two growing conditions (open field and low plastic tunnel), three sowing dates (October 15th, November 1st and November 15th) and 14 elicitor treatments. The seedlings were treated with different elicitors after 20, 30 and 40 days after sowing. The data of morphological, physiological, and biochemical parameters was documented, and pooled data of two years was subjected to statistical analysis. The combination of the Pusa Bahar variety sown on October 15th and treated with elicitor (T12) and grown under low plastic tunnel conditions showed superior performance in various parameters including plant spread, number of flowers per plant, bud diameter, bud length, flower diameter, yield per plant, shelf life, relative water content and dry matter accumulation. Additionally, the Pusa Bahar variety sown on November 15th and subjected to the same elicitor treatment and grown under low plastic tunnel conditions displayed earliness in bud initiation and highest flower longevity. Under a low plastic tunnel, the Pusa Narangi Gainda variety sown on November 1st and treated with the same elicitors (T12) exhibited the maximum plant height and internodal length, while sowing on November 15th and treated with salicylic acid @ 300 ppm + AM (T10) resulted in earliness to first flowering. The maximum total chlorophyll content and total carotenoid content were recorded in Pusa Bahar variety sown on Nov. 15th and treated with T12 and planted under low plastic tunnel conditions, whereas, the highest GPX, soluble protein content, total phenol content, proline content, catalase content was recorded in Pusa Narangi Gainda variety sown on Nov. 15th, under open field conditions with T12 treatment. The Pusa Bahar variety sown on 15th October and treated with COS @ 200 ppm recorded maximum root colonization. Additionally, the Pusa Bahar variety, sown on Oct. 15th and treated with COS @ 200 ppm + AM achieved the highest net profit and benefit-cost ratio under low plastic tunnel conditions.

Studies on tree species for urban landscape and air pollution tolerance in Delhi

This study was conducted to investigate the physiological, biochemical, and anatomical responses of seven tree species in different locations in Delhi. The Air Pollution Tolerance Index (APTI) and Anticipated Performance Index (API) were used to assess the tolerance levels of these species. In winter, *Ficus religiosa* (23.23) exhibited the highest APTI at the polluted Income Tax Office (ITO), while *Azadirachta indica* (14.01) showed the lowest APTI. In summer, *Ficus religiosa* (21.04) again had the highest APTI at polluted locations, and *Polyalthia longifolia* (11.14) was identified as the most sensitive to air pollution. Maximum API was observed in *F. religiosa* (93.75) during winter at ITO. Stomatal studies revealed *Azadirachta indica* with the highest stomatal density (205.33 μm^{-2}) and index, while *Alstonia scholaris* (78.33 μm^{-2}) had the lowest stomatal density. *A. indica* also displayed the longest stomata. Species with lower APTI and API values, such as *Polyalthia longifolia*, were considered sensitive bioindicators, while those with higher values (*F. religiosa* and *Pongamia pinnata*) were deemed tolerant to air pollution, making them suitable for urban landscaping. A questionnaire survey based on public perception highlighted preferences for easily cultivable, evergreen, aesthetically pleasing, summer-blooming, medium-height trees with columnar growth habits. The conclusion emphasized the significance of aesthetic appeal, growth form, soil parameters, and resistance to urban environments in tree selection for urban landscapes. Urban landscape planners can utilize these findings to enhance residents' satisfaction, manage green spaces effectively, reduce air pollution, provide ecosystem services, and improve overall urban landscapes.

Standardization of vertical soil-less system for quality cut flower production of gerbera var. Arka Nesara

With the burgeoning population, plummeting cultivable area and escalating water demand, there is an urge to shift from the conventional soil-based cultivation to the vertical soil-less system thus augmenting the plant density and crop yield potential with improved water and nutrient use efficiency. Gerbera (*Gerbera jamesonii*), belonging to the family Asteraceae has greater scope in the Indian floriculture export and hence there is a need to improve the factor productivity of gerbera by adopting suitable soil-less system, substrate, nutrient solution and light regulation. In the present investigation carried out at ICAR-IIHR, Bengaluru, aggregate wick system with pots on ground performed better with respect to vegetative growth and flower quality with greater water (83.46 % over drip system) and nutrient use efficiency. Also, plants grown on Arka fermented cocopeat: FYM: rice husk (1:1:1 v/v) with the supply of modified nutrient formulation supplied at TDS of 600 ppm during vegetative stage and 1000 ppm during flowering stage resulted in maximum leaf area, hastened flowering, yield and flower quality. Further, plants of gerbera var. Arka Nesara grown in vertical structures oriented towards east-west direction deploying aggregate wick system on pots with the above-identified substrate and nutrient solution showed superior performance with respect to plant growth, yield, flower quality and economic returns. With respect to plant density, the vertical system accommodated around 30 plants in an area of 1.35 m 2 while, conventional system housed only 10-12 plants. Moreover, the overall yield per ground floor area in vertical farming system is almost 2.5 times higher than that of the conventional system.

Photoperiodic crop regulation in chrysanthemum (*Chrysanthemum morifolium* Ramat.)

The present experiment was carried to study the influence of different photoperiodic responses in chrysanthemum varieties, Autumn White and Diana Orange for two seasons. The two spray Chrysanthemum varieties, were exposed to three different day length extension treatments in a semi-climate controlled greenhouse with incandescent lamps from 6:00 p.m. to 10:00 p.m. for 10, 15, and 20 days, with four replications. The findings on growth and flowering were taken at various intervals (0, 15, 30, 45, and 60 days). The most significant increases in plant height (95.79 and 85.18 cm), inter nodal length (4.41 and 4.08 cm), stem diameter (0.66 and 0.61 cm), number of leaves per plant (39 and 34.07), leaf area (262.52 and 249.42 cm^2) and leaf area index (3.22 and 3.04) were observed in the varieties, Autumn White and Diana Orange when subjected to day length extension for 20 days at 60 days after planting.Plant growth parameters, including crop growth rate (0.146 and 0.115 g cm^{-2} day^{-1}), relative growth rate (0.095 and 0.081 g g^{-1} day^{-1}) at the 45 days after planting, and net assimilation rate (3.64 and 3.23 mg cm^{-2} day^{-1}) at 30 days after planting, exhibited their highest values in the early stages when subjected to day length for 20 days compared to control. A prominent increase in gaseous exchange parameters like net photosynthetic rate (14.56 and 13.16 µmol CO_2 m^{-2} s^{-1}), internal CO_2 (335.38 and 326.38 µmol CO_2 m^{-2} s^{-1}), transpiration rate (8.87 and 8.25 µmol H_2O m^{-2} s^{-1}), and stomatal conductance (0.095 and 0.075 0.095 µmol m^{-2} s^{-1}) was found in Autumn White and Diana Orange at 45 days after planting with the highest duration of the day length (20 days) in different photoperiodic treatments over the control. Results clearly showed the 20 days, day length extension resulted in the highest chlorophyll (a, b, and total) at 60 days after planting in Autumn White (2.325, 0.786, and 3.162 mg g^{-1} FW), followed by Diana Orange (2.284, 0.723, and 3.072 mg g^{-1} FW). However, the lowest chlorophyll content was found in the control group. At the longest photoperiod exposure, the maximum chlorophyll 'a/b' ratio was measured 60 days after planting (3.22 and 3.17) in Autumn White and Diana Orange. Photoperiodic acclimation for flower induction was confirmed by an increase in chlorophyll a/b ratio when chlorophyll content decreased in response to nitrogen. Diana Orange had the highest catalase (21.63), peroxidase (376.51), and SOD (40.35) activity at 60 days after planting, followed by Autumn White (catalase, peroxidase, and SOD, 20.33, 353.79, and 37.33) during the 20 days of day-length exposure.

Theme 4: Micropropagation of Flower Crops for Mass Multiplication

Standardization of protocol for *in vitro* mass multiplication of *Tagetes minuta* L.

Three genotypes of tagetes minuta L. (wild marigold) i.e., TM-1, TM-2, and TM-3 were assessed for their *in vitro* establishment, mass proliferation, rooting, and acclimatization ability. MS medium enriched with 125 mg L^{-1} of PVP, 125 mg L^{-1} of casein hydrolysate, 0.05 mg L^{-1} of GA_3, 0.025 mg L^{-1} of NAA, and 40 gL^{-1} of sucrose supplemented with 16.10 mg L^{-1} putrescine, recorded the best results. This study has proved the effectiveness of putrescine over the conventionally used growth regulators (BAP) for *in vitro* establishment. For shoot proliferation, the culture medium {MS + GA_3 (0.025 mg L^{-1}) + NAA (0.01 mg L^{-1}) + PVP (125 mg L^{-1}) + casein hydrolysate (125 mg L^{-1}) + sucrose (40 g L^{-1}) + agar (8g L^{-1})} enriched with different levels of putrescine significantly improved the *in vitro* proliferationover the culture medium enriched with different levels of BAP and the control. For the first time, the efficacy of silver nanoparticles (AgNPs) was assessed for the *in vitro* proliferation of *Tagetes minuta* genotypes. While comparing the efficacy of three different sizes of AgNPs i.e., 60 nm, 40nm, and 20 nm, it was observed that 0.1 mg L^{-1} of 20 nm AgNPs was found to be the most effective in improving the growth, proliferation, and rooting of different wild marigold genotypes. Among the three genotypes of wild marigold, TM-2 has shown better *in vitro* establishment and shoot proliferation potentials than TM-1 and TM-3. While comparing the efficacy of two auxins i.e., NAA and IBA, for *in vitro* root induction from shoots, it was observed that IBA was way more effective than NAA. The developed protocol will pave the way for basic research on the application of *in vitro* flowering, *in vitro* pollination & somatic hybridization etc. in marigold breeding.

Standardization of protocol for *in-vitro* production of lilium (*Lilium longiflorum* T.) cv. Gran Paradiso bulbs through bioreactor

The present investigation was carried out to standardize a protocol for *in-vitro* production of bulbs through continuous immersion type bioreactor. The study revealed that, inner bulb scales were found more effective than the outer scale explants for culture establishment. Pre-treatment to inner scale explants with carbendazim (0.2%) + Mancozeb (0.2%) + Streptocycline 300 ppm for 2.5hr followed by surface sterilization with ethanol for 120 sec combined with 0.1% $HgCl_2$ for 7 min was found best for minimizing contamination. MS medium supplemented with BAP + NAA (1.0 + 0.2 mg L^{-1}) for 21 days resulted in highest per cent direct shoot organogenesis (97.00%). Maximum per cent induction of callus (81.62%) was recorded from MS + Picloram (0.50 mg L^{-1}) + NAA (0.30 mg L^{-1}). The calluses were best proliferated in the MS + Picloram (0.50 mg L^{-1} + 0.30 mg L^{-1}). Highest daughter bulblets were induced from the media MS + 3% sucrose + BAP (1.00 mg L^{-1}) + NAA (1.00 mg L^{-1}). Further, stage I bulblets (4-10 g) were developed to stage stage III (20-30 g) inside the bioreactor with different concentrations of sucrose (3 %, 6 % and 9 %). In this, 9% sucrose was found best for 4g bulblet to develop in to 23.74g bulb in weight. The bioreactor bulbs were 100% rooted in the media containing MS + activated charcoal (1.0 mg L^{-1}). 100 % plant survival was found in glass bottles containing polypropylene caps. Morphological characters like number of flower buds, flower bud diameter, number of leaves, stem thickness and stalk length of both (*in vitro* and *in vivo*) were found on-par with each other when compared. Cold treatment to bulbs at 2-4**°C** was found most effective method to break the dormancy followed by GA_3 3 mg/L with a sprouting rate of 92.47% and 98.33% in (4-10 g) and (15-20 g) size bulbs, respectively. Among the biochemical parameters tested, a sharp decrease in abscisic acid (ABA), increase in GA_3 and total sugars content were observed in both the size of bulbs during dormancy release. Molecular study revealed that, ISSR- 843, ISSR-848, ISSR-854, ISSR-881, ISSR-899, and ISSR-900 were found promising and the plantlets regenerated from this protocol were true to type.

List of contributing students and Chairpersons of their research advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Maryam Firdous (21646)	M.Sc.	Standardization of protocol for *in vitro* mass multiplication of *Tagetes minuta* L.	Dr. Reeta Bhatia Dey	ICAR-IARI, New Delhi
2.	N. Balaji (21647)	M.Sc.	Studies on performance of warm-season turf grasses under treated wastewater	Dr. S. S. Sindhu	ICAR-IARI, New Delhi
3.	Sanghita Roy (21648)	M.Sc.	Studies on *in-vitro* responses to salt stress tolerance in rose (*Rosa* spp.)	Dr. Namita	ICAR-IARI, New Delhi
4.	Kusuma M. V. (21649)	M.Sc.	Study on drought tolerance in chrysanthemum (*Chrysanthemum morifolium* Ramat.)	Dr. Gunjeet Kumar	ICAR-IARI, New Delhi
5.	Vallarasu S. (21650)	M.Sc.	Effect of 5-azacytidine and plant growth regulators on dormancy and flowering in lilium (*Lilium x hybrida* L.)	Dr. Mast Ram Dhiman	ICAR-IARI, New Delhi
6.	Chaithra (21651)	M.Sc.	Studies on *in vitro* response of French marigold (*Tagetes patula* L.) genotypes to salt stress	Dr. Sapna Panwar	ICAR-IARI, New Delhi
7.	Srajana Pradhan (11028)	Ph.D.	Induction of doubled haploids in marigold through androgenesis	Dr. Kanwar Pal Singh	ICAR-IARI, New Delhi
8.	Soudamini Karjee (11030)	Ph.D.	Standardization of protocol for *in-vitro* production of lilium (*Lilium longiflorum* T.) cv. Gran Paradiso bulbs through bioreactor	Dr. C. Aswath	**ICAR-IIHR, Bengaluru
9.	Uzma Mehraj (11254)	Ph.D.	Induction of doubled haploids through androgenesis and characterization of doubled haploid based hybrids for qualitative and quantitative traits in marigold (*Tagetes erecta* L.)	Dr. Kanwar Pal Singh	ICAR-IARI, New Delhi
10.	Sangeetha Priya S. (11500)	Ph.D.	Standardization of vertical soil-less system for quality cut flower production of gerbera var. Arka Nesara	Dr. C. Aswath	**ICAR-IIHR, Bengaluru
11.	Koppala Deepthi (11502)	Ph.D.	Induction of doubled haploids in marigold (*Tagetes erecta* L.) for thermotolerance	Dr. Kanwar Pal Singh	ICAR-IARI, New Delhi
12.	Rayavarapu Tejaswi (11503)	Ph.D.	Studies on mitigation of cold stress in marigold (*Tagetes erecta* L.)	Dr. Kanwar Pal Singh	ICAR-IARI, New Delhi
13.	Harendra Kumar Yadav (11506)	Ph.D.	*In-vitro* and *in-vivo* mutagenesis for commercial traits in rose (*Rosa* × *hybrida* L.)	Dr. Namita	ICAR-IARI, New Delhi
14.	Lokendra Singh (11507)	Ph.D.	Studies on tree species for urban landscape and air pollution tolerance in Delhi	Dr. S. S. Sindhu	ICAR-IARI, New Delhi
15.	Vaishali C (11768)	Ph.D.	Photoperiodic crop regulation in chrysanthemum (*Chrysanthemum morifolium* Ramat.)	Dr. M.C. Singh	ICAR-IARI, New Delhi

**Outreach Institute

Fruit Science

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Prof. Manish Srivastav

The Division of Fruits and Horticultural Technology has made substantial strides in advancing horticulture, particularly in the domain of fruit crops. The division's contributions are noteworthy, especially in terms of pioneering research endeavors and offering viable solutions to challenges within the fruit industry. The Division of Fruits and Horticultural Technology places a significant emphasis on human resource development in the field of horticultural research. This focus is primarily channeled through post-graduate teaching programs that target key areas considered crucial in the advancement of horticulture, specifically in the context of fruit crops. This approach not only contributes to knowledge expansion but also fosters the development of skilled professionals who can actively contribute to the growth and innovation of the horticultural sector. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Genetical Studies and Characterization

Study on association between pulp colour composition and seed based traits in guava (*Psidium guajava* L.)

The present investigation aimed to characterize guava hybrids for pulp colour, biochemical constituents, and seed related traits. Five guava parental genotypes, viz., Hisar Surkha (HSU), Punjab Pink (PP), Black guava, Pant Prabhat (PPT) and Shweta (SH) and their 42 hybrids were used in the present study. Coloured guava parents and their hybrid were rich in pigment as compared to white pulped ones. Among hybrid, maximum lycopene (11.372 mg/100g) was found in PP/BG-19-15-18. Maximum total anthocyanins were found in PP/BG-19-19-6 (4.027 mg/100g) and HSU/SH-19-19-8 (2.362 mg/100g). Among pink pulped hybrid, total carotenoids ranged from 0.728 mg/100g to 2.362 mg/100g, whereas; among white pulped hybrid it ranged from 0.183 mg/100g to 2.180 mg/100g. PPT/HSU-19-23-12 contained considerably higher ascorbic acid content (280 mg/100g). Among pink pulped hybrid, three hybrids, namely, PP/BG-19-15-18, PP/BG-19-19-6, and HSU/SH-19-19-8 were found promising. Among white pulped hybrid, three hybrids namely PPT/BG-19-21-13, PP/SH-19-24-17, PPT/HSU-19-22-13, and PP/SH-19-11-2 were found promising. PP/BG-19-23-8 (2530.97 N) and PP/SH-19-16-6 (352.21 N) had overall maximum and minimum seed hardness. The guava genotypes, PP, PP/BG-19-15-1, PP/HSU-19-13-21, PPT/BG-19-21-18, PPT/BG-19-20-6, PPT/BG-19-19-20, PPT/BG-19-21-14 had higher seed hardness more than 2000 N. A non-significant correlation was found between selected seed parameters and pigments among studied genotypes.

Characterization of a set of interspecific citrus hybrids Orangelo (*Citrus maxima* × *Citrus sinensis*)

Twenty-four interspecific citrus orangelo hybrids were characterized based on the DUS guidelines. More than 80% hybrid population had ovate leaf lamina shape. However, two hybrids expressed obovate and SCSH 13-13 and CRH 20-11 showed orbicular and elliptic leaf lamina shape. The largest pedicel length, petal length and diameter of opened flower were observed in SCSH 3-10, while petals were widest in SCSH 9-20. Majority of the hybrids (54.17%) showed spheroid fruit shape, while more than 75% hybrids witnessed green-yellow (RHS N-144A) peel at maturity. The seeds per fruit varied from 8 to 60. Grouping based on morphological traits showed that most of orangelos (21 hybrids) and their parents were clustered together. PCA analysis showed that morphological quantitative traits leaf lamina length, leaf lamina width and their ratio, leaf lamina thickness and pedicel length, accounted for 77.76% of the cumulative variability. Based on the physico-chemical data, all the 24 orangelo along their parents showed two major clusters A and cluster B at similarity value of 0.56. Out of 24 orangelo hybrids, five hybrids, namely, SCSH 3-10, SCSH 9-20, SCSH 11-15, SCSH 21-10 and CRH 20-11 had better qualitative characters. A total of 50 *de novo* EST-SSR were validated, and 19 primers were polymorphic with a total of 38% polymorphism. The amplicon size ranged from 100 bp in NRCH3 to 300 bp in NRCH49. The trait specific marker NRCH21 had the highest allelic frequency (0.96), while it was lowest (0.52) in NRCH6 and NRCH8. Further, of the 19 primers, highest and lowest PIC values were found in NRCH9 based primers (0.48) and NRCH21 (0.07), respectively. The gene diversity ranged from 0.07 to 0.55, being highest (0.55) in NRCH9. The phylogenetic tree provided the important information regarding genetic relationship in 24 orangelo hybrids with their four parents.

Morpho-biochemical and molecular characterization of segregating population of litchi (*Litchi chinensis* Sonn.)

Litchi, a valuable subtropical fruit, belongs to the *Sapindaceae* family. The evaluation of the current range of variation is a fundamental requirement for effective crop improvement initiatives in the future. The present study titled was undertaken at research farm, ICAR-Research Complex for Eastern Region, Farming Systems Research Centre for Hill and Plateau Region (FSRCHPR), Plandu, Ranchi, Jharkhand. The study aims to achieve the objectives to identify and validate the genome-wide SSRs markers in litchi and characterize the litchi segregants based on morphological, biochemical, and genome-wide SSRs. The study included a total of forty genotypes of litchi and were subjected to assessment in a randomized block design with three replications. The results showed a significant variation for leaflet length and width, rachis length, petiole length, seed shape, seed length, seed width, inflorescence length and width, fruit length and width, fruit pulp content (%), fruit weight, shape of fruit shoulder, shape of fruit tip, TSS, acidity (%), ascorbic acid content, antioxidant activity, total phenol content, reducing sugar, non-reducing and total sugars content (%). A total of 150 SSRs primers was selected from whole genome sequence of litchi through krait software and from that finally 50 single band amplified primers were selected for characterization and among that 26 primers were showing polymorphism. SSR profiling data revealed average allele number of 3.31 alleles/ locus and PIC value in the range of 0.16 to 0.57. Cluster analysis grouped the litchi germplasms into 2 major cluster in cluster I, two germplasm were there (ICAR-RCER-LS-19/7 and 6/4) and rest were in the cluster II. Based on principal component analysis, 10 PCs were showing 71.08% of variation in the germplasm. It was noted that this new set of SSRs proved to be highly informative, serving as a valuable DNA marker resource for upcoming molecular research in litchi.

Studies on physico-biochemical characterization of mango genotypes in response to fruit fly infestation and related volatile profiling

The present investigation was aimed to study the population dynamics of natural fruit fly infestation in homogenous and mixed orchards. Fruit fly populations peaked in mango plantations between June and July, coinciding with the ripening time. The occurrence of humid conditions, rainfall and fruits characteristics were found to influence the dynamics of fruit fly. The seasonal trap captures of male fruit flies showed a moderately significant negative correlation (-0.612*) with maximum but significant positive correlation with the minimum temperature (0.701**). However, a positive correlation was observed between relative humidity (r = 0.924**) and rainfall (r=0.721**) with the fluctuations of fruit fly populations across all the monitored orchard sites. While, based on fruit infestation percentage and larval density; Langra was found to be immune, while Pusa Prathiba, Bombay Green, Neelum, Olour, and Pusa Lalima (Highly resistant); Dashehari and Himsagar (resistant); Amrapali (moderately resistant); Chausa and Mallika (susceptible), whereas Totapuri, Tommy Atkins, and Pusa Manohari are found to be highly susceptible. The physical parameters, such as fruit weight, length, and diameter, did not significantly correlate with fruit infestation. However, physical parameters such as peel thickness (r = -0.776**), sap volume (r = -0.654*), fruit firmness (r = -0.604*), and bio/allele-chemical traits sucks as total phenols (r = -0.68**), total flavonoids (r = -0.72**), ascorbic acid (r = -0.82), and total tannins (r = -0.75**) displayed significant negative correlations with the intensity of fruit infestation. Additionally, *Bactrocera dorsalis* infestation showed significant upregulation of GPX, SOD, and PPO activity compared to healthy tissue, except for CAT, which was found to be higher in healthy tissue. The upregulation was higher in immune (Langra), highly resistant (Pusa Prathibha, Bombay Green, Neelum, and Olour) which could explain their greater resistance to fruit fly infestation followed by resistant group (Pusa Lalima, Dashehari, Himsagar). The transcriptome analysis revealed 544 DEGs upregulated and 414 DEGs downregulated in Langra in comparison to Tommy Atkins.

Evaluation of pummelo (*Citrus grandis* L.) progenies for bitterness and rind thickness

The present investigation was carried out to identify potential progenies based on physico-chemical and molecular attributes amongthe hybrids and half-sib progenies of pummelo. Based on their precocity, regular bearing, yield and quality attributes, a total of 47 hybrids from cross combination Acc.12 X Acc.19, 55 hybrids from cross combination Acc.3 X Acc.19 and 92 half-sibs were selected for further studies. Based on biochemical and sensory evaluation, it was observed that, H17-3, H17-5 and H17-9 from cross combination Acc.12 X Acc.19; H23-4 and H23-11 from cross combination Acc.3 X Acc.19; and HS46-13 and HS48-12 the half-sibs from Acc.12 were found to be superior with higher TSS (9.87ºB, 10.10ºB, 10.53ºB, 9.3ºB, 9.7ºB, 10.32ºB and 10.34 ºB respectively)and less bitterness. The progenies HS48-12 and H23-11 consisted a very thin rind could be exploited as breeding stock/ new hybrids for commercial cultivation. Out of 76 SSR markers, fifteen were polymorphic of which ten markers showed PIC values with more than 0.5 which can be used for hybridity confirmation, diversity analysis and for DNA fingerprinting. The marker CiBE0246 showed possible linkage with ascorbic acid content and fruit weight with the hybrids. The changes in the nucleotide sequence genes responsible for bitterness showed variation in bitterness/ sweetness of the fruit which further confirmed through LCMS analysis. Through Chi-square analysis, it was observed that the inheritance of rind thickness and sweetness followed Mendelian ratio of 3:1 while pulp colour intensity and pulp colour uniformity were found to be co-dominant in nature with a ratio of 1: 1.

Phenotypic evaluation and mapping of genomic regions governing yield and their component traits in mango

Biparental progeny population were evaluated for vigour, flowering, yield, and biochemical traits. The hybrid 'H-13-5' had the maximum plant height (10.11 m), stem girth was maximum in 'H-1-6' (132.21cm), and 'H-13-1' had the largest canopy spread (9.77 m). The hybrid 'H-13-4' exhibited the highest bark-wood ratio (7.59). Hybrid 'H-1-9' had the highest stomatal density (797 stomata/mm^2) as a dwarfing trait. Regarding reproductive characteristics, hybrid 'H-11-4' produced the maximum number of fruits (2.51) per panicle. With a more significant fruit retention percentage of 62%, the hybrid 'H-11-1' showed improved fruit retention on the tree. The tree with the higher fruit output, hybrid 'H-1-8', produced 43 kg of fruit per tree. The hybrid 'H-1-5' produced the maximum size of fruits (317 g/ per fruit). There was considerable diversity among hybrids in terms of morphology, blooming, fruiting, and production. Paternal effects were more noticeable than maternal effects for some features, and certain traits exhibited common tendencies. Twelve high-performing hybrids, including 'H-1-8', 'H-1-5', 'H-12-8', 'H-1-3', 'H-22-1', 'H-15-1', 'H-13-4', 'H-19-1', 'H-13-5', 'H-4-9', 'H-3-6', and 'H-12-6', were found to be better. The molecular characterization of mango hybrids using MSSRs revealed high heterozygosity. These markers have significantly contributed to our understanding of genetic variability and relatedness among mango hybrids. Mapping of QTLs for vegetative and fruiting character were useful in identifying 18 QTLs associated with nine important related traits. The QTLs related to vegetative growth parameters were distributed across eight chromosomes, *i.e.*, 3. 5, 7, 13, 15, 19 and 20. Similarly, QTLs governing flowering and fruiting related traits were located on chromosome 4, 7 and 15 with a significant LOD (2.04 to 4.01) value and explained 13.39 to 30.68 per cent phenotypic variation in the population.

Evaluation and characterization of Arka Sahan custard apple progenies for self-fruitfulness

In Custard apple breeding, understanding self-fruitfulness is crucial for productivity and quality. Among 1113 progenies, diverse traits were observed, including plant height (0.8 m to 4.2 m), growth habits (erect or spreading), and leaf morphology (elliptic, ovate, lanceolate). Only 56 progenies displayed stable self-fruitfulness. Further analysis of selected progenies revealed varied fruit attributes, such as length (6.0 cm to 9.1 cm), pulp weight (109.5 g to 243.8 g), seed percentage (0.9% to 7.7%), and biochemical composition. Phenotypic and genetic diversity were assessed, with higher PCV indicating phenotypic diversity and higher GCV suggesting genetic diversity. Heritability estimates ranged from 5.01 to 88.82 for different traits, and genetic advance as a percentage of the mean varied from 1.04 to 37.39, indicating potential for genetic improvement. The study also focused on flowering traits and pollen morphology in Arka Sahan custard apple progenies. Flowering occurred from March to July, with variations in petal length, peduncle length, and angles of petal opening between self-fruitful and unfruitful progenies. Anthesis and anther dehiscence timing differed. Pollen morphology analysis revealed differences in monads, dyads, tetrads, and pollen viability between the two groups. Self-fruitful progenies exhibited higher pollen germination and longer pollen tube lengths. Additionally, the research addressed unfruitfulness in Annona, identifying factors like anthesis timing, anther dehiscence, and pollen traits. SSR marker analysis identified homozygosity in parents and highlighted two polymorphic markers, LMCH-38 and LMCH-102, with notable inheritance patterns in the progeny. These findings offer insights for future breeding.

Theme 2: Flowering and Pollination Studies

Studies on the pollen micro-morphology, storage behaviours, and cross-compatibility of grape (*Vitis* spp.) genotypes

The knowledge of pollen morphology, suitable storage condition, and species compatibility is vital for a successful grapevine improvement programme. Ten *Vitis* genotypes, important for scion and rootstock improvement programmes were studied for their pollen structure and pollen storage. The morphology of pollen was analyzed with a scanning electron microscope (SEM). Pollen viability was tested by the 2,3,5-triphenyltetrazolium chloride (TTC) and germination was analysed by *in vitro* assays. The results revealed variations in pollen micro-morphology in ten genotypes, with distinct pollen dimensions, shapes, and exine ornamentation. Pollen of *Vitis parviflora* Roxb. and Dogridge were acolporated, which did not germinate on *in vitro* media. The remaining eight genotypes exhibited tricolporated pollen which showed well *in vitro* pollen germination. Storage temperature and duration interactions showed that, at room temperature, pollen of most of the grape genotypes can be stored for up to one day only with an acceptable pollen germination rate (>30%). However, storage for up to seven days was successfully achieved at 4°C, except for ‘Pearl of Csaba’. The most effective storage conditions were found to be at –20°C and –196°C (in liquid N_2), enabling pollen storage for a period of up to 30 days and can be used for pollination to overcome the challenge of asynchronous flowering. In cross-compatibility studies, four interspecific combinations were analysed for their compatibility among which, *V. parviflora* Roxb. × Pusa Navrang and *V. parviflora* Roxb. × Salt Creek showed high cross-compatibility, offering their potential use for grape rootstock breeding. However, *V. parviflora* Roxb. × Male Hybrid recorded the lowest compatibility index among studied crosses. In the case of self-pollinated flowers from *V. parviflora* Roxb. and *V. parviflora* Roxb. × Dogridge, pollen failed to germinate on the stigma due to male sterility caused by acolporated pollen. As a result, the flowers of these genotypes functioned as females, which makes them ideal female parents for grape breeding without the need for the tedious process of emasculation.

Studies on floral development and reproductive biology in grapevine

The investigation was conducted on six years old grapevine plants. The origin and development of uncommitted primordia (anlagen), inflorescences, tendrils, shoots, and flowers in several grapevine genotypes have been investigated by histology and scanning electron microscopy. In brief, the flowering process of grapevine is divided into three main steps: i) Formation of uncommitted primordia or anlagen (Stages 0 to 1); ii) Differentiation of uncommitted primordia to form inflorescence or tendril or shoot primordia (Stages 2 to 7); and iii) Differentiation of flowers (Stages 8 to 11). The effect of open-, self-, and cross-pollination on metaxenic (berry) and xenic (seed) traits in grapevine genotypes were examined. All of the genotypes exhibited adequate *in vitro* pollen viability and germination percentages. Seven different cross-combinations were used on the grape variety ‘Pusa Navrang'. A significantly higher percentage of berries were set and retained through open and self-pollination. Among the six pollen genotypes, ‘Beauty Seedless’ was found to improve certain agronomic traits in ‘Pusa Navrang’, such as berry set, berry retention, berry and seed sizes, and seed number per berry. These results showed that the examined grape genotypes had significant metaxenic and xenic effects. The ‘Beauty Seedless’ was found most effective pollinizer for the metaxenic and xenic effects. Hence, ‘Beauty Seedless’ may be a desirable option in both quality grape production as well as breeding studies and may be suggested as a pollen parent to improve certain agronomic traits. The RNA-Seq study of three grape genotypes namely, Male hybrid (male (M)), Hur (female (F)), and ‘Pusa Navrang’ (hermaphrodites (H)) at E-L 15 and E-L 17 stages, identified several DEGs associated with the flower development and regulation. The metabolic pathways such as anther dehiscence, protein processing in endoplasmic reticulum, SNARE interactions in vesicular transport, plant hormone signal transduction, AMPK signaling pathway, MAPK signaling pathway, and ABC transporters were found to be highly enriched with the identified DEGs.

Theme 3: Mutagenesis Studies

In vitro mutagenesis and validation of mutants using molecular markers in Kinnow mandarin

The present investigation was conducted with the objectives to standardize *in vitro* regeneration protocol, *in vitro* mutagenesis protocol and M_1 population development. The direct organogenesis and premature abscission free micro-shoots could be induced from hardwood nodal segment cultured on silver supplemented medium (MS + BAP 2.5 mg L^{-1} + GA_3 10 mg L^{-1} + silver thiosulfate 5 mg L^{-1}). Embryogenic callus induction from outer integument of transitional stage seed on medium containing MS + activated charcoal 200 mg L^{-1} after vertical cut at chalazal end was standardized. The standardized *in ovulo* nucellus culture technique includes the collection of >4 mm ovules from stage III (>21to ≤25 mm diameter) fruits followed by *in ovulo* explant preparation and inoculation on somatic embryo induction cum maturation medium (DKW + Kinetin 5.0 mg L^{-1} + malt extract 1000 mg L^{-1}). Transfer of cotyledonary embryos from the above medium to germination cum conversion medium (MT + GA_3 2.0 mg L^{-1} + NAA 0.5 mg L^{-1} + spermidine 100 mg L^{-1} + CW 10%) followed by preconditioning of germinated seedlings in the liquid medium and plantlet establishment on a potting medium (cocopeat: vermiculite: perlite, 2:1:1). The integument derived embryogenic calli based suspension culture system includes habituation of calli on plant bio-regulators free medium, suspension culture of habituated calli in PBR free medium for somatic embryogenesis followed by maturation of obtained embryos on solid medium (MT + NAA 0.5 mg L^{-1} + coconut water 10%) and remaining step of germination to acclimatization follows *in ovulo* nucellus derived DSE system protocol. Gamma irradiated and EMS treated optimized explants of DSE and ISE system showed the optimum dose at 80 Gy (DSE) and 100 Gy (ISE) for gamma irradiation, while for EMS it was 0.5% EMS for 5 hr. (DSE) and 0.1% EMS for 3 hr. (ISE). The DSE system was found superior with respect to short mutant regeneration cycle, elimination of deleterious mutants and high M_1 population recovery. From the detailed investigation it can be concluded that DSE system is highly beneficial for both gamma irradiation and EMS induced *in vitro* mutagenesis.

In vitro mutagenesis and validation of mutants using molecular markers in sweet orange cv. Mosambi

In present investigation, different types of explants from the field-grown 4-year-old mother plants of sweet orange cv. Mosambi were taken for culture initiation. Experiment was conducted to standardize the protocol from the different explants followed by the second experiment to standardize the LD_{50} in gamma and EMS treated callus. This involves the identification of putative mutants which were subjected to molecular analysis using SSR markers for identifying true mutants. Ovular segments were proved as the best explant for indirect somatic embryogenesis. Among the different stages of the fruit growth, the 5th stage (49.54, 44.94 mm w×l, 65 ±5 DAP) was standardized as the most effective stage, so as to get true-to type plantlets. The best callus induction from ovular segments was recorded from MT + 2,4-D (2.0 mg L^{-1}) + Kin (0.5 mg L^{-1}) + ME (500 mg L^{-1}) and embryogenesis from MT + NAA (0.1 mg L^{-1}) + BAP (3.0 mg L^{-1}) + ME (500 mg L^{-1}) + CW 10%. Addition of GA3 to MT medium fortified with BAP (3.0 mg L^{-1}) + GA3 (1.0 mg L^{-1}) enhanced the germination of embryos and the MS + NAA (5.0 mg L^{-1}) + IBA (1.0 mg L^{-1}) + Phloroglucinol (100 mg L^{-1}) resulted maximum rooting percentage. The callus from the ovular segments was subjected to mutagen treatment with gamma irradiation and EMS of different concentrations to standardize the LD_{50}. The LD_{50} for gamma radiation was standardized at 60 Gy and for EMS at 0.3% for 3 h. The survival percentage, the other callus related parameters and the biochemical observations were showed declining trend with an increase in concentrations of mutagen. The putative mutants were subjected to the molecular markers for confirmation of mutants. Among the 34 primers used, only 4 primers i.e., CIBE 5720, GT 03, AMB 01 and AG-14 were polymorphic, highly informative for genetic variation analysis of the mutagen treated callus population and the control plant.

Theme 4: PGRs, Abiotic Stress Management and Crop Production

Impact of plant growth regulators in relation to cold tolerance and flowering in papaya (*Carica papaya* L.)

Papaya is a species sensitive to low temperatures because it originated in tropical environments. An experiment was carried out to know the effect of PGRs on physiochemical parameters and the flowering of papaya var. Pusa Peet during 2022-23 in insect-proof net house and open field conditions with foliar application of two levels of salicylic acid (75 and 100 ppm) and thiourea (250 and 300 ppm) under factorial RBD. The growth conditions and chemical treatments have shown marked significance in different morpho-physiological and biochemical parameters. The growth conditions were significant for morphological parameters like plant height, number of active leaves, average internodal length and plant diameter. At the same time, it was non-significant for many of the flowering parameters recorded. Maximum plant height was recorded in plants raised in net house (60.95 cm) compared to open house conditions (47.85 cm). The chemical treatments were also significant for parameters like membrane stability index, relative water content and biochemical parameters like proline activity, catalase activity, protein content etc. The highest membrane stability index was recorded in the plants treated with salicylic acid – 100 ppm (61.41%). The relative water content also was observed to be high in control plants. In contrast, the least values were recorded for plants treated with salicylic acid 75 ppm, which could help prevent intracellular ice formation in papaya plants. The mean catalase activity was higher in control plants (1.51 µmoles H_2O_2 hydrolyzed mg^{-1} TSP min^{-1}) than in other chemical treatments. Compared to other treatments, the pollen viability was maximum in plants treated with salicylic acid 100 ppm (50.45%). The chemical treatments remarkably affected the papaya plants cold tolerance and improved papaya's morphological, physiological, and biochemical parameters. Among different treatments, thiourea 300 ppm and salicylic acid 75 ppm were most influential in mitigating cold tolerance. However, flowering-related parameters are positively influenced by chemical treatments of salicylic acid 100 ppm.

Drought stress tolerance studies in mango (*Mangifera indica* L.)

In the present research, different polyembryonic mango genotypes and reciprocally grafted contrasting mango genotypes were evaluated under water deficit. One-year-old polyembryonic rootstocks were exposed to normal irrigation and drought conditions for 28 days. The higher decrease in leaf area and leaf area ratio was found in Kurukkan (25.92%) and K-5 (17.76%), respectively. OLOP-Z-6/2 and OPK-3-7/12 showed a decrease in specific leaf weight. Genotype K-5 and Kurukkan showed a lesser decline in photosynthetic rate, while transpiration rate was inhibited more in K-5 (61.0%). Two drought-tolerant and one susceptible genotype were grafted reciprocally in all combinations were also tested under water deficit. Reduction in LA and SLA was lower in Olour/K-5, while reduction in LAR, LA and SLA was lower in Olour/Kurukkan. Kurukkan/Olour showed no increment under moisture deficit conditions in R/S ratio. Antioxidant enzymatic activity, level of MDA and H_2O_2 increased under drought in all stionic combination with varying degrees of enhancement. All plant growth parameters were increased by application of chemicals in the susceptible Olour but at varying degrees, however, a mixed response was observed in the tolerant genotype. A higher positive impact of spd was observed on the number of leaves, plant height, SLA, and LAR in tolerant genotype K-5. Moreover, SA priming showed a higher increase in stem diameter, leaf area, SLW and LFW in tolerant genotype K-5. Chlorophyll ‘a’ to ‘b’ ratio was reduced in K-5 by both chemicals but lower reduction by SA while in Olour it was increased by both chemicals with more increment (>10%) by SA. The SA spray was more effective in improving TS (>68%) compared to non-treated plants and SA-treated plants. The *CAT*, *POD*, *APX*, and *GR* upregulated more by SA application in K-5, while in Olour, spd spray upregulated more antioxidant enzymatic activity compared to control, but it inhibited *APX* in K-5. A higher reduction (25%) in MDA and H_2O_2 was reduced more (> 40%) in K-5 noted by SA priming as compared to control.

Salt tolerance behaviour of sweet orange cv. Pusa Sharad on different citrus genotypes

The impact of sodium chloride on sweet orange cv. Pusa Sharad (PS) grafted on eleven different rootstocks were evaluated. Irrigation water containing 30 and 60 mM of sodium chloride was applied to scion-rootstock combinations in comparison to control till the onset of salt injury symptoms i.e., 42 days. Under salinity stress, the PS scion grafted onto CM, X9, C47, N1, and N3 rootstocks exhibited minimum reduction in the scion height, leaf area ratio, root to shoot ratio, total chlorophyll content, total carotenoid content, transpiration rate, photosynthesis rate, internal CO_2 concentration and stomatal conductance as compared to PS scions grafted onto JK, C12, N2, N4, N5, and TC rootstocks under 60 mM NaCl stress. The highest accumulation of osmolytes such as total soluble sugars, proline, total phenol, was recorded on Pusa Sharad on CM, C47 and X9. The scanning electron microscope reviled that under NaCl stress, there was irregular wax deposition on the leaves of Pusa Sharad grafted on JK and TC, resulting in a non-uniform covering of the leaf surface. Interestingly, structural damages in guard cells induced by 60 mM of NaCl stress were minimal in Pusa Sharad grafted on CM and X9 when compared to those grafted on JK and TC. The gas chromatography-mass spectrometry results resulted sugars, sugar alcohols, and fatty acids significantly increased in Pusa Sharad when grafted onto rootstocks X9, CM, C47, and N1, compared to those grafted onto JK, C12, TC, and N5. The differential expression of genes revealed that the predominant genes for encoding salt-responsive proteins governing ion transport proteins (primarily NHX1 and HKT1 genes), chloride ion (Cl^-) homeostasis (CCC1 gene), the synthesis and accumulation of protective proteins (LEA2 gene), and the antioxidative mechanisms for scavenging reactive oxygen species (ROS), predominantly involving APX. The finding of our study concluded that the Pusa Sharad grafted onto CM, C47, X9, N1, and N3 demonstrated greater NaCl tolerance compared to those grafted onto JK, C12, N2, N4, N5, and TC.

Effects of tree age and heading back on mango (*Mangifera indica* L.) cv. Amrapali

Amrapali trees having different tree ages (10, 20, and 30 years), and Amrapali trees headed back 5, 10 years ago with non-headed back trees as control trees were used for the studies. The physiological and fruit growth related parameters were studied. It was evident that the nitrogen content was maximum in 20 years old trees of Amrapali (1.38%) which was statistically *at par* with nitrogen content in leaf tissues of 10 years old trees (1.29%). Similarly, maximum phosphorus (0.22%) was observed in 10 years old trees and had a significant difference with phosphorus content in 20- and 30-years old trees. Photosynthetic pigments Chl ‘a’,’b’ and their ratio were recorded higher in 20-year-old trees, whereas total chlorophyll was elevated in 30-years old trees. On fresh and dry weight basis higher reducing sugar was noted in 10-year-old trees, non-reducing in 20-years old and total sugar in 20-years old trees. Total number of panicles, malformed panicles, healthy panicles, malformation percentage, fruit per trees, and estimated yield were observed in 30 years old trees, while number of the male flower and hermaphrodite flowers per healthy panicle, fruit retention, fruit length, fruit width, fruit volume, fresh and dry weight of fruit, TSS and acidity recorded maximum in 10-year-old trees. In response to heading back treatments, chlorophyll ‘a’ ‘b’ and total chlorophyll content was elevated in trees headed back 5 years ago and diminished in trees headed back 10-years ago than control. However, fruit length, width and volume were more in trees headed back 5 years ago compared to control. In trees headed back 10 years ago had higher titratable acidity while it was lowest in trees headed back 5 years ago. Based on present findings, it is concluded that Amrapali trees attaining an age of more than 20 years may suffer from poor fruit quality and must be subjected to severe pruning for rejuvenation.

Effect of *Tephrosia* biomass mulching on mango (*Mangifera indica* L.) under the rainfed upland condition

Tephrosia candida (Roxb.), a leguminous shrub, has been identified as a promising perennial plant that could produce leafy biomass as a consequence of research done at ICAR-RCER FSRCHPR, Ranchi. The objective of the present study was to investigate if *Tephrosia* biomass mulching may increase mango productivity and soil fertility in the EPHR. The study included four treatments comprising of mulching with different quantity (7.5, 5.0, 2.5, 0.0 kg fresh biomass of *Tephrosia candida* per sqm area of the tree basin). Among all the treatments studied it was found that the treatment T1 resulted in the maximum soil pH, soil EC, soil available nitrogen, soil available phosphorus, soil exchangeable potassium, DTPA-extractable micronutrients (Cu, Fe, Mn and Zn). T1 also exhibited the highest soil enzymatic activities including soil dehydrogenase and soil fluorescein diacetate, soil microbial biomass carbon content, soil total organic carbon, oxidizable organic carbon and soil organic carbon fractions, plant growth, leaf parameters and fruit quality parameters. Also, it was revealed that the effect of mulching does not vary significantly concerning total sugars, reducing sugars, non-reducing sugars and TSS. In contrast, the control group exhibited a higher value for total antioxidant activity and total phenolic content. In terms of the effect of mulching on the phenological behaviour of mango, the treatments did not vary significantly, however the treatment T4 (control) had achieved early physiological maturity. The treatments T1, T2 and T3 were found equally effective for all the parameters studied and consistently higher than the control. The study on the *Tephrosia* litter decomposition pattern revealed that around 50% of the mulch biomass could naturally decompose within approximately 0.74 years, while a significant 99% degradation could occur over approximately 5.35 years. Hence, mulching the mango tree basin with 5.0 kg fresh biomass of *Tephrosia candida* per sq.m is found to be most efficient in improving the soil physical, chemical and biological properties.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Pooja (21652)	M.Sc.	Study on association between pulp colour composition and seed based traits in guava (*Psidium guajava* L.)	Dr. Madhubala Thakre	ICAR-IARI, New Delhi
2.	Prabhanjan Bhanudas Rane (21653)	M.Sc.	Studies on the pollen micro-morphology, storage behaviours, and cross-compatibility of grape (*Vitis* spp.) genotypes	Dr. Madhubala Thakre	ICAR-IARI, New Delhi
3.	Laya P. (21654)	M.Sc.	Impact of plant growth regulators in relation to cold tolerance and flowering in papaya (*Carica papaya* L.)	Dr. Jai Prakash	ICAR-IARI, New Delhi
4.	Raushan Kumar (21655)	M.Sc.	Characterization of a set of interspecific citrus hybrids Orangelo (*Citrus maxima* × *Citrus sinensis*)	Dr. Nimisha Sharma	ICAR-IARI, New Delhi
5.	Harshit Kumar (21656)	M.Sc.	Effects of tree age and heading-back on mango (*Mangifera indica* L.) cv. Amrapali	Dr. Manish Srivastav	ICAR-IARI, New Delhi
6.	Madhumati V. (60105)	M.Sc.	Effect of *Tephrosia* biomass mulching on mango (*Mangifera indica* L.) under the rainfed upland condition	Dr. Bikash Das	#ICAR-IARI, Jharkhand
7.	Saiket Dey (60106)	M.Sc.	Morpho-biochemical and molecular characterization of segregating population of litchi (*Litchi chinensis* Sonn.)	Dr. Mahesh Kumar Dhakar	#ICAR-IARI, Jharkhand
8.	Theivanai M. (11038)	Ph.D.	*In vitro* mutagenesis and validation of mutants using molecular markers in Kinnow mandarin	Dr. O.P. Awasthi	ICAR-IARI, New Delhi
9.	Reena Prusty (11263)	Ph.D.	*In vitro* mutagenesis and validation of mutants using molecular markers in sweet orange cv. Mosambi	Dr. O.P. Awasthi	ICAR-IARI, New Delhi
10.	Megha R. (11508)	Ph.D.	Studies on physico-biochemical characterization of mango genotypes in response to fruit fly infestation and related volatile profiling	Dr. S. K. Singh	ICAR-IARI, New Delhi
11.	Sandeep (11509)	Ph.D.	Drought stress tolerance studies in mango (*Mangifera indica* L.)	Dr. A.K. Dubey	ICAR-IARI, New Delhi

12.	Nitin P.S (11512)	Ph.D.	Evaluation of pummelo (*Citrus grandis* L) progenies for bitterness and rind thickness	Dr. M. Sankaran	**ICAR-IIHR, Bengaluru
13.	Jnapika K.H. (11514)	Ph.D.	Phenotypic evaluation and mapping of genomic regions governing yield and their component traits in mango	Dr A. Nagaraja	ICAR-IARI, New Delhi
14.	B.H. Sushmitha (11516)	Ph.D.	Evaluation and characterization of Arka Sahan custard apple progenies for self-fruitfulness	Dr. T. Sakthivel	**ICAR-IIHR, Bengaluru
15.	Ashok Dhakad (11517)	Ph.D.	Studies on floral development and reproductive biology in grapevine	Dr. V. B. Patel	ICAR-IARI, New Delhi
16.	Kripa Shankar (11783)	Ph.D.	Salt tolerance behaviour of sweet orange cv. Pusa Sharad on different citrus genotypes	Dr. O.P. Awasthi	ICAR-IARI, New Delhi

#IARI off campus

**Outreach Institute

Post Harvest Management

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Prof. Ram Asrey

The Division with a multidisciplinary approach has mandate of integration of production with postharvest management, development of appropriate handling and storage protocols. Valorisation of horticultural and arable crops through processing and waste utilization, transfer of technology, consultancy to both public and private sectors are also the mandated activities of the division. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Postharvest Management of Fresh Fruits and Vegetables

Exogenous brassinosteroids application for regulation of fruit ripening and quality in mango (*Mangifera indica* L.)

The results obtained showed that BRs (80 ng/g) treated fruits had significant lower PLW (13.00%) and higher firmness (4.82 N) and retained higher AA content (21.32 mg/100g), TPC (11.14 mg GAE/100g) and AOX (0.88 µmol Trolox /g FW) value. Under cold storage of 24 days, the higher dose of BRs (80 ng/g) displayed better quality characteristics. Fruits treated with 80 ng/g exhibited comparatively lowest PLW (5.89%), lowest CI (0.15%), EL (36.19%) along with the less activities of cell wall degrading enzymes, and MDA content. Similarly, brassinazole (BRz) (0.8 µg/L) displayed lower fruit weight loss (9.18%), higher AA (20.90 mg/100g), TPC value (10.89 mg GAE/100g) and AOX value (0.91 µmol Trolox/g FW) at ambient storage. Amongst doses, 1-MCP (300 nl/L) lowest PLW (5.48%) and higher colour value, fruit firmness along with suppressed rate of respiration (59.99 mL CO_2/kg/h) and ethylene (0.99 C_2H_4 mL/kg/h). The same dose maintained higher AA content (20.50 mg/100g), TPC (10.71 mg GAE/100g), AOX value (0.90 µmol Trolox/g FW) with least cell wall degrading enzyme activities. The same concentration also elevated the activity of antioxidants enzymes like SOD, CAT, POD and PPO.

Effect of hot water treatments and MAP on the storage life of mango (*Mangifera indica* L.) cv. Banganapalli

Mango (*Mangifera indica* L. family Anacardiaceae), being climacteric fruit, ripens after harvest and the shelf life varies between 4 to 8 days at ambient temperature and 2-3 weeks at optimum low temperature of 13°C, depending upon the varieties. The present investigation is to integrate different HWTs (which is also one of the quarantine treatments in mango export) in Banganapalli mangoes with different cold storage temperatures, with MA packaging and chemical pre-treatments in order to understand its scope in achieving maximum storage life with quality maintenance. Among different HWTs tried, 48°C for 60 min (QHWT) and 55°C for 10 min treated fruits performed better than control. Fruits could be stored up to 4 weeks and 10 days in 13°C and room temperature, respectively without affecting quality. Best results were obtained when mangoes were packed in micro-perforated (0.005 % perforation) Cryovac PD-961 films after QHWT, and stored at 13°C. Combination of QHWT with SA (2.5 mM) pre-treatment and micro-perforated PD-961 film package reduced chilling injury in mangoes at 8°C storage.

Postharvest interventions for reduction of pesticide residues in apple

The farmers use an indiscriminate amount of pesticides to prevent infection from various pests and diseases during the growing season of apple fruits. Their residues may be toxic to consumers and fetch poor returns to farmers due to rejection of consignments. The present study was conducted to elucidate the effect of physical, chemical and processing techniques on pesticide residue degradation from apple fruit while maintaining their optimum quality attributes during a 90 days cold storage period. The influence hot water, gamma irradiation and chemical treatment on the degradation of pesticide residues was evaluated along with an assessment of quality attributes. Increasing hot water temperature and duration yielded a significant reduction in pesticide residues (90-98%) from apple fruit. The results of recovery ranged from 75.18 to 119.17% with a 4.19 to 12.72% relative standard deviation. Among the pesticides dithianon, malathion and dimethoate were found to be most susceptible to the treatment. Accelerated dissipation of azoxystrobin, carbendazim, chlorpyriphos and tebuconazole with increasing doses of irradiation from 0.25 to 1.kGy was observed (ranging between 0.69 to 84%) while chlorpyriphos and thiacloprid dissipation ranged between 8.77 to 86. 94%. A significant decline in t½ of pesticides degradation was observed upon subjecting fruits to gamma rays at 0.75 and 1.0 kGy. Among the chemical treatments, peroxyacetic acid (0.008%), oxalic acid (0.1%) and sodium hypochlorite (0.01%) significantly influenced the dissipation of pesticide residues by 70 to 98% during the 90 day storage period of apple fruits. Sterilization of juice in absence of potassium metabisulfite (-KMS) exhibited the maximum dissipation of pesticide residues. Ascorbic acid added (+AA) frozen as well as concentrated pulp showed the maximum dissipation (50 to 100%) of pesticides at the termination of the experiment. Upon processing, azoxystrobin, difenoconazole, hexaconazole, tebuconazole, dimethoate, chlorpyrifos and malathion dissipated faster in comparison to carbendazim.

Eco-friendly approaches for managing postharvest quality and diseases in stored guava fruit

Guava (*Psidium guajava* L.) fruit is an abundant source of phytonutrients including carotenoids, vitamin C, minerals and polyphenols. The present study was intended to maintain quality and manage postharvest diseases in 'Barafkhana' guava using melatonin, brassinosteroids and ultraviolet-C (UV-C) treatment. The results showed that 600 µmol L^{-1} melatonin treatment was found effective in maintaining lower weight loss (PLW), better firmness and lower respiration rate. Further, it enhanced the activities of superoxide dismutase, catalase and ascorbate peroxidase, while malondialdehyde and hydrogen peroxide content kept under check. Likewise, the 60 ng g^{-1} brassinosteroids treatment was efficient in delaying PLW, respiration rate and ethylene evolution. Further, these concentrations also recorded higher biochemical and quality parameters including total soluble solids and antioxidants. Additionally, UV-C dose of 2.0 kJ m^{-2} and 10.00 kJ m^{-2} were effective in controlling *Colletotrichum gleosporoides* and *Rhizopus stolonifer* infection, respectively under in vivo conditions. Further, 2.0 kJ m^{-2} UV-C irradiation significantly maintained the fruit quality during storage. The current investigation inferred that the melatonin (600 µmol L^{-1}), brassinosteroids (60 ng g^{-1}) and UV-C irradiation (2.00 kJ m^{-2}) were significant in enhancing the shelf-life, and maintaining postharvest quality of 'Barafkhana' guava fruits under cold storage.

Physical elicitors for quality retention and anthracnose disease suppression in papaya fruits

Papaya (*Carica papaya* L.) is recognized as a functional food rich in enzymatic and non-enzymatic antioxidants. To address postharvest challenges and minimize residual effects, eco-friendly interventions were explored. Five experiments were conducted: the first and second involved UV-C radiation (0.8 to 2.8 kJ m^{-2}) to control anthracnose *in vitro*, with doses above 2.0 kJ m^{-2} showing complete inhibition in vitro. However, it was not entirely effective in preventing in vivo disease incidence as the UV-C irradiation induced scalding and damage to the peel, favouring disease incidence. In the third and fourth, pre-inoculated fruits were ozonized (1.5 to 3.0 mg L^{-1}) to control anthracnose *in vivo*. The aqueous ozone treatment, significantly reduced respiration, ethylene evolution, and extended shelf life by up to 20 days in cold storage. Additionally, the ozonation treatment substantially delayed the activity of pectinolytic enzymes throughout storage period. The fifth experiment combined ozone (2 mg L^{-1}) with guar gum coating (0.3% GG), enhancing shelf life to 8 days at ambient storage with acceptable quality which is two days more than control and ozone and coating treatment alone. Overall, these eco-friendly interventions show promise in preserving papaya quality and managing postharvest diseases.

Standardization of maturity indices and post-harvest protocols for domestic and export marketing of avocado (*Persea americana* Mill.)

The aim of study was to determine the optimum maturity, ideal cold storage temperature and suitable pre-storage treatment to extend the storage life with better retention of fruit quality. Findings of the study revealed that avocado fruit followed the sigmoidal growth curve during its growth and development phase. During storage at different temperatures (5 °C, 9 °C, 12 °C and ambient condition), fruits stored at 9 °C showed maximum storage life (21 days) with better quality retention in both the accessions. Whereas, under ambient condition fruits remained in good condition only for 7 days in CHES−HA−I/I and 4 days in CHES−HA−VII/I. Among pre-storage treatments, 1-MCP (500 ppb) exhibited promising effect on extending the storage/shelf life of avocado fruit. From the present study it is concluded that avocado fruits grown under Bengaluru, Karnataka conditions can be harvested between 140-150 DAFS when fruit fat content reaches 16.00 to 19.07 g/100g. Untreated fruits can be stored at 9 °C up to 21 days without chilling injury and it can be extended up to 42 days with pre-storage treatment (1-MCP 500 ppb) with least change in quality, lowest spoilage and weight loss. This information can help the avocado fruit growers, traders and exporters in planning harvest, storage, marketing and export.

Theme 2: Processing of Horticultural Crops

Green technology for chlorophyll extraction from pea pod shells

Processing industries of garden pea generate huge amount of waste in the form of empty pods which makes up about 30 - 40 % of fresh weight of the vegetable. Such waste has an attractive nutritional profile with potentiality of use in food industry. The present study was carried out to maximise the extraction of chlorophyll from fresh pea pod pomace by ultrasonication, metal complexing followed by enzyme-assisted extraction. Blanching of pomace and ultrasonication at 50% amplitude were given as pretreaments to maximize chlorophyll recovery from the fibrous matrix. Suitable zinc salt concentration for zinc-chlorophyll complex formation, temperature treatment and pH of pea pod pomace were selected on the basis of maximum chlorophyll content recovery as well as the brightest green hue of the extract. For enzyme-assisted extraction, different levels of enzyme concentration (20, 40 and 60 IU/g), incubation time (60, 120 and 180 min) and incubation temperature (30, 45 and 60°C) were selected to maximize chlorophyll yield in extract. Optimization studies revealed 49.975 IU/g cellulase addition, at 30°C incubation temperature for 60 min incubation increased the chlorophyll recovery in the extract by 56 % as compared to control. The extracted pigment was subjected to varying processing regimes of pH, temperature and light exposure. Stabilized pigment showed better stability in adverse processing conditions in comparison to control. Storage temperature of the stabilized chlorophyll below 25°C under dark conditions at pH 7.0 was found to be the best to get maximum stability of the pigment for its effective utilization as a natural green colourant.

Valorization of persimmon through novel dehydration techniques

Persimmon (*Diospyros kaki* L.) is a nutrient-rich tropical fruit, known for its antioxidants. To ensure year-long availability of this fruit, addressing its limited storage life during the climacteric phase and enhance its value, persimmons were osmo-dehydrated using sucrose, and low-calorie polyols: erythritol, and xylitol at various concentrations (30-60%) and temperatures (50-70 ºC). Effect of processing parameters (concentration, temperature and ultrasonication) on moisture ratio kinetics and quality of candied persimmon was determined. Logistic model was found effective for predicting moisture ratio during the osmodehydration process. Higher osmotic temperatures and ultrasound reduced osmo drying time considerably. Ultrasound-assisted dehydration in sucrose solution exhibited higher water loss and solid gain compared to xylitol and erythritol solutions. To convert the osmosed persimmon to candy, the osmotically dehydrated persimmon slices were subjected to further drying using tray dryer, infrared dryer, or vacuum fryer. Overall, it was concluded that highly acceptable low-calorie candy could be prepared from persimmon fruit at par with sucrose-osmosed candy using polyols erythritol and xylitol. Ultrasonication and infrared drying reduce processing time while enhancing acceptability. The most acceptable persimmon candy was obtained through ultrasound-assisted osmo dehydration in 50% erythritol solution followed by infrared drying.

Utilization of overripe banana powder for development of puffed extruded snack

Overripe banana (*Musa* x *paradisiaca* L.) is a rich source of sugar which can be used as a natural sweetener in foods. Understanding the gaps, the research was conducted which included a protocol for foam mat drying powder development from overripe banana and utilization of this powder as a functional additive for extruded snacks. We compared four foaming agents i.e., egg albumin, casein, soy and whey protein at a constant concentration level. Based on their foam stability, expansion, and density; egg albumin was found the best. Under second objective, process parameter comprising 26% banana flour with 200 rpm screw speed and 16% feed moisture, was reformulated and validated with the values predicted by the model. The proximate composition of extruded snacks showed that the developed snack is a fair source of dietary fiber with a slightly sweet tinge of overripe banana flour without any added sugar. Arrhenius model was used for shelf -life prediction of control, optimized powder, and optimized extruded snack under accelerated shelf -life study. The predicted shelf life was 6, 4 and 9 months for control, foam mat dried powder and optimized extruded snack, respectively at 30°C and 75% RH.

Ultrasound-assisted extraction (UAE) of pectin from citrus peels: Techno-functional and bioactive characterization

Pectin is a functional bioactive ingredient derived from citrus and apple pomace. The current trend emphasizes environmentally friendly methods for the sustainable utilization of food waste. For this, pectin was obtained from sweet lime and pummelo peels through ultrasound-assisted extraction (UAE) method and optimized using Response Surface Methodology (RSM). The optimal UAE conditions are sonication time = 9.38 minutes, power = 44.01%, and a liquid: solid ratio (L:S) = 46.79:1, yielded higher pectin (26.35%) with a high galacturonic acid content (69.11%) from pummelo pectin (PP) as compared to sweet lime pectin (SLP). The extracted pectin exhibited food-grade quality, featuring a low methoxyl pectin (LMP) (50%), and high functional quality in terms of phenolic content and antioxidant activity. PP had superior rheological and gelling properties than SLP. Both the pectin's demonstrated high biological activity in inhibiting lipid deposition in HepG2 cells and low cytotoxicity in MTT assay. The findings suggest that a LMP can be used for formulating low glycaemic foods, fabrication of low-fat mayonnaise using PP has been demonstrated to manage type 2 diabetes and obesity. Overall UAE merits promising prospects in comparison to traditional extraction methods due to its higher efficiency, shorter processing time and clean operation.

Development of nanocellulose based edible coating

An attempt was made to extract nanocellulose from rice husk by chlorine free/green method. Response surface methodology was used to optimize material moisture (15-35% d.b.), hydrothermal temperature (130-

150ºC) and screw speed (250-450 rpm). Cellulose content and lignin content were: 1646.45 mg/100g and 1.310 mg/100g, respectively. Response surface methodology was used to optimize NaOH concentration (2-4%), H_2O_2 concentration (15-25%) and oxalic acid concentration (5-15%). Cellulose, hemicellulose and lignin yields were: 80.54%, 10.57% and 8.46%, respectively. Nanocellulose was further obtained by ultrasonication. Nanocellulose yield was 71.32%. Nanocellulose yield obtained by standard method was 53.32%. Nanocellulose based edible coating was formulated. Response surface methodology was used to optimize RHN concentration (1-5%), Tween 80 concentration (0.1-0.5%) and glycerol concentration (5-15%). Contact angle, surface tension and turbidity were: 30.12 º, 26.39 mN/m and 166.83 NTU, respectively. PLW, lightness, hue angle, chlorophyll, respiration rate for 15 days storage of uncoated kale leaves varied from 0 to 42.23%, 34.01 to 65.67, 127.25 to 101.22º, 55.04 to 5.14 SPAD unit, 17.03 to 89.33 mL.CO_2 kg^{-1} h^{-1}, respectively while that for coated kale leaves varied from 0 to 19.36%, 33.27 to 45.12, 127.76 to 116.54º, 55.06 to 28.74 SPAD unit, 6.02 to 54.27 mL.CO_2 kg^{-1} h^{-1}, respectively.

Supercritical fluid extraction of oleoresins from *Capsicum chinense* (Bhut Jolokia): Characterization and encapsulation

Capsaicin, the dominant pungent compound in hot chilies, is widely used as a flavoring agent, preservative, and active compound in packaging film and functional foods.. The present investigation aimed to optimize a clean and green method for extracting capsaicin through supercritical fluid extraction (SFE) method using two different co-solvents; a) ethanol and b) rice bran oil (RBO). RSM was used to evaluate the effect of input variables (temperature, pressure, and time) on the responses; capsaicin content (CC) and global yield (GY) for SFE with ethanol as co-solvent, and CC and γ-oryzanol (GO) for SFE with RBO as co-solvent. The optimized SFE condition (68.31°C/347.98 bars/102.50 min) using ethanol as a co-solvent resulted in capsaicin-rich oleoresin (CO) displaying CC of 367.14 mg/g and GY of 7.23 %. Alternatively, when using RBO as the co-solvent, the optimal SFE condition (70°C /225 bar/110 min) produced capsaicin-rich RBO (CRBO) containing CC of 201.37 mg/g and GO 9.01 mg/g. Encapsulation efficiency (EE) of COM and CRBOM were 66.03 and 73.95 %, respectively. The CRBOM showed excellent retention of capsaicin (80.48 %) and GO (80.62 %) higher than COM under accelerated storage (90°C for 60 min), owing to its higher EE. Overall, the valorization of Bhut Jolokia for extraction of capsaicin opens a new window for its commercial exploitation in food industries.

Pectin from jackfruit waste: Extraction, functional characterization and its application as food coating

In this study, jackfruit peels used for pectin extraction through ultrasonication (UAE) and microwave-assisted extraction (MAE) process and optimized through response surface methodology. Optimized MAE conditions (power, 320W; time, 2.59 min; oxalic acid concentration (OA), 0.23N) achieved maximum pectin yield (PY, 15.32%), galacturonic acid (GalA, 74.57%) and degree of esterification (DE, 25.14%). Whereas, optimized UAE conditions (power 30%; time 12.23min; and OA 0.129N) achieved 12.04% PY, 68.65% GalA, and 38.11% DE. Significant ($p \leq 0.05$) differences were observed in the quality of pectin. Overall, the jackfruit pectin was food grade (GalA & 65%), low-methoxyl pectin similar to commercial pectin. Pectin was used to develop active packaging films using tapioca starch incorporated with black carrot extract (BCE). The WVP, oxygen permeability and elongation at break was minimum at 2% BCE concentration while exhibited highest tensile strength. Active packaging film significantly imparted oxidative stability of chia and flax seed oil by decreasing peroxide and total oxidation value. Biological activities further substantiate the high functionality of jackfruit pectin justifying its use in formulating low-calorie foods. Overall, results strongly suggest the practical utility of pectin in foods, and for fabrication of biodegradable packaging for environmental sustainability.

Theme 3: Processing of Arable Crops

Encapsulation of chia seed oil (*Salvia hispanica* L.)

In present study, the process of freeze-drying was employed for the encapsulation of chia seed oil (CSO) using three sets of wall matrix combinations, modified tapioca starch (MTS), maltodextrin (MD) and gum Arabic (GA) with whey protein concentrate (WPC) as a common wall material in all three combinations. Encapsulation efficiency (EE) and α-linolenic acid content (ALA) were evaluated for all runs. In set I (MTSWPC), the EE and ALA content of microcapsules were mostly influenced by wall material ratio and oil content. Whereas, in sets II (MDWPC) & III (GAWPC), all three independent variables significantly affected the response variables. The optimized conditions for OCSO I microcapsule resulted in high EE (97 %), ALA content (59.54 %), and a Ω-3:Ω-6 ratio (3.34). The optimized conditions of OCSO II yielded EE of 81.23 %, ALA of 61.85 %, and a Ω-3:Ω-6 ratio of 3.44, whereas that for OCSO III was 83.69 %, 60.04 %, and 3.34, respectively. The wall material composition MD:WPC::25:75 was found to be the best combination with an oil loading of 9 % and EE 81.23 %. The EE of MDWPC was confirmed through fatty acid composition, oxidative, thermal stability, and oil release. The encapsulated CSO with a balanced Ω-3:Ω-6 ratio can be used as a functional ingredient in foods for health benefits.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	S. Mounika Manisree (21703)	M.Sc.	Green technology for chlorophyll extraction from pea pod shells	Dr. Shruti Sethi	ICAR-IARI, New Delhi
2.	Ranjani M (21704)	M.Sc.	Valorization of persimmon through novel dehydration techniques	Dr. Shalini Gaur Rudra	ICAR-IARI, New Delhi
3.	Narola Ajay Rameshbhai (21705)	M.Sc.	Utilization of overripe banana powder for development of puffed extruded snack	Dr. Alka Joshi	ICAR-IARI, New Delhi
4.	Vathsala. V (21706)	M.Sc.	Ultrasound-assisted extraction (UAE) of pectin from citrus peels: Techno-functional and bioactive characterization	Dr. Charanjit Kaur	ICAR-IARI, New Delhi
5.	Anamika Thakur (10663)	Ph.D.	Development of nanocellulose based edible coating	Dr. Abhijit Kar	ICAR-IARI, New Delhi
6.	Nirmal Kumar Meena (10704)	Ph.D.	Exogenous brassinosteroids application for regulation of fruit ripening and quality in mango (*Mangifera indica* L.)	Dr. Ram Asrey	ICAR-IARI, New Delhi
7.	Anushree Anand (11104)	Ph.D.	Effect of hot water treatments and MAP on the storage life of mango (*Mangifera indica L.*) cv. Banganapalli	Dr. D. V. Sudhakar Rao	**ICAR-IIHR, Bengaluru
8.	Vishnu Anand (11109)	Ph.D.	Encapsulation of chia seed oil (*Salvia hispanica* L.*)*	Dr. Charanjit Kaur	ICAR-IARI, New Delhi
9.	Vikono Ksh (11110)	Ph.D.	Supercritical fluid extraction of oleoresins from *Capsicum chinense* (Bhut Jolokia): Characterization and encapsulation	Dr. Charanjit Kaur	ICAR-IARI, New Delhi
10.	Ajit Kumar Singh (11588)	Ph.D.	Postharvest interventions for reduction of pesticide residues in apple	Dr. Shruti Sethi	ICAR-IARI, New Delhi

11.	Menaka M. (11853)	Ph.D.	Eco-friendly approaches for managing postharvest quality and diseases in stored guava fruit	Dr. Ram Asrey	ICAR-IARI, New Delhi
12.	Vinod B. R. (11855)	Ph.D.	Physical elicitors for quality retention and anthracnose disease suppression in papaya fruits	Dr. Ram Asrey	ICAR-IARI, New Delhi
13.	Vivek Saurabh (11593)	Ph.D.	Pectin from jackfruit waste: Extraction, functional characterization and its application as food coating	Dr. Charanjit Kaur	ICAR-IARI, New Delhi
14.	Vittal Kamble (11595)	Ph.D.	Standardization of maturity indices and post-harvest protocols for domestic and export marketing of avocado (*Persea americana* Mill.)	Dr. C. K. Narayana	**ICAR-IIHR, Bengaluru

**Outreach Institute

Vegetable Science

21

Prof. R.K. Yadav

The Division of Vegetable Science has the mandate to conduct applied and strategic research on improvement of vegetable crops; to impart postgraduate education and training for human resource development; to disseminate information on recent advances in vegetable crops; to provide advisory and consultancy services on crop and seed production technology and improvement of vegetable crops; to collect, evaluate, purify and preserve the bio-diversity material related to different vegetable crops; to utilize the desirable superior genotypes in the breeding programme. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Genetic Diversity and Nutritional Studies

Study on morphological, biochemical and molecular diversity in vegetable soybean [*Glycine max* (L.) Merrill]

Thirty-four vegetable soybean genotypes were evaluated at the ICARRCER research field in Plandu, Ranchi, and Jharkhand for green pod yield, yield-related traits, as well as nutritional and anti-nutritional characteristics. Pod pubescence was observed in all genotypes except for AGS-332, AGS-339, NRC-105, and Karune. AGS-610 was noted as the earliest to reach the first green pod harvest stage (R6 stage). Among these genotypes, AGS-458 exhibited a promising pod yield of 0.39 kg/plant and seed yield of 0.22 kg/plant, akin to the prominent variety Swarna Vasundhara, making it a noteworthy Basmati flavoured genotype. Additionally, AGS-459 and AGS-404 showed promise for both graded green pod yield and green seed yield. In terms of nutritional and antinutritional factors, AGS-292 stood out for having the lowest trypsin inhibitor activity. AGS-190 emerged as a promising genotype for oil extraction and the oxidative stability of oil (with 18.6% oil content, 52.10% oleic acid, and 23.16% linoleic acid). The study also revealed high genetic diversity and heritability in various traits. Additionally, a correlation analysis demonstrated strong and statistically significant relationships ($p = 0.01$) between traits like plant height, days to first harvest, days to reach fifty percent flowering, the number of primary branches per plant, and graded green pod yield per plant. Genetic divergence analysis focusing on 12 green pod yield traits could group 34 genotypes into seven clusters, with AGS-459 (in cluster VI) and AGS-332 (in cluster VII) identified as the most distinct genotypes. These divergent genotypes hold promise as potential parents in hybridization programs aimed at developing high-yielding vegetable soybean lines and varieties. The Polymorphic Information Content (PIC) values of SSR markers ranged from 0.06 (Satt 707, Satt 546) to 0.72 (Satt 367), with an average PIC value of 0.49.

Genetic diversity studies in pointed gourd (*Trichosanthes dioica* Roxb.) for yield & quality attributes

Forty-six distinct genotypes of pointed gourd were evaluated at ICAR-Research Complex for Eastern Region, Plandu, Ranchi, Jharkhand. Analysis of variance revealed that all the 46 pointed gourd genotypes varied significantly for all fruit yield and quality traits. Attributes like fruit per plant, harvest frequency, pulp seed ratio, and total phenol content are significantly and positively correlated to total fruit yield (t/ha).Total fruit yield (t/ha) has the maximum contribution towards genetic diversity observed in this study. Seven principal components were derived through linear transformation, collectively explaining about 78.27 percent of the variation. The polymorphic information content (PIC) values of the primers, ranging from 0.35 to 0.45, indicated a moderate level of genetic diversity among the genotypes. Variety Swarna Alaukik and among genotypes HAP-79, HAP-70 were highlighted as promising ones for the yield related attributes and genotypes HAP-106 for quality traits. The promising genotypes have the capability to be employed in upcoming breeding initiatives. As a result, these genotypes can be advocated for cultivation in the Eastern Plateau and Hill Region, aiming to safeguard the nutritional well-being of the local population in that area.

Diversity analysis and nutritional profiling of garden pea (*Pisum sativum var. hortense* L.)

Analysis of variance and mean performance for pod yield and its components showed significant differences among 94 accessions of garden pea for all characters indicating the presence of a wide range of variability in genotypes. PCV values were slightly greater than GCV, indicating very little influence of the environment on their expression. High estimates of genotypic and phenotypic coefficient of variation were found for the characters viz., pod yield per plant, 10 pod weight, plant height, and internode length. High heritability coupled with genetic advance as percent of mean was observed for plant height, internode length, number of seeds per pod, 10 pod weight, number of pods per plant and pod yield per plant. In correlation studies, it was observed that pod yield per plant showed a significant positive association with the number of pods per plant, number of seeds per pod, 10 pod weight, pod length and pod width. In the correlation study of biochemical traits pod yield per plant shows a positive correlation with Sugar and moisture. The positive direct effect on pod yield per plant was exhibited by 10 pod weight followed by the number of pods per plant, and pod length. In cluster analysis, all the accessions were classified into six clusters. To gain a broader perspective on the data, principal component analysis (PCA), was employed which identified five principal components (PCs) that accounted for over 79% of the total variation among the traits. Based on yield performance, Pusa Prabal and 2021/PMVAR-8 were found to be the superior yielding genotypes. GP 1102 and JP 625 were found to be promising for nutritional traits.

GABA (γ-Amino Butyric Acid) profiling and in-vitro regeneration protocol optimization in tomato (*Solanum lycopersicum* L.) genotypes suitable for protected environment

GABA (γ-Amino Butyric Acid) profiling was done in 75 tomato genotypes grown under protected condition at three fruit maturity stages, i.e., green stage, turning stage, and ripe stage. DTH-475 (orange coloured fruit) exhibited the highest GABA content (28.06 mg g-1 DW and 1459.55 µg g-1 FW) during the green stage. Analysis of 75 genotypes revealed significant genetic diversity in terms of yield, quality parameters, and fruit colour. In optimization of *in-vitro* regeneration protocol for Pusa Ruby and K-63 genotypes was also attempted. In case of Pusa Ruby, the highest survival percentage was achieved with a 10-minute pre-treatment of 4% NaOCl, resulting in 84.3% survival. *In vitro* cultured hypocotyls of Pusa Ruby demonstrated successful protection from contamination with the same NaOCl pre-treatment. In K-63 tomato, shoot tips exhibited the highest survival (81.1%) when subjected to 10 minutes of 4% NaOCl treatment. The regeneration frequencies of Pusa Ruby and K-63 were calculated using different explants and growth media compositions. NAA was found effective in enhancing regeneration frequency. Callus initiation from shoot tips was faster in Pusa Ruby compared to K-63. Lower levels of auxins and cytokinins led to prolonged callusing duration, while higher doses reduced the time needed. IBA was more effective than NAA in inducing early rooting. Pusa Ruby exhibited the highest rooting percentage (84.8%) with specific media composition. These findings hold implications for selecting suitable genotypes for their use in tomato breeding programmes as well as advancing in-vitro regeneration techniques.

Genetic diversity and heterosis studies in okra [*Abelmoschus esculentus* L. (Moench)] for yield and quality attributes under Eastern Plateau region of India

The present work was carried out at ICAR-IARI Jharkhand during Kharif-2022. The analysis of variance for morphological and quality traits indicated that there was significant diversity among the genotypes for the majority of the characteristics being examined. Yield per plant, was observed maximum in genotype Pusa bhindi-5 (358.49 g). Three genotypes namely Pusa Bhindi-5 and Kashi Kranti recorded minimum incidence of Bhindi YVMV at 90 days after sowing (DAS). Although yield was positively correlated with the total number of fruits per plant, fruit weight and plant height, however, yield revealed a significant and negative relationship with the YVMV disease incidence. Among quality traits, a negative and significant correlation was observed for yield per plant with that of ascorbic acid and a positive correlation with mucilage content. Cluster analysis using both morphological and biochemical traits grouped 45 okra genotypes into six different clusters with a maximum of 21 genotypes in Cluster VI. Diversity using 30 polymorphic SSR primers revealed a mean allelic variation of 1.9 alleles per locus. Further, neighbour joining (NJ) cluster analysis grouped 72 genotypes of okra into two major clusters. Cluster I containing a majority of the cultivated types of okra and was clearly distinct from the wild types grouped under Cluster II. Heterosis and combining ability effects revealed that Kashi Kranti and DOV-7 best parent for yield per plant, while cross combination KRK/GKLF-20×Pusa Sawani was found best hybrid on the basis of both SCA effect and per se performance for number of branches and yield per plant. Hybrid KRK/GKLF-20×Pusa Sawani exhibited maximum positive and significant heterosis over mid parent (32.84%), better parent (31.37%) and commercial check (31.37%). The present study has showed tremendous scope for commercial exploitation of heterosis in okra under the Eastern Plateau Region of India.

Morphological, biochemical and molecular characterization of okra genotypes for yield and quality traits

The results of analysis of variance of 55 diverse okra genotypes indicated substantial variation among the genotypes for most of the traits examined. Notably, carotenoid content and chlorophyll a exhibited high values for genetic coefficient of variation (GCV), heritability, and genetic advance. Correlation studies revealed significant correlations of yield (q/ha) with yellow vein mosaic virus disease (-0.32**), internode length (- 0.47**) and days to 50% flowering (-0.53**) in negative direction, while positive correlations were observed with fruit length (0.34**) and fruit weight (0.38**). Regarding quality traits, ash (-0.22*), mucilage (-0.27**), and calcium content (-0.16*) displayed negative and significant correlations with yield (q/ha). Based on morphological traits, the 55 okra genotypes were grouped into six different clusters, with cluster 1 having the most genotypes. Similarly, for quality traits, eight divergent clusters were formed. Principal component analysis of morphological traits revealed that five principal components contributed to a total variability of 83.76%. In the molecular study, 10 SSR markers exhibited polymorphism, resulting in 20 alleles being detected. The polymorphic information content (PIC) was determined to be 0.599, with PIC values ranging from 0.076 in primer OKRA SSR 69 to 0.778 in primer OKRA SSR 67. However, almost all inter primer binding site (iPBS) markers were found to be polymorphic, resulting in a total of 66 alleles. The average polymorphism information content (PIC) was 0.401 with value ranging from 0.373 to 0.485 and the average expected heterozygosity is found to be 0.428 with value ranging from 0.161 in iPBS 2383 to 0.499 in iPBS 2384, iPBS 2225 and iPBS 2077 respectively. The cluster dendrogram based on molecular marker analysis grouped 79 okra genotypes in two major clusters.

Genetic analysis of yield, yield parameters and downy mildew resistance in ridge gourd [*Luffa acutangula* (Roxb.) L.]

Ridge gourd is an important cucurbit globally but its production is hampered by various diseases, notably downy mildew. To address this, an experiment was conducted from 2020 to 2023 at ICAR-Indian Institute of Horticultural Research aimed at identifying downy mildew resistant sources, studying the genetics of yield and downy mildew resistance, and identifying molecular markers linked to downy mildew resistance loci. Ten ridge gourd varieties and 13 advanced breeding lines were screened for two kharif seasons, identifying ten moderately resistant lines based on the percent disease index (PDI). Notably, IIHR-DMR-18-4-4 and IIHR-DMR-18-65-1 exhibited lower disease severity (PDI: 23.46 and 24.03) than Pusa Nutan (PDI: 73). Combining ability and heterosis studies for yield, related traits, and downy mildew resistance revealed non-additive gene action, except for specific traits. Deepthi and IIHR-DMR-18-65-2 were good general combiners and crosses Deepthi x IIHR-DMR-18-4-4 and Pusa Nutan x IIHR-DMR-18-65-1 were specific combiners for yield. Crosses Deepthi x IIHR-DMR-18-4-4 and Pusa Nasdar x IIHR-DMR-18-65-2 showed promising yields with the highest heterosis.Six-generation mean analysis of crosses Jaipur Long x IIHR-DMR-18-4-4 and Arka Prasan x IIHR-DMR-18-4-4 indicated the presence of epistasis. In Jaipur Long X IIHR-DMR-18-4-4, dominant gene effects (h) and additive x dominance effect (j) were observed, while in Arka Prasan x IIHR-DMR-18-4-4, additive x additive gene interaction (i) and dominant gene effects (h) showed greater magnitude with a duplicate nature of epistasis in both crosses. Reciprocal recurrent selection is suggested for improving downy mildew resistance in ridge gourd. Using 462 SSR markers in 288 F_2 populations of Jaipur Long x IIHR-DMR-18-4-4, polymorphic SSRs were identified through Bulk Segregant Analysis (BSA). SSR-RG-56 and SSR-RG-61 markers showed significant genetic associations with downy mildew resistance (p-value <0.05), with SSR-RG-56 as a major marker (R^2> 10). Hence, IIHR-DMR-18-4-4 can serve as a valuable resistance source.

GABA (γ Amino butyric Acid) profiling and optimization of in vitro regeneration protocol in tomato (*Solanum lycopersicum* L.) genotypes suitable for protected environment

Seventy-five tomato genotypes were screened at different stages (green and turning stages) for GABA, an important amino acid with roles in neurotransmission and stress resistance. Notably, K-44 had the highest GABA in green 15.70 mg/g dw, while K-73 had the lowest 9.15 mg/g dw. Turning stage GABA ranged from 7.07 mg/g dw K-49 to 11.14 mg/g dw K-147. Certain genotypes like K-63, K-69 and K-70 maintain stable GABA levels during ripening despite the general decrease in GABA content. Among the three yellow genotypes, K-63 flat yellow had the highest GABA expression, followed by K63 round and K-63 normal yellow. In optimization of in-vitro regeneration, the critical role of the right explant length selection was noticed for achieving optimal callus induction outcomes. The focus was then shifted to the influence of culture media on callus and shoot multiplication from nodal explants, and different concentrations of BAP were employed. The effects of culture media on shoot multiplication were examined. Overall, the importance of factors like explant length and growth regulators in achieving successful callus induction and subsequent shoot multiplication in tissue culture was emphasized by these experiments. The critical influence of various factors on successful tissue culture-based plant regeneration was demonstrated by the study. From explant length to growth regulator concentrations, each parameter was shown to play a crucial role in determining callus induction, shoot multiplication, and root formation. These findings contributed to the broader understanding of plant tissue culture techniques, their optimization, and their potential applications in improving crop traits and cultivar development.

Genotypic and photo-temporal response of vegetable-based microgreens on its nutritional and biochemical properties

Microgreens are young plants that emerge from vegetable, herb, or wild species seeds and are consumed at the stage when their cotyledons or first true leaves have fully expanded within 7 to 21 days after germination. The present was carried out with ten different genotypes which were grown in black plastic shallow trays using cocopeat media only. They were given three different light treatments (100% white, 50% blue + 50% white, and 50% red + 50% white light). Finally, samples were taken in two different stages (7 days and 12 days after germination) to undergo nutritional and biochemical analysis. Red cabbage stood out as the most favourable genotype due to its elevated levels of essential phytochemicals such as vitamin C, carotenoids, phenols, and the antioxidant FRAP. Furthermore, the red amaranth ranked as the second most promising genotype in our investigation due to its high content of dry matter, anthocyanin, and important minerals (magnesium and iron). Harvesting, the second stage, which occurs twelve days after germination, emerged as the most favourable. This stage exhibited the highest concentrations of the desired phytochemicals. However, for achieving high antioxidant activities (FRAP and DPPH), as well as for phenols, calcium, and copper content, the first stage, occurring seven days after germination, proved to be the most advantageous. Regarding the light treatment, both Light II (50% blue + 50% white) and Light III (50% red + 50% white) conditions proved to be more advantageous for the desired phytochemicals when compared to Light I (100% white) conditions. Important phytochemicals like vitamin C, phenols, DPPH, and calcium were found in the highest quantities when exposed to Light III. Conversely, Light II was the optimal choice for carotenoids, anthocyanin, and crucial minerals such as magnesium, iron, and zinc.

Theme 2: Biotic Stress Tolerance

Molecular mapping of watermelon bud necrosis orthotospovirus resistance gene(s) and evaluation of fruit quality traits in watermelon [*Citrullus lanatus* (Thunb.) Matsum & Nakai]

Watermelon bud necrosis orthotospovirus (WBNV) resistant watermelon prebred line ‘DWM-45’ (*Citrullus lanatus var. citroid*) was crossed with commercially popular but WBNV susceptible variety 'Arka Manik' to produce F_1, F_2, BC1P1 and BC1P2 populations. In the screening experiments against WBNV under the natural epiphytic and artificial inoculation conditions P1, F1, and BC1P1 showed greater WBNV resistance. Segregation analysis indicated Mendelian ratios of 3: 1, 1: 0, and 1: 1 for F2, BC1P1, and BC1P2 populations, respectively confirming the resistance in DWM-45 governed by single dominant gene. To map the WBNV resistance gene(s) governing resistance in DWM-45, 210 markers were tested and we found 15 SSR markers showing polymorphism between P1 and P2. One SSR marker i.e., BVWS02365 was able to differentiate between resistant and susceptible bulks and individual resistant and susceptible plants in the F_2 generation, following a Mendelian ratio of 1: 2: 1 confirming single dominant gene resistance. The BVWS02365 marker displayed a significant LOD score of 29.47 in single marker analysis, indicating strong linkage (6.8 cm) to the WBNV resistance gene (Wb-1). With respect to the genetics of fruit quality traits, monogenic inheritance for fruit shape, rind colour, rind pattern, seed coat colour, and flesh colour at margin and carpellar regions were recorded. Flesh taste followed two-gene dominant epistasis, while complex genetic control with epistatic digenic interactions influenced traits like fruit length, fruit width, fruit weight and Total Soluble Solids. From the results it was concluded that the resistance to WBNV in ‘DWM-45’ is governed by single dominant gene, therefore simple selections can be useful for the improvement of this trait and DWM-45 can be used as source of resistance in WBNV resistance breeding of watermelon. The identified linked marker ‘BVWS02365’ can be used for marker assisted selection to fasten the WBNV resistance breeding in watermelon.

Studies on inheritance for fruit yield related traits and molecular mapping of downy mildew resistance genes in cucumber (*Cucumis sativus* L.)

Generation mean analysis showed non-significance scaling test indicating the absence of epistatic interaction and higher presence of additive/dominance effect in the cross DC-773 × DC70, thus revealing that the downy mildew resistance in the genotype DC-70 was controlled by a single recessive gene. The scaling test was significant and epistatic interactions were observed for all the fruit yield related traits. Complimentary epistasis was observed for node number of male flower, node number of female flower, fruit diameter, number of fruits per plant and yield per plant. Whereas, duplicate epistasis was observed for days to male flower opening, days to female flower opening, days to fruit set, days to fruit harvest, fruit length, average fruit weight and vine length. The gene effects of yield traits of six generations revealed that the magnitude and direction of gene effects varied in the cross DC-773 × DC-70. This suggested the need to exploit heterosis and/or selection of beneficial segregants through pedigree method for the improvement of fruit yield per plant in cucumber. By QTL-seq approach, several QTLs associated with downy mildew resistance were identified on chromosomes 3 and 6. About 383 SNP and 14 InDel markers were identified in the region from 29.00 to 29.90 Mb (0.9 Mb) of chromosome-3. In the region from 20.30 to 21.20 Mb (0.89 Mb) on chromosome 6, 180 SNPs and 16 InDel markers were identified with Δ (SNP index) value of 0.388. A total of nine putative candidate genes on chromosome-3 and three putative candidate genes on chromosome-6 directly involved in downy mildew disease resistance were identified. These findings highlight the effectiveness of the QTL-seq approach for rapid QTL detection and provide valuable QTL regions for further fine mapping of downy mildew resistance and other traits in cucumber.

Genetic and biochemical analyses of resistance to Squash Leaf Curl China Virus in pumpkin (*Cucurbita moschata* Duchesne ex Poir.)

On the basis of morphological symptom on pumpkin leaf in the field at New Delhi and electron microscopy analysis indicated presence ofBegomovirus and Crinivirus infections respectively.Finaly molecular analysis identified the presence of predominant viruses like Squash Leaf Curl China Virus (SLCCV), and a novel virus, Cucurbit Chlorotic Yellows Virus (CCYV). CCYV was confirmed as a new emerging virus. The DNA-A and DNA-B component of PV-1 isolate of SLCCV exhibited sequence identities ranging from 95.0% to 98.7% & 88.0% to 96.1% with five Indian strains of SLCCV and 90.3% to 91.5% & 86.8% to 90.1% with ten Chinese SLCCV strains, indicating its close genetic association with Indian and Chinese SLCCV isolates, respectively. The sap inoculation method for SLCCV transmission was developed. Buffer III, consisting of phosphate buffer, β-mercaptoethanol, and Na2SO3, showed the highest severity of symptoms and incidence of infection in the susceptible pumpkin variety Pusa Vishwas. The summer season was found to be the most favourable for virus transmission, and plant parts such as expanded leaves, middle leaves, and stem exhibited higher infectivity compared to other parts. During 2021 and 2022, based on challenge inoculation studies, three pumpkin genotypes (DPU-41, DPU-43, and DPU-133) showed high resistance (VI = 0) to SLCCV and CCYV while Pusa Vishwas showed high susceptibility. The inheritance studies of six generations involving susceptible and resistant genotypes revealed that resistance to SLCCV in the genotypes DPU-41 and DPU-43 is governed by a single dominant gene. The resistant genotypes (DPU-41, 43 and DPU-133) consistently exhibited higher levels of total phenols, DPPH, FRAP, polyphenol oxidase, and catalase than Pusa Vishwas throughout the entire observation period (from 96 hours to 300 hours) after inoculation with viruliferous and aviruliferous whiteflies independently.

Introgression of YVMV and ELCV resistance from wild *Abelmoschus* species in okra (*Abelmoschus esculentus* L.)

Based on natural epiphytotic field screening of 24 accessions from five different *Abelmoschus species* for YVMV and ELCV, four accessions of different wild species, namely *A. moschatus* (IC 141055) and *A. manihot var tetraphyllus* (IC-90476-1), *A. caillei* (SKM) and *A. ficulneus* (Sel 1) were found highly resistant. These resistant accessions were crossed with cultivated genotype Pusa A-4 to develop F_1 and $BCIF_1$ populations. F_1 plants were found resistant to YVMV and ELCV. In crossability studies, direct cross with wild parents using Pusa-A4 as a female parent had higher rate of crossing efficiency than their reciprocal. Crossing efficiency was maximum in Pusa-A4 and *A. ficulneus* (Sel 1) with F_1 seeds germination of 82%. Pollen viability was maximum in Pusa A-4 (98.04 %) and lowest (1.94% to 46%) in interspecific F_1 (Pusa A-4 × *A. moschatus* (IC 141055). However, in its $BC1F_1$ population {[Pusa A-4 × *A. moschatus* (IC 141055)] × Pusa A-4} pollen viability improved (16.98% to 52.36%). In molecular screening of parental population, out of 45 pairs of microsatellite markers (SSRs), 28 primer pairs were identified to be polymorphic with average polymorphic information content of 0.36. Maximum polymorphic information content 0.56 was found to be in markers Okra SSR 121 and Okra 56. Among the genotypes used, for screening *A. tetraphyllus* (Sel 1) was widely related with Pusa A-4 with the genetic distance value 80. Hybridity of the F1 (Pusa A-4 x A. moschatus (IC 141055) was confirmed with these markers. On molecular screening of BCIFI {[Pusa A-4 x *A. moschatus* (IC 141055)] x Pusa A-4} population using these markers resulted polymorphic information content of 0.26. It was found that for F_1 development, cultivated okra should be used as female parent and large number of backcrosses should be made to get better success.

Pathogen identification and management of emerging foliar disease of kharif onion

Kharif and late kharif onion contributes around 40% of total production. From the randomly collected diseased leaf samples, six isolates of the pathogen responsible for leaf yellowing in kharif onions were obtained using single spore isolation. These isolates demonstrated variations in mycelial growth, conidial size, beak length, and septal numbers. Conidia shape ranged between obclavate to obpyriform to ellipsoidal. The average mycelium width ranges in between 3.58 to 4.86 µm, average size of conidia in between 25.12–33.33µmL and 11.02–17.9 µm, average beak length size in between 6.16–10.9 µm and number of septation ranged between 1-4 (horizontal) and 0-3 (vertical). Molecular analysis based on Internal Transcribed Spacer (ITS) region sequencing confirmed the morphological identifications, ensuring the accurate identification of the pathogen as *Alternaria alternata*. A similarity percentage of more than 99% was observed in almost all the isolates after sequencing and comparing the sequences retrieved from the Gene Bank using NCBI BLAST program. Pathogenicity tests on the kharif onion genotype KP-427 confirmed that all tested *A. alternata* isolates were pathogenic to kharif onions. Two genotypes, N. Local and L-9200, exhibited immune reactions, suggesting their potential for disease resistance and scope in future crop improvement program. *Trichoderma harzianum* was isolated from rhizosphere soil of the immune genotype (N. Local). The bio-efficacy of isolated *Trichoderma harzianum* and commercial formulation *Trichoderma viride* was studied under in-vitro condition against *Alternaria alternata*. In vitro study revealed *Trichoderma viride* as an effective bioagent in inhibiting the growth of *A. alternata* with inhibition of 63.03% followed by *T. harzianum* with inhibition of 60%, providing a promising route for sustainable disease control. Under in-vivo condition *Trichoderma viride* exhibited highest percent disease inhibition (45.95%) at 14 days after inoculation. Kkharif onion crops can be effective managed by employing both resistant genotypes and biocontrol agents.

Morpho-genetic diversity in onion, *Stemphylium vesicarium* and screening onions against Stemphylium leaf blight

Stemphylium leaf blight, caused by Stemphylium vesicarium affect both the bulb yield and the seed quality of onion. Significant variations were observed among the Stemphylium vesicarium isolates collected from different locations in terms of colony diameter, mean radial growth rate, and sporulation on PDA and PCA media. The conidiophores of Stemphylium vesicarium isolates displayed a wide range of dimensions, with lengths ranging from 28.45 µm to 80.45 µm and breadths ranging from 2.86 µm to 7.60 µm. Similarly, the conidia exhibited variations in size, colour, and shape, with length ranging from 23.31 µm to 43.18 µm and breadth ranging from 12.84 µm to 23.13 µm. 15 RAPD primers generated a total of 192 banding patterns. SV4, OPL5, and SV5 were identified as the most polymorphic primers. In the phylogenetic analysis, 20 isolates obtained from diseased onion leaves formed a distinct cluster and exhibited sequence similarity with ex- type sequences of Stemphylium vesicarium. Additionally, two isolates from diseased garlic samples showed sequence similarity with ex-type sequences of Stemphylium eturmiunum. Results of one hundred and fifty-seven genotypes revealed a significant variation among the morphological and biochemical traits studied. Fifteen genotypes were identified as moderately resistant. Further, biochemical analysis revealed that total foliar phenol content, pyruvic acid, catalase, and peroxidase increased up to 20 days after inoculation (DAI) and thereafter declined. Protein content was highest in the initial stage and declined at 10, 20, and 30 DAI. Correlation analysis showed a highly significant and negative correlation of PDI with total foliar phenol content (TFPC), pyruvic acid, catalase, peroxidase, and protein content. The polymorphic information content (PIC) values of the tested markers in this study ranged from 0.23 to 0.59, with 46.15% of the markers having PIC values higher than 0.5, indicating their high informativeness for genetic analysis.

Studies on genetics of resistance to gummy stem blight in watermelon [*Citrullus lanatus* (Thunb.) Matsum. & Nakai]

Gummy stem blight (GSB) caused by the fungus *Stagonosporopsis cucurbitacearum* (syn. *Didymella bryoniae*), is a devastating disease in watermelon all over the world. In India, various reports are available in several cucurbits except for watermelon. In this study, the pathogen causing GSB in watermelon was identified, isolated and characterized both morphologically and molecularly. The fungal isolate was registered as NAIMCC-TF 2438 with the NCBI accession number MN396362. A total of 266 genotypes were screened to identify the resistant sources for this disease. Among the genotypes IIHR-617 (IC 482276), IIHR-82, IIHR-545, BIL-53 and IIHR-556 were found to be resistant. Two most resistant genotypes IIHR 82 and IIHR 617 were chosen for the crossing with a highly susceptible parent Arka Manik to study the genetics of resistance. Results showed that Complementary type epistasis is present in IIHR82 × Arka Manik whereas, duplicate type in IIHR 617 × Arka Manik combinations. Whole genome sequencing of the resistant bulk, susceptible bulk and resistant parents for the population IIHR-617 × Arka Manik and IIHR 82 × Arka Manik was performed. Three extremely significant genomic regions were identified for the population IIHR 617 × Arka Manik and six were found for the population IIHR 82 × Arka Manik, conferring resistance to GSB. Significant differences were observed among the grafted entries and checks for disease incidence when the identified resistant variety was used as a rootstock for grafting and watermelon hybrid NS-295 as scion. Rootstocks evaluated for yield, quality and GSB incidence showed an improvement in terms of TSS, flesh colour, total carotenoids and lycopene content among the grafted entries as compared to non-grafted controls. Two suitable GSB-resistant rootstock combinations and the QTLs behind the complex resistant phenotype were identified which will provide direct benefit to watermelon growers as well as for breeding resistant varieties.

Mapping of anthracnose (*Colletotrichum* spp.) fruit rot resistance genes in *Capsicum* spp.

Two virulent local isolates of chilli, namely *C. trumcatum*'IIHR Ct-1' and *C. gloeosporioides* 'IIHR Cg-1' were able to infect the susceptible accessions (IHR4491) in both the wound *in-vitro* pin prick (37.1%) and field spray (35.3%) methods while the accessions PBC80 (1.0%; 1.9 %) and PBC81(0.8%, 1.57%) showed resistant reaction. These *C. truncatum* resistant accessions upon challenged with 'IIHR Cg-1' isolates expressed resistant reaction while PBC80 (9.57%) showed break down under *in-vitro* bioassay. The absence of nuclear resistance gene for *C. gleosporiodes* in PBC80 was confirmed. The chi square goodness of fit revealed the dominant epistatic gene model in 3R:13S inhibitory action for *C. truncatum* resistance. A resistant reaction was expressed in the absence of recessive inhibitory gene at one locus (*ANRCT1_anrct2 anrct2*). Resistance to *C. gloeosporioides* 'IIHR Cg-1'isolate was expressed when the susceptible genes at a locus is in homozygous recessive condition (*ancg1 ancg1ANCG2_*) or both the genes (Susceptible and modifier) are in homozygous recessive condition (*ancg1ancg1 ancg2 ancg2*). The mapping of 360 mortal populations with the abundant SNPs using the DArTSeq™ technology through Diversity Array technologies, Canberra, Australia produced 8644 SNPs spanning across the consensus linkage map covering all the twelve chromosomes of chilli. Out of which nineteen SNPs also known as QTNs; Quantitative Trait Nucleotides were significantly linked with chilli anthracnose fruit rot resistance. The chromosome 2 carries five associated SNPs while chromosome 6 carries seven SNPs. The search in pepper pan genome identified PR protein and transcription factor groups such as NBS-LRR regions. The five receptors *ie*., CCR4 or STPKs, LRR-RLKs, GsSRK, TIR and CRK identified on the anthracnose resistant region of chromosome 2 were pattern recognition receptor (PRRs) that were activated by the *Colletotrichum* spp. to produce PAMP-triggered immunity (PTI) on resistant lines.

Studies on interspecific hybridization in *Abelmoschus* species

Wild relatives of okra confer a good source of resistance for breeding programs, especially for traits linked to biotic and abiotic stresses. *Abelmoschus esculentus* cv. 'Pusa Sawani', a cultivated okra variety, was crossed with three wild accessions viz. *A. manihot var. tetraphyllus* (IC 90476-1), *A. moschatus* (IC-141055) serrated leaf type and *A. moschatus* (IC141040) non-serrated leaf type to develop interspecific population. Interspecific F_1s were confirmed for hybridity using SSR primers and flow cytometry. Cross compatibility were found when cultivated (Pusa Sawani) was employed as a female (seed parent). In pollen studies, both cultivated and wild parents exhibited high pollen viability and less variability in pollen diameter. Greater fruit set (78%) and crossing efficiency (50.34%) were obtained from the cross of 'Pusa Sawani' × IC 90476-1. The interspecific F_1s had vigorous plants with normal flowers and fruits; but sterile and no seed setting. The infertile F_1s were treated with 0.1% colchicine (colchiploidisation) to restore fertility. The results of the study will help in advancing knowledge about directionality of hybridization, improvement of quality traits, use of molecular tools and hybrid vigour to generate improved pre-breeding material/genetic stock(s) in cultivated from wild okra. To develop an *in vitro* regeneration protocol, five popular okra cultivated genotypes, two wild species, and interspecific hybrids were taken. Out of 64 different combinations of regeneration media, NAA and IBA in the concentration of 0.5-1mg/L and kinetin 1-1.5mg/L proved to be effective media for epicotyl and embryo culture in cultivated okra, wild species, and their interspecific derived F_1 hybrids. Regeneration efficiency in cultivated genotypes through epicotyl culture ranges from 40% to 65 and by embryo culture ranges between 25% to 65%, respectively. The success of apical shoot culture and embryo culture in okra was influenced by the genotype, growth hormones and their concentrations.

Phylogenetic studies in Indian luffa species

Four Luffa species viz. *Luffa acutangula* Roxb., *Luffa cylindrica* Mill., *Luffa graveolens* and *Luffa echinate* were used in this study. The seed dormancy was overcome by scarification coupled with GA3 treatment @ 200ppm in *Luffa graveolens* and scarification along with KNO_3 treatment @ 0.2% in *Luffa echinata*. Floral parameters of parental Luffa species had considerable variation with resulting F_1 hybrids with intermediate in flower size, corolla colour and ovary surface. For yield related traits higher level of variability was observed for fruit length (3.73-28.17cm), fruit width (2-3.72cm), average fruit weight (3.79-151.67cm) and number of fruits per plant (11.43-92.93). Cross incompatibility was found between *Luffa acutangula* × *Luffa echinata* due to both pre- and post-fertilization barriers. The sterility of F_1 hybrids was either due to the absence of viable pollen grains (*Luffa graveolens* × *Luffa cylindrica*, *Luffa acutangula var. hermaphrodita* × *Luffa graveolens*) or non-dehiscence of anthers (*Luffa cylindrica* × *Luffa graveolens*, *Luffa cylindrica* **×** *Luffa echinata* and *Luffa acutangula* × *Luffa graveolens*) and also due to the result of meiotic abnormalities and frequency of higher number of univalents in Pollen Mother Cells (PMCs). The cluster dendrogram based on molecular markers separated *Luffa cylindrica, Luffa graveolens* together in same cluster and *Luffa acutangula, Luffa echinata*, *Luffa acutangula var. amara*, *Luffa acutangula var. hermaphrodita* in second cluster. Cytological examination of Pollen Mother Cells of *Luffa cylindrica* × *Luffa graveolens* reflected maximum number of 5 to 9 bivalents per cell at diakinesis/metaphase I stage. Brewbaker and Kwack medium with 10% sucrose was found to be optimal medium for in vitro pollen germination for *L. acutangula*, *L. cylindrica* and *L. echinata* and BK medium with 3% sucrose for *L. graveolens*. Among different storage conditions, cryopreserved (−196˚C) pollen showed significantly higher viability.

Validation and fine mapping of quantitative trait loci for watermelon bud necrosis orthotospo virus resistance in watermelon

Watermelon Bud Necrosis orthotospo Virus (WBNV) transmitted by thrips pose a threat to year-round production in traditional watermelon production areas. Currently, no varieties, or hybrids have resistance to WBNV. Therefore, it is crucial to map QTLs and develop WBNV-resistant varieties. Using the BSA-QTL sequencing method, confirmed the presence of 2 QTLs on chromosomes 2 and 3, consistent with our previous findings. These regions have shown persistent and significant involvement in WBNV resistance over multiple years. Among three parents used for study the BIL-53 showed the highest resistance, followed by BIL-99 and BIL-135. The frequency distribution of AUDPC across all populations demonstrated a continuous distribution, underscoring the quantitative character of this trait. In population I (BIL-53 X IIHR 140-152), families 57, 60, 69, 75 and 76 displayed WBNV resistance in the summer of 2023. Fine mapping of QTLs successfully narrowed down the QTL region to 292kb (1.15cM) on chromosome 2 and on chromosome 3 were narrowed down to 512kb (0.9cM). Candidate gene analysis identified important genes within QTL regions of chromosome 2, Notably, F-box/LRR-repeat proteins, and Nicotinate phosphoribosyl transferase-like protein were found, playing roles in defense responses. Chromosome 3 was identified as significant for hosting QTLs/candidate genes related resistance genes with NBS-LRR genes, Calmodulin binding protein-like proteins, F-box -LRR protein genes, programmed cell death protein, Aspartokinase I, stress regulated protein and harpin-induced proteins were present in QTLs identified on chromosome 3, suggesting their key roles in defense against WBNV. The study suggests BIL-53 as resistant parent options for breeding WBNV-resistant varieties. Markers like WMSSR2-5, WMSSR2-26, WMSSR3-130, and WMSSR3-2, tightly linked to WBNV resistance, hold potential for marker-assisted breeding for enhanced fruit quality traits and WBNV resistance in watermelon.

Theme 3: Abiotic Stress Tolerance

Studies on physio-biochemical response and expression analysis of selected genes under drought stress condition in cucumber (*Cucumis sativus* L.)

Six cucumber genotypes were selected and categorized into three drought-responsive groups, namely tolerant (DGC-21 and WBC-23-2), intermediate (Pusa Uday and Punjab Naveen) and susceptible (DG-59 and PPC-6) to drought. These genotypes were grown hydroponically and subjected to osmotic stress induced by transferring them to a PEG solution. It was noticed that leaves were more sensitive to drought stress compared to stems and roots. Tolerant genotypes, DGC-21 and WBC-23-2, exhibited the ability to maintain higher relative water content, membrane stability index, and osmotic potential in leaves, stems, and roots susceptible DG-59 and PPC-6 genotypes. 122 Tolerant genotypes also displayed elevated photosynthesis and transpiration rates in contrast to the susceptible and intermediate ones. The latter groups showed elevated levels of malondialdehyde and hydrogen peroxide in leaves, stems, and roots, while proline levels slightly increased. In stark contrast, tolerant genotypes WBC-23-2 and DGC-21 exhibited substantially higher proline content. Enzymatic activity was generally higher in tolerant genotypes. Notably, strong correlations were observed between osmotic potential, malondialdehyde, hydrogen peroxide, and membrane stability index in leaves, stems, and roots. Expression analysis indicated that all the genes showed maximum expression after 48 h of stress. The tissue-specific expression of hormones like auxin may contribute to stress tolerance, and increased expression of ethylene-responsive transcription factors, particularly in tolerant genotypes, was linked to drought stress response of tolerant genotype. Moreover, the expression analysis confirmed the crucial role of heat shock proteins in stress tolerance. MYB transcription factor, tonoplast intrinsic proteins may have contributed to drought tolerance. Expression of some enzyme related gene showed higher expression in susceptible genotype. These findings contribute to advancing our understanding of how plants cope with drought stress and potentially lay the groundwork for targeted strategies to enhance stress tolerance in cucumber plants.

Physiological and molecular characterization for high temperature tolerance in garden pea

Eighty-six garden pea (*Pisum sativum var. hortense*) genotypes were screening at high temperatures for yield related traits in phytotron (controlled) and field condition (uncontrolled). In controlled screening in the growth chamber, 34 and 7 genotypes were identified as tolerant during the seedling and reproductive stages, respectively. Independent field screening during heat stress season (Jan-Aprilat 39/16.4°C) 15 genotypes could survived and set pods and only nine were found to have >60% pollen viability. The identified 15 tolerant, 15 moderately tolerant and 15 sensitive genotypes were further characterized using nine physiological and biochemical traits under heat tolerance. The average canopy temperature in heat stress conditions was 56.32% higher than in the normal season, and sensitive genotypes showed 6.32 % higher canopy temperature than tolerant genotypes. Similarly, MSI was found to be decreased by 44.51% in sensitive genotypes. The MDA and H_2O_2 contents were found to be increased more in sensitive genotypes. The enzymes superoxide dismutase and catalase showed increased activity of 69.61% and 8.89 times respectively. However, total sugar content was found to be decreased by 5.67% in tolerant genotypes and 11.75% in sensitive genotypes. It was observed that the key physiological and biochemical traits like relative water content, greenness index, membrane stability index, malondialdehyde, hydrogen peroxide, superoxide dismutase and catalase could be used as an identification index for heat tolerance. In molecular diversity studied, markers 16213, psaa219, and psmpb16 recorded the highest number of alleles per loci (10 alleles), and the marker psmpaa67 had a major allele frequency of 0.95. The highest PIC of 0.81 was observed in the marker psmpsad141. The garden pea genotypes were grouped into four populations by structure analysis. The genotypes viz. EC-

598646, EC-598638, 2019/PMPM-4, GP-61, GP-902, GP-912-II, EC-598649, GP-48, EC-677211, EC-598654, GP-1104, EC-677214, GP-57, GP-915-II and EC-598602 were identified as tolerant under heat stress.

Mapping of QTLs for heat tolerance in hot pepper (*Capsicum annuum* L.)

The F_1 derived by crossing DLS-161-1 (heat tolerant) and DChBL-240 (heat susceptible) was selfed to generate the F_2. DLS-161-1 performed significantly better for various heat stress related parameters, like plant height (60 cm), number of fruits per plant (180.33), canopy temperature depression (3.34°C) membrane stability index (65.99%), pollen viability (92.10%), photosynthetic rate (20.73 µmol CO_2 m²/sec.) guaiacol peroxidase (564.99 U/gm F.W) and catalase (711.90 U/gm F.W) compared to DChBL-240. A wide range of variation was observed in the F_2 population for all the studied traits in high temperature conditions indicating the quantitative nature of heat tolerance. In genotyping of F_2 through genotyping by sequencing (GBS) using Illumina Hiseq platform 67.21 Gb raw sequencing data was generated and aligned against reference genome (*Capsicum annnum*). Variant calling with UGBS- GATK pipeline resulted in identification of 5806 polymorphic SNP markers. These markers were grouped into 12 linkage groups. QTL analysis with composite interval mapping revealed a total of 145 QTLs for 24 different traits. Finally, 21 QTLs having more than 10% PVE (Phenotypic Variance Explained) were identified for 9 morphological, 3 physiological and 2 biochemical traits and were considered as major QTLs. Within the 64 QTLs 23,990 candidate genes were identified, of which 20,770 genes have been annotated to different databases. Among the annotated genes under heat stress, the majority belong to the bhLH transcription factor family (9.04%). In addition, a total of 4,18,491 SSR loci were identified within 64 QTLs. Investigation of relative expression pattern of different *Capsicum annuum* specific heat shock protein genes (HSP genes) revealed upregulation of two genes, namely, CaHSP2271 (26.8-fold) and CaHSP3 (5-fold) in DLS-161-1 under high temperature conditions (44°C) which suggests that these two HSP genes might have contributed to the greater ability of DLS161-1 to tolerate heat stress compared to the susceptible parent (DChBL-240).

Understanding the physio-biochemical and molecular basis for high-temperature tolerance in cucumber

A set of 123 cucumber germplasm was evaluated in a growth chamber (40°C/35°C) for two subsequent seasons in the seedling stage. Based on their response in the seedling stage, 5 highly tolerant and 5 highly susceptible were selected for screening and field evaluation. Experiment conducted under two different temperature stress (35/30°C and 40/35°C) for important physiological and biochemical traits revealed that tolerant genotypes were able to maintain high chlorophyll retention, stable membrane stability index, higher retention of water content, stability in net photosynthesis, high stomatal conductance and transpiration in combination with less canopy temperatures under high temperature stress. Accumulation of biochemicals like proline, protein and antioxidants like SOD, catalase and peroxidase was the underlying biochemical mechanisms for high temperature tolerance. Besides, expression of the important heat shock proteins (HSPs), aquaporins (AQPs), photosynthesis related genes were conducted in two selected contrasting genotypes (WBC-13, Tolerant: DGPC-59, Susceptible) at different stress conditions. Upregulation of photosynthesis related genes, signal transduction genes and heat responsive genes (HSPs) in tolerant genotype indicate the molecular network associated with heat tolerance in cucumber. Among the HSPs, higher accumulation of HSP70 and HSP90 were recorded in the tolerant genotype, WBC-13 under heat stress condition indicating their critical role. Besides, Rubisco S, Rubisco L and CsTIP1b were upregulated in the tolerant genotypes under heat stress condition. Therefore, the HSPs in combination with photosynthetic and aquaporin genes were associated with heat stress tolerance. In GWAS analysis significant QTLs for chlorophyll, membrane stability index, dry weight and canopy temperature were identified for heat stress conditions. The annotation of candidate genes indicated that most of these QTLs are linked with important functional genes, which control solute transport through the cell membrane and other plant biochemical activities related to heat stress tolerance in cucumber.

Biochemical and molecular studies of curding and flowering behaviour in cauliflower

Based on its temperature requirement for curd initiation cauliflower is classified as Early (20-27 °C), Mid-early (16-20 °C), Mid-late (12-16 °C), and Late (10-16 °C). Curding and flowering in cauliflower are under the regulation of complex pathways governed by various internal (age, hormone, autonomous) and environmental (temperature) factors and interactions governing them. Therefore, the present investigation was carried out with twelve varieties/genotypes (three from each maturity group) sown five times at monthly intervals starting from 30th July to 30th November 2022 and observed for eight morphological traits and seven developmental transitions. The decrease in temperature caused a reduction in the morphological traits and duration of developmental transitions, which further increased with the rise in temperature. Analysis of endogenous gibberellins was performed in one variety of each group at six developmental transitions starting from seedling to bolting stages, and in the second experiment at 20-day intervals starting from 65 days after sowing (DAS) to 125 DAS. Higher GA content was observed at bolting, seedling and curd initiation stages, suggesting its connection with curd induction and stalk elongation. GA content at the full curd stage was higher in curd tissues than leaf tissues, while at the bolting stage, it was similar in leaf and stalk tissues. Expression analysis of fourteen curding and flowering-related genes was performed in four varieties as of gibberellin analysis at four-time intervals from 65 DAS to 125 DAS. Expression of BoVRN2, BoFUL-d, BoREM1, BoFT, BoCAL, CCE1, BoTFL1 and BoLFY genes showed significant differences between Indian and snowball (European) cauliflower varieties. The information generated through the present investigation will help in understanding the role of investigated determinants of curding and flowering in cauliflower to widen its growing plasticity.

Theme 4: Standardization of Production System

Evaluation of chilli genotypes for yield and quality parameters under net and open field condition

Thirty chilli genotypes were compared under netted and open field conditions and it was found that qualitative traits like plant habit, anthocyanin coloration and leaf and fruit color intensity showed variations under netted conditions while other showed consistency. Quantitative parameters, including plant height, plant spread, length of the main stem and total fresh fruit yield per plant, displayed significant differences between the two conditions. Netted cultivation increased values for plant height, plant spread and total fruit yield, whereas traits like days to flowering, fruit length, fruit diameter, and average fruit weight remained relatively stable. Under netting fruit quality parameters, revealing notable increases in capsaicin and capsanthin content, as well as vitamin C content. In terms of growth-related parameters, several traits such as leaf mass per plant, leaf number per plant, NDVI scores, root mass per plant, root volume and flower diameter exhibited substantial improvements under net conditions. Conversely, leaf surface area, length, and width of leaf blade, as well as root surface area, remained largely unchanged. Physiological parameters, including photosynthetic rate and total chlorophyll content, showed significant increases and stomatal conductance and transpiration rate, on the other hand, decreased under net conditions. These findings highlight the potential benefits of netted cultivation in enhancing yield, fruit quality and various growth-related and physiological traits in chili production. The study emphasizes the importance of considering protected cultivation as a viable option to optimize chilli farming, offering valuable insights for both small and marginal farmers in India. High potential performers under net conditions included DChBL-42, DChV-

274, DChBL-233, PC 2062, and DChBL-72(A), while DChBL42, DChBL-72(A), DChBL-72(B), DLS-20-11, and DLS-161-1 excelled in the open field.

Evaluation of lettuce (*Lactuca sativa* L.) genotypes for various agro-morphological, yield and biochemical traits under different production conditions

Sixteen lettuce (*Lactuca sativa* L.) genotypes were evaluated for various agromorphological, yield and biochemical traits under different production conditions. The application of 100 ppm GA_3 enhanced seed germination (67.21% and 88.63%), seedling length (6.68 cm and 7.61 cm), seed vigour index (463.39% and 693.76%), shoot length (3.80cm and 5.22 cm) and root length (3.36 cm and 2.24 cm) after 5 and 10 days of seed germination respectively. V9 (Lollo Rossa) showed highest seed germination, seed vigour index, seedling length, shoot length and root length. Agro-morphological and yield traits like plant height, plant canopy spread, number of leaves, leaf length, leaf width, fresh plant biomass and yield/m² was highest in soil under protected condition. Whereas root length and root weight were highest in soilless medium under protected condition. Biochemical traits like total soluble solids, respiration rate and chlorophyll content were found to be highest in soil under open condition. Whereas, antioxidant activity, moisture content, total carotenoid content and ascorbic acid content were highest in lettuce grown in soil under protected condition. Among varieties, V9 (Lollo Rossa) had highest total soluble solids and ascorbic acid content and V11 (Red Salad) had more respiration rate and total carotenoid content in leafy types. Among head types, V16 (Great Lakes) had highest total soluble solids, chlorophyll content and total carotenoid content, V15 (Butterhead Green) had highest antioxidant activity and ascorbic acid content. With respect to economics, cost of cultivation under open condition was 150 Rs/m² and 275 Rs/m² under protected for all the varieties. The Gross Income, Net Returns and Benefit Cost Ratio was highest in V9 (Lollo Rossa) and lowest in V12 (Red Rose) in leafy types. Among head types, highest and lowest Gross Income, Net Returns and Benefit Cost Ratio was observed in V16 (Great Lakes) had and V15 (Butterhead Green)

Optimization of time of planting and plant geometry for quality seed production of broccoli (*Brassica oleracea var. italica* Plenck) cv. Pusa Purple Broccoli-1

The experiment was conducted in broccoli variety Pusa Purple Broccoli-1 in Split Plot Design (SPD) with three different dates of transplanting and plant geometry viz. T1 (10th October), T2 (10th November), T3 (10th December) and 45×30 cm, 45×45 cm, 60×30 cm, 60×45 cm. The earliest head initiation, marketable head maturity, number of flower stalks and maximum height of flower stalk were recorded ideal in T1 (10th October) transplanting and 60×45 cm (S4) spacing. The seed yield-related parameters like the number of siliqua per plant, average length of siliqua, number of seed set per siliqua, seed yield per plant, seed yield per plot, seed yield per hectare resulted highest in 10th October (T1) transplanting with 60×45 cm (S4) planting geometry. The seed quality attributes are test weight of seed, seedling shoot length, root length, total seedlings length, vigour index I, vigour index II was exhibited highest in 10th October (T1) transplanting with 60×45 cm (S4) planting geometry and the minimum was observed in 10th December (T3) transplanting with 60×45 cm (S4) planting geometry. While the lowest value of electrical conductivity was recorded from 10th October (T1) transplanting and 60×45 cm (S4) planting geometry. The interaction between the date of transplanting and planting geometry were significant for majority of characters except head maturity, per seed set in bagging, per cent seed set by hand pollination, average number of seed per siliqua, shoot and root length of seedling, total seedlings length, seedlings dry weight and electrical conductivity. Thus, based upon experimental findings it is concluded that the seed crop broccoli cultivar Pusa Purple Broccoli-1 should be transplanted on 10th October with the spacing 60×45 cm obtained higher seed yield of 323.63 kg/ha and B:C cost ratio of 22.4:1 with better seed quality traits and biochemical compounds of head.

List of contributing students and Chairperson of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc/ Ph.D	Title of the Thesis	Chairperson	Institute
1.	Swagata Nandi (21718)	M.Sc.	Studies on physio-biochemical response and expression analysis of selected genes under drought stress condition in cucumber (*Cucumis sativus* L.)	Dr. Shyam Sundar Dey	ICAR-IARI, New Delhi
2.	Ankita Saha (21719)	M.Sc.	Genotypic and photo-temporal response of vegetable-based microgreens on its nutritional and biochemical properties	Dr. J.K. Ranjan	ICAR-IARI, New Delhi
3.	Luhana Sohamkumar Chetandas (21720)	M.Sc.	Biochemical and molecular studies of curding and flowering behaviour in cauliflower	Dr. Shrawan Singh	ICAR-IARI, New Delhi
4.	Dharmendra Kumar Verma (21722)	M.Sc.	Evaluation of chilli genotypes for yield and quality parameters under net and open field condition	Dr. Arpita Srivastava	ICAR-IARI, New Delhi
5.	Kishor Varotariya (21723)	M.Sc.	Optimization of time of planting and plant geometry for quality seed production of broccoli (*Brassica oleracea* var. *italica* Plenck) cv. Pusa Purple Broccoli-1	Dr. B. S. Tomar	ICAR-IARI, New Delhi
6.	Dharavath Ram Babu (21724)	M.Sc.	Gamma amino butyric acid profiling (GABA) and standardization of *in-vitro* regeneration protocol in tomato (*Solanum lycopersicum* L.) genotypes	Dr. Zakir Hussain	ICAR-IARI, New Delhi
7.	Thushal. R. Y. (21725)	M.Sc.	Evaluation of lettuce (*Lactuca sativa* L.) genotypes for various agro-morphological, yield and biochemical traits under different production conditions	Dr. Awani Kumar Singh	ICAR-IARI, New Delhi
8.	Sparsh Nathoo (21736)	M.Sc.	Morphological, biochemical and molecular characterization of okra genotypes for yield and quality traits	Dr. R. K Yadav	ICAR-IARI, New Delhi
9.	Barnali Majumder (50083)	M.Sc.	GABA (γ Amino butyric Acid) profiling and optimization of *in vitro* regeneration protocol in tomato (*Solanum lycopersicum* L.) genotypes suitable for protected environment	Dr. P. K Singh	#ICAR-IARI, Assam
10.	Nabanita Roy (50084)	M.Sc.	Diversity analysis and nutritional profiling of garden pea (*Pisum sativum* var. *hortense* L.)	Dr. Brij Bihari Sharma	#ICAR-IARI, Assam
11.	Wahengbam Zenith Singh (50085)	M.Sc.	Pathogen identification and management of emerging foliar diseases of *kharif* onion	Dr. Sabina Islam	#ICAR-IARI, Assam
12.	Ankit Kumar Sinha (60119)	M.Sc.	Genotypic divesrsity studies in pointed gourd (*Trichosanthes dioica* Roxb) for yield and quality attributes	Dr. A.K.Singh	#ICAR-IARI, Jharkhand
13.	B. R. Vasavi Devi (60120)	M.Sc.	Genetic diversity and heterosis studies in okra [*Abelmoschus esculentus* L. (Moench)] for yield and quality attributes under Eastern Plateau region of India	Dr. Krishna Prakash	#ICAR-IARI, Jharkhand

14.	Devireddy Meghana (60121)	M.Sc.	Study on morphological, biochemical and molecular diversity in vegetable soybean [*Glycine max* (L.) Merrill]	Dr. Rabi Sankar Pan	#ICAR-IARI, Jharkhand
15.	Arvind Nagar (10626)	Ph.D.	Phylogenetic studies in Indian luffa species	Dr. A. D. Munshi	ICAR-IARI, New Delhi
16.	Vishwanath Bidaramali (11354)	Ph.D.	Studies on inheritance for fruit yield related traits and molecular mapping of downy mildew resistance genes in cucumber (*Cucumis sativus* L.)	Dr. Amish K. Sureja	ICAR-IARI, New Delhi
17.	Dhananjay A Hongal (11619)	Ph.D.	Understanding the physio-biochemical and molecular basis for high-temperature tolerance in cucumber	Dr. Shyam Sundar Dey	ICAR-IARI, New Delhi
18.	Santhiya S (11620)	Ph.D.	Introgression of YVMV and ELCV resistance from wild *Abelmoschus* species in okra (*Abelmoschus esculentus* L.)	Dr. R. K Yadav	ICAR-IARI, New Delhi
19.	Aruna T (11622)	Ph.D.	Mapping of QTLs for heat tolerance in hot pepper (*Capsicum annuum* L.)	Dr. Manisha Mangal	ICAR-IARI, New Delhi
20.	Janani R (11624)	Ph.D.	Physiological and molecular characterization for high temperature tolerance in garden pea	Dr. B. B Sharma	ICAR-IARI, New Delhi
21.	Chauhan Shohaib Sheikh Ayub (11626)	Ph.D.	Molecular mapping of watermelon bud necrosis orthotospovirus resistance gene(s) and evaluation of fruit quality traits in watermelon [*Citrullus lanatus* (Thunb.) Matsum & Nakai]	Dr. Harshwardhan Choudhary	ICAR-IARI, New Delhi
22.	Bichhinna Maitri Rout (11628)	Ph.D.	Genetic and biochemical analyses of resistance to Squash Leaf Curl China Virus in pumpkin (*Cucurbita moschata* Duchesne ex Poir.)	Dr. Amish K. Sureja	ICAR-IARI, New Delhi
23.	Rahul Chandel (11633)	Ph.D.	Morpho-genetic diversity in onion, *Stemphylium vesicarium* and Screening onions against Stemphylium leaf blight	Dr. Anil Khar	ICAR-IARI, New Delhi
24.	S. Bhargav Kiran (11884)	Ph.D.	Studies on inter-specific hybridization in *Abelmoschus* species	Dr. R.K. Yadav	ICAR-IARI, New Delhi
25.	Sourav Mohapatra (11132)	Ph. D.	Studies on genetics of resistance to gummy stem blight in watermelon [*Citrullus lanatus* (Thunb.) Matsum. & Nakai]	Dr. E.S.Rao	**ICAR-IIHR, Bengaluru
26.	B. Vanlalneihi (10900)	Ph. D.	Mapping of anthracnose (*Colletotrichum* spp.) fruit rot resistance genes in *Capsicum* spp.	Dr. K. Madhavi Reddy	**ICAR-IIHR, Bengaluru
27.	Lavanya (11631)	Ph. D.	Genetic analysis of yield, yield parameters and downy mildew resistance in ridge gourd [*Luffa acutangula* (Roxb.) L.]	Dr. B. Varalakshmi	**ICAR-IIHR, Bengaluru
28.	Yathish (11623)	Ph. D.	Validation and fine mapping of quantitative trait loci for watermelon bud necrosis orthotospo virus resistance in watermelon	Dr. M. Pitchaimuthu	**ICAR-IIHR, Bengaluru

#IARI off campus

**Outreach Institute

Session VI: School of Social Sciences

Thesis Summary

Discipline	**Number of Thesis Submitted**	
	M.Sc.	**Ph.D.**
Agricultural Economics	07	09
Agricultural Extension	06	14
Agricultural Statistics	08	07
Bioinformatics	06	08
Computer Application	05	03
Total	**32**	**41**

SCHOOL OF SOCIAL SCIENCES

Convenor: Dr. Monika A. Joshi, Professor, Division of Seed Science & Technology
Co-convenor: Dr. Shruti Sethi, Principal Scientist, Division of Food Science & Post harvest Technology

Chairperson: Dr. V.V. Sadamate, Former Adviser Agri., Planning Commission

Dr. V. V. Sadamate graduated from Pune Agriculture College (1973) and did his Masters & Ph.D in Agricultural Extension from ICAR-IARI, New Delhi in 1975 and 1979, respectively. Dr. Sadamate did his Post Doc from Michigan State University, US as Fulbright Senior Research Scholar and availed Advanced Agriculture Extension and Management training at Wisconsin, Cornell & Royal Institute of Public Administration (RIPA) London, UK. He worked with ICAR as Junior Scientist (1978-1982) and with the Ministry of Agriculture (1982-2005) as Director and then Additional Commissioner (Extn). He joined the Planning Commission as Advisor Agriculture (2006-2013) and handled formulation /implementation of XIth & XIIth Plan for Agriculture & Allied Sectors. He has published 50 research papers, 50 technical papers and over 100 Agriculture Planning Reports. He has contributed significantly in developing/operating extension innovations and reforms. Dr. Sadamate superannuated from Ministry of Agriculture in May, 2013. Subsequently, he worked as Principal Consultant, FAO, New Delhi (2013) and with the Ministry of Rural Development as Agricultural Convergence Expert, Watershed Management World Bank Project (2014-16), as Member Doubling Farmer Income Exercise (Extension Sub-Group 2018-19), GOI. He is associated with IARI as an Adjunct faculty (2014 onwards). Presently, Dr. Sadamate is working as Independent Agriculture Extension Specialist: Consultancies, Policy Advocacy, Extension Reforms & Innovations; is Vice President INSEE, Nagpur, Life Member, ISEE, New Delhi, TAAS, New Delhi, and CHAI, New Delhi; Senior Member, National Council for Climate Change, Ahmedabad and Chair/member of various RACs/Academic Councils/BOM of several institutes.

Agricultural Economics

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Prof. Alka Singh

The Division of Agricultural Economics, a constituent of the School of Social Sciences of Indian Council of Agricultural Research-Indian Agricultural Research Institute, was established in 1960. The mandate of the Division is to conduct research in frontier areas and serve as a center for academic excellence in post-graduate education. Since its inception, the Division has been making contributions in basic and applied research with significant implications for agricultural policy. The research contributions of the Division have been globally recognized and many of the alumni occupy positions of repute in national and international organizations. The research focus of the Division has been continuously reoriented to address contemporary development challenges. The early research of the Division focused on farm business analysis, efficient allocation of resources, supply response, input demand analysis, and marketing efficiency. To address the challenges and opportunities of the Green Revolution, research on capital formation, labor employment, farm mechanization, rural credit needs, yield gap analysis, price policy and subsidy issues, and efficient management of natural resources was undertaken. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Technology, Resource and Environment

Economic assessment of human-wildlife conflicts in agriculture

Human-wildlife conflicts (HWC) are defined as any interaction between wildlife and humans that causes harm to humans, wild animals, or property. This study attempts to explore the farmer's perception about wildlife damage in agriculture, various management strategies adopted by farmers, the pattern, determinants and extent of economic losses in agriculture and examines the farmer's WTP to prevent HWC while also analysing the existing compensation schemes for wildlife damage. The study is based on primary data collected from 426 farmers residing in villages surrounding the Eco sensitive Zone (ESZ) of Bannerughatta National Park (BNP), Karnataka. The study also made use of data on number of HWC cases and compensation paid, cropping intensity and area under mulberry cultivation which was collected from published sources. The study used descriptive statistics and Poisson regression to analyze the determinants of HWC, the contingent valuation method was followed to estimate willingness to pay, and the agricultural damage function of the ragi crop was analyzed using beta regression. Elephants and wild boars were reported to be major depredators causing significant crop losses. Amount of crop loss varies from 9.28% in mulberry to 50.13% in case of paddy and, while the loss is 29.50 % in case of ragi which is the major crop. There is a lack of scientific mechanism in fixing compensation for each crop, and it takes a minimum of 6 months to 18 months to receive the compensation. Farmers are willing to pay an extra premium of 1.30 % towards PMFBY if crop loss due to HWC is covered under the scheme. So, the study suggests the inclusion of crop loss due to HWC under PMFBY and faster implementation of the scheme in all the states with significant HWC cases to reduce the losses.

Climate change vulnerability and risk management in agriculture of Maharashtra

The crop production in Maharashtra remains highly vulnerable due to climate-related stressors such as drought, floods, and monsoon variability. This study analyses the level of agricultural vulnerability at the district level and the impact of climatic and non-climatic variables on the production of major crops. The vulnerability of farm households to different production risks and the impact of risk management strategy on farm income and risk exposure were also examined using NSS 77th round data. The study developed the Composite Agricultural Vulnerability Index (CAVI) using seven indicators that show regional disparity. Marathwada and Western Vidarbha region were more vulnerable, while Konkan, Western Maharashtra, and Eastern Vidarbha were comparatively less vulnerable. The Konkan region shows a lower potential crop loss and Western Maharashtra has better adaptive capacity to cope with climate change. There is an increasing trend of maximum and minimum temperatures in all the regions. Except for sugarcane, all the crops (rice, sorghum, pigeon pea, gram and cotton) had shown a significant negative effect of an increase in temperature (net of maximum and minimum temperature) on crop yield. Whereas rainfall had a significant effect on only rice, sorghum, sugarcane, and gram crops. However, the rainfall effect was not sufficient to compensate for the negative effect of the increase in temperature. The farm households were more exposed to the drought risk (42 %), followed by insect pests (11 %). Among all production risks, flood resulted in the highest per-hectare loss of output, followed by drought and insect pests. Access to information determines the adoption of a risk management strategy. The expenditure on different farm inputs positively influences the gross value of output per hectare. Furthermore, the endogenous switching regression results suggested that adopting horticultural crops as a risk management strategy has significantly improved farm income for adopters and reduces the risk of crop failure.

Conjunctive use of farm pond and groundwater and its implications on farm economy in semi-arid region of Karnataka

The success of crop production is intricately tied to the efficient conservation of soil moisture in situ and ex-situ, along with the harvesting, storage, and reuse of surplus runoff water for supplemental irrigation and groundwater recharge. The study employs both primary and secondary data to assess the adoption and discontinuance of Farm Ponds (FPs) in four dry zones of Karnataka, to evaluate irrigation growth sources, groundwater trends, and construct a groundwater vulnerability index and identify factors influencing FP adoption and reasons for discontinuance. In the Central, Southern, and Eastern dry zones, wells exhibit a positive trend, signaling a decline in groundwater tables across seasons. Chikkaballapur is identified as hydrologically and socio-economically vulnerable, while Koppal is highly susceptible to droughts. Farmers generally have positive perceptions of FPs, but obstacles like high initial investments, accidents, and land wastage impede adoption. The Endogenous Switching Regression Models reveals that the additional irrigation through rainwater harvested in FPs positively impacts red gram and ragi yields. Partial budgeting analysis demonstrates the financial feasibility of FPs with a 90 percent subsidy, and social cost-benefit analysis indicates a B:C ratio of 1.23% at a 5% discount rate. Respondents express positive preferences for provisioning and regulating services of FPs, and Discrete choice experiments to estimate willingness to pay (WTP) through a random parameters logit model report impressive WTP values for increased yields, groundwater recharge, and drought mitigation services. Preventative measures are vital in Hilly, Coastal, and Transitional zones with high groundwater extraction rates. Rainwater harvesting structures are key in districts like Kolar and Chikkaballapur to complement groundwater irrigation. A holistic GIS approach is recommended for Farm Pond (FP) construction. Policies should prioritize successful watershed and FP adopters, emphasizing behavioural shifts and increasing social capital for success of FPs.

An economic analysis of food systems and food security in Sierra Leone

Despite many efforts to address hunger and malnutrition, many developing nations, including Sierra Leone, are still grappling with food insecurity and low nutrition among low-income households. This study delves into food security, malnutrition, and food systems in Sierra Leone. The study uses secondary data such as CFSVA (2020), SLDHS (2019) and FAOSTAT (2000-2020). Various statistical methods, including diversity indices, CARI console and regression models, are used to understand food systems' complexity and impact on nutrition and food security. The study also conducts a systematic literature review on various policies related to food security by India to device suitable policies for Sierra Leone. The crop production trends indicate an upward trend in cereals, roots, tubers, and vegetables; fruit and sugar production remain stable, while oil crops and pulses give low output. Regarding diversity, the North West region had the highest average crop Simpson index of diversity at 20.50 and an average production diversity score of 3.6, indicating a diverse range of crops and livestock were being cultivated in that region. Overall, the entire dataset had a mean PDS of 3.03, indicating a moderate level of production diversity across all the surveyed areas. The beta regression shows that crop diversity is positively influenced by irrigation, household income, access to credit, and storage availability. Regarding dietary diversity, cereals and protein sources are the most commonly purchased items, accounting for 31.4% and 11.0% of food expenditure, respectively and roots and tubers make up 6.0%, which indicates major share of expenditure is for food. Regarding food security, the CARI Console model shows that 35.8% of households in Sierra Leone are food secure, while 62.2% are insecure. Two pivotal lessons emerge from India's food security policies and programs are the power of collaboration across sectors and precise targeting mechanisms that deliver subsidised food to the neediest households.

Estimating the economic and environmental benefits of direct seeded rice in Karnal district of Haryana

Direct-seeded rice (DSR) has been widely adopted in many South and East Asian countries owing to its water and labour-saving characteristics. The government of India and research communities are focussing on DSR as a potential technique to provide environmental benefits along with its economic advantage in terms of increased yield and reduced cost of cultivation. This study examined the potential benefits of DSR with plot-level data of rice growers of the Karnal district of Haryana. The share of DSR area to the total rice area of the district was highest in Sirsa (8.7%) district, followed by Fatehabad (3.14%) and Jind (2.87%). In Karnal, DSR contributed 2.09% to the total rice area, whereas the state share of DSR was a mere 1.93%. In DSR plots, the yield was estimated to be lesser by 4.28 quintals per ha. DSR plots used 50.47% fewer labor hours and 42.6% less irrigation water than Puddled Transplanted Rice (PTR). A saving on the cost of land preparation by 20%, sowing/transplanting by 75% and an increase in weed control expenses by 81% were estimated in the DSR plots, resulting in the cost of cultivation (Cost A2 + FL) saving by 13% compared to PTR farmers. A saving of 2638.39 kg CO_2 equivalent per hectare was observed in DSR plots compared to PTR plots. Issues like heavy weed infestation, unavailability of seed drills on time & and their limited use under heavy rainfall conditions during sowing, land leveling, etc., were the significant drivers compelling them to opt for PTR over DSR. Government schemes encouraged the adoption of DSR in Haryana to a greater extent. However, remunerating the farmers in congruence with their contribution to the ecosystem services regarding carbon-saving and water-saving can promote the adoption of DSR as an alternative to traditional rice at a broader scale.

Institutions and Technologies for Enhancing Efficiency and Equity of Groundwater Irrigation in India

To combat groundwater over-exploitation and reduce reliance on diesel and electricity, some demand management policies have been introduced including micro-irrigation technologies and solar-powered pumps. The present study attempted to examine groundwater irrigation development and assess the impact of agricultural electricity subsidies on groundwater use and agricultural production in India using secondary data. The impact of the informal groundwater market, micro-irrigation technologies and solar-powered pumps on the efficiency and equity of groundwater irrigation was assessed using primary data collected from the arid and sub-humid regions of Rajasthan. The phenomenal expansion in the net irrigated area under tubewells has augmented the total net irrigated area in the country over the years. In India, the number of groundwater extraction structures has increased, but their growth has slowed over time. Deep tubewells have shown the highest increment, which may be due to the relatively cheap availability of electric energy sources. Renewable sources like solar-operated pumps and micro-irrigation technologies have been growing. The agricultural electricity subsidies contributed to increasing the cropped area and production, but also contributed to the decline in the groundwater resources. Further, water sellers and water buyers were found to have benefitted by participating in the water markets. Participation in the groundwater market have a positive effect on the efficiencies of the irrigated farm. Farmers using micro-irrigation technologies and both electricity and solar energy sources were estimated to be having higher physical and economic groundwater irrigation productivity. Micro-irrigated farms also had the highest efficiency scores. Micro-irrigation might have led to a reduction in the groundwater use per acre, but the amount of groundwater use per farm have not fall concomitantly because of the higher irrigation intensity. The Jevons paradox for the micro-irrigation technologies was found to be present in the sub-humid region and on the farms cultivating high-value crops in the arid region.

Theme 2: Agricultural Markets and Value Chain

Impact of blending of edible vegetable oils on rapeseed and mustard crop in Bharatpur district of Rajasthan - An economic investigation

In 1990, the Indian Union Health Ministry permitted the mixing of edible vegetable oils to produce a better ratio of saturated to unsaturated fatty acids and to reduce the ill effect of erucic acid present in mustard. The decision had a big impact on the market for pure mustard oil. Because of the reduction in income, farmers became reluctant to grow the crop. Whereas the permission to blend has benefited a variety of oils, particularly refined oil and contributed to India's increased reliance on oil imports during the past 20 years. The Food Safety and Standards Authority of India (FSSAI) had decided to impose ban on blending of mustard oil from 8 march 2021. In this context, this study assesses the impact of blending on area, production and prices of rapeseed & mustard and the major factors affecting acreage response using Nerlovian lagged adjustment model. A qualitative assessment was done to study the impact of blending ban on processors using NVivo software. The growth rate of area, production and yield of Rapeseed & Mustard in India has significantly reduced after blending was allowed whereas the instability has reduced. The growth in production before blending was mainly due to an increase in acreage, whereas, after blending, it was yield driven. Before blending, the coefficients of farm harvest price and yield for Rapeseed & mustard were both highly significant and substantial in magnitude, while post-blending there was a decrease. After the ban on blending, the acreage, production and farm harvest prices have significantly increased as compared to the projections made without ban. The processing industry has faced an increase in costs and decrease in returns due to lack of remunerative prices after the blending ban. The major constraints faced by the processors are unhealthy blending practices and the wrong labeling of mustard oil.

Performance analysis of e-NAM and its impact on price realization in Rajasthan and Haryana

The central government launched e-NAM to ensure efficient price discovery. Utilising both primary as well as secondary data, present study explores the countrywide implementation status of e-NAM, trade concentration across states and crops, impact of e-NAM on price realization at the national level and identifies the determinants of e-NAM trade. The primary survey focused on Haryana and Rajasthan, which account for over 50% of the total e-NAM trade in the country in 2020-21 covering specific crops such as paddy and bajra. The sample consisted of 240 farmers, 32 traders, 40 commission agents, and mandi officials of the respective markets. The findings indicate a remarkable twenty-fold increase in e-NAM trade value over the five years from 2018-19 to 2022-23 at the national level. The HHI index reveals monopolies in dry fruits and spices, particularly in Odisha and Andhra Pradesh. In terms of the total trade value, Haryana (19.5%) has the highest share in 2022-23, followed by Punjab (18.1%), Rajasthan (17.5%), and Andhra Pradesh (14.7%). Notably, on a value basis, Haryana excels in the cereals trade, Punjab in the pulse trade, Rajasthan in the fruits and oilseeds trade, and Andhra Pradesh in the vegetable trade in the year 2022-23. The Wilcoxon price difference test unveils positive significant price differences in 15 cases, while 12 cases show negative significant differences, comparing e-NAM prices with AGMARKNET prices. The state level panel data analysis demonstrates that farmer participation and traders' concentration positively impact e-NAM trade performance at the state level. For paddy farmers, APMC prices surpass other marketing channels by Rs. 308/quintal. But for bajra, it was Rs. 62.5/quintal lower than other channels.

Competitiveness, concentration and capacity utilization of oilseeds processing industry

An efficient oilseed processing industry is a prerequisite for maximizing economic returns to the producer and ensuring a fair price for the consumer. There is a great deal of interdependence between oilseed production and the oilseed processing industry, and they complement each other in meeting people's demands. The performance of the Indian oilseed processing industry can be improved through efficient operation of the enterprises with minimum wastage of key resources and full utilization of available capacity. In this backdrop, this study assesses the trade competitiveness of the edible oil complex, examines the changes in the distribution and concentration of the oilseeds processing industry over time and space, and crushing capacity utilisation and its determinants in the oilseeds processing industry. The nominal protection coefficient (NPC) is employed to calculate the trade competitiveness, revealing a competitive disadvantage for oilseeds and edible oil in the international market, while most oilcakes exhibit a competitive advantage, except for soybean-derived oilcakes. The tabular analysis is employed to categorize oilseed processing industries based on size, products, turnover, regional distribution, and commodity-specific distribution. The Herfindahl-Hirschman Index (HHI) measures industry concentration, illustrating a decrease over time, indicative of more evenly distributed market power among competitors. Frontier production function analysis, two-stage estimation, uncovers that nearly 78% of oilseeds are used for crushing, yielding 34% edible oil and 66% oil cake. Industry growth, though stagnant in terms of units, exhibits increased production value due to rising demand. Privately owned enterprises dominate, predominantly in urban regions, with Vegetable oil and fat (VOM) manufacturers leading in both unit number and processed output value. Andhra Pradesh, Gujarat, and Maharashtra emerge as key states for industry establishments. Capacity utilization hovers at 34%, highlighting the need to address obstacles hindering sector growth, including internal inefficiencies and raw material cost escalation. The industry's existing technical efficiency stands at 53%.

A multi-stakeholders analysis of e-marketing of agricultural commodities

The e-marketing aims at creating competitive prices and market information dissemination by bringing transparency in the system. The study assesses the present status of e-marketing (ReMS and e-NAM) implementation in the country based on data collected from multiple sources. The primary data for the study was collected through personnel interviews with 240 farmers and 60 intermediaries from two different regions; Karnool in Andhra Pradesh (AP) and Chitradurga in Karnataka. Statistical tools such as tabular analysis, difference-in-difference, coarsened exact matching, logit regression, and the Garrett ranking method were employed for data analysis. The impact analysis using DID shows that groundnut prices increased by 4.7 and 9.7 % in AP and Karnataka due to e-marketing, respectively. The factors such as land holding, access to extension services, and farm experience positive, whereas the age of the farmer and distance to the market negatively determine farmers' participation in e-marketing. Farmers' major sources of market information were newspapers and television. The major constraints faced by farmers are the dissemination of market information and robust physical infrastructure in the market. The major constraints faced by the traders and commission agents include the challenges in strategic procurement in quality and quantity of desired commodities and the adoption of electronic processes of bidding and online money transfers. Farmers believe that e-marketing has led to increased transparency in the system and heightened competition among traders and commission agents. There is a need to create awareness among all stakeholders, including farmers, commission agents, and traders, about the direct payment mechanism to the bank account through online transfer. This can facilitate seamless and secure payment processes and ensures that farmers receive their dues promptly. In general, e-marketing has a positive impact on farmers' income. However, there is scope for further improvement to enhance the efficiency of the marketing process.

A multi-market and multi-regional analysis of important cereals in India: A partial equilibrium approach

The current study uses the cereal outlook model to generate market projections for the rice, wheat, and maize crops up to 2040–2041, to find if the supply can meet the demand, and if India can remain as a food surplus country under the dynamic socio-economic, physical, technological, and institutional frameworks. The study examined historical data (from 1980–1981 to 2017–18) using the multi-commodity, multi-market, partial equilibrium analysis to generate the outlook, and conducted two simulations to comprehend the impact of growth on cost of cultivation, and MSP on the area, production, consumption, trade, and stocks of commodities. The study also addressed the important policies that have an impact on the trade of grains. To create market forecasts, the study modelled the area and yield equation at the regional level. The market outlook on rice, wheat and maize crops indicates a surplus production and growing demand for these commodities in future. It was predicted that the total consumption demand of rice would reach about 117.59 million tons(mt) while its aggregate production to grow from 106.22 mt during 2017-18 to 139.54 mt by 2040-41. Similarly, the aggregate demand for wheat is predicted to grow by 42.12 mt while the production to reach 115 mt, whereas the aggregate demand of maize was predicted to increase by 33.06 % over the base year and the supply is predicted to increase by 33%. Additionally, the model emphasizes productivity gain as a primary source of future output growth. The study suggests for cereal plus farming system, enterprise and varietal diversification to ensure nutritional security, rationalization of excess cultivation area under cereals, strengthening and development of long-term agricultural infrastructure, promotion of secondary agriculture and strengthening of food value chains and attaining allocative efficiency in food distribution and rightful targeting of food beneficiaries.

Impact of India and European Union FTA on Indian agriculture

Free-trade agreements (FTAs) are legally binding agreements between governments to create a tariff-free trade zone. A nation gets benefited from FTAs when trade creation exceeds trade diversion. In this context, this study examines the impact of India and European Union FTA on Indian agriculture, estimates trade intensity and competitiveness of agricultural commodities, identify agricultural trade potential, and analyze the effects of tariff liberalization on trade creation and diversion. Export, and import intensity index and Symmetric Revealed Comparative Advantage were used to assess Indian agricultural goods' competitiveness with the EU using secondary data. The study used Gravity model to identify trade determinants and potential, and the World Bank's SMART model to analyze agricultural trade between India and the EU ex ante. Netherlands, Italy, and Germany were India's top EU agricultural trading partners due to their strategic port positions and well-developed market infrastructure for Intra EU trade. Indian exports to the EU were mostly fish, coffee, tea, meat, spices, and cotton. India imported EU vegetable oil, raw hides, skin, leather, and animal fodder. Reducing EU agricultural tariffs in India will enhance EU-India agricultural trade by US$ 1541.2 million. Trade creation, which accounts for 85% of the trade effect, is expected to outweigh trade diversion, hence will largely benefit India's agriculture and associated sectors. Gravity model projections were less than unity, indicative of the agricultural commodity trading potential between India and the EU. India must increase indigenous producer competitiveness. Policies that promote limited liberalisation with sensitive lists of agro-commodities, strengthen agro-market infrastructure, and provide financial access and technical support to agricultural stakeholders can boost productivity, efficiency, and profitability, helping Indian producers compete with imports. India can plan and decide intelligently to preserve domestic producers and consumers by analyzing trade creation and diversion consequences. The India-EU FTA is a win-win for agricultural trade.

Theme 3: Institutional Innovations and Rural Livelihood

Economic evaluation of seed production of field crops in north India: Institutions, technology and markets

Seed security can be stated as a precondition to achieve food security. This study was proposed to understand the seed production process and its impact on farm economy, and to explore the different models of contractual seed production. Over time, there has been a notable increase in the availability of cereals and pulses seeds, while the availability of quality oilseed seeds has declined. This shift has been accompanied by a decrease in the public sector's contribution to quality seed availability for cereals and oilseeds, excluding pulses. Farmers predominantly rely on local markets or their own farm-produced seeds to meet the seed requirement. Seed production often incurs higher cultivation costs, but, realise significantly higher gross and net incomes per acre due to the premium prices commanded by quality seeds. There is scope to improve the technical efficiency of both seed and grain production. However, seed production found to be relatively profitable and technically efficient. Among different seed production models, the IARI-SPU channel was found to be the most efficient in terms of market efficiency. There are disparities between seed and grain producers in technology adoption. Seed producers are high adopters while, grain producers are partial or low adopters of different technologies and practices. The multinomial logistic regression analysis underscored the size of land holding and training received influence farmers' participation in seed production models. IARI-SPU farmers perceive higher price realization, recognition, networking, and technical support as positive aspects of the model but faced challenges related to late payments and contract conditions. Seed licensing firm participants found assurance in contracts but experienced issues with contract compliance and output rejection. FPO-engaged farmers appreciated payment reliability and market access but encountered challenges related to technical guidance, payment delays, and input costs. NSC-affiliated seed growers benefited from higher prices and market assurance but faced late payments and transportation cost hurdles.

Study of determinants of performance of farmer producer organization in India

FPOs are gaining attention for elevating farmers' incomes. In 2019, India's government introduced a scheme aiming to establish 10,000 FPOs. However, research on FPO performance determinants mainly employs quantitative methods, offering limited insights. This study emphasizes the need for qualitative research to understand FPO dynamics better. It gives the status of FPOs using NABARD, SFAC, and MCA databases up to April 2023. Maharashtra leads with 35% FPOs, followed by Uttar Pradesh at 15%. About 92% of FPOs are active, but 3.2% are inactive, with respect to meeting the compliance posed for an FPC. Through a systematic review, performance determinants of FPO were identified and validated through convergent interviews with successfully performing FPOs. In order to select the successful performing FPO, a focus group discussion was conducted. Year on year revenue growth rate of more than 25%, Profit growth rate of 20- 30%, increase in the number of products dealt, growth of active farmer members over total farmer members and increase in input procurement were identified as key criteria for an FPO to be called as good performer. Based on this, five successful FPOs were selected through snowball sampling with a sample size of 5 participants each (3 farmer members, 1 BoD member, and 1 CEO), making the total sample size 25. Telephonic interviews were transcribed and content analysis was done using NVivo, reveals the vital role of transparent communication in addressing farmers' growth-based needs including efficient input access and market reach services provided to the farmer members for the success of FPOs. In conclusion, policy recommendations stemming from this study centre on fostering transparent communication, addressing members' needs, and capitalizing on technology-driven platforms. By nurturing these elements, policymakers can empower FPOs to play an even more transformative role in India's agriculture landscape, driving economic empowerment and progress among farmer constituents.

A study of determinants of performance of agribusiness start-ups in India

India emerged as the fastest-growing economy with the third-largest startup ecosystem in the world and at the same time, a strong stream of research is required for policy advocacy to increase the success rate of startups. It becomes essential to identify the factors that are responsible for the performance of startups. In this context, the present study focused on assessing the landscape of the startup ecosystem of India with a focus on agribusiness, identifies performance determinants of start-ups and maps performance determinants of agribusiness start-ups. The secondary data was collected from start-ups in India to prepare a report on start-ups' growth trends in the agribusiness sector and overall sector from 2016 to 2023, as well as other relevant parameters. For funding and start-up growth rate, various reports were used. For a systematic literature review, PRISMA 2020 methodology was used, and for characterizing and mapping agri-start-ups' performance determinants, content analysis was done using Nvivo-14 software. As the results indicated, funding for agri-start-ups increased continuously even with external constraints in the ecosystem in the previous years. The major funding source for start-ups was venture capital funding. The determinants were classified into three categories of personal, organizational, and external factors, and the most important performance determinants were product market fit and effective business model. There is a need to inculcate innovation and entrepreneurial culture in HEIs to develop better technologies. Incubators shall be focused on providing mentoring support regarding making a good product market fit and building appealing business models. Various pre-incubation programs shall be organized to sensitize the youth to conduct environmental scanning before getting into product development. A bottom-up approach shall be introduced while assessing the needs of the market.

Changing rural employment pattern and its implications on farm economy

As farm labour constitutes a major share in cost of cultivation, changing wages and physical availability of labours have definite implications on farm economy. The present study analyses the changing structure of rural workforce, trends in agricultural wages and rate of substitution between agricultural labour and machinery. The worker-population ratio (WPR) and share of rural areas in total employment have declined over the years. Agriculture remains as the predominant employer in rural areas, despite rising employment diversification. Rural workforce is dominated by male workforce. During COVID induced lockdown period both male and female workers in agriculture increased significantly due to the large-scale reverse-migration of labours from urban to rural areas, hence agriculture provided cushion to the workers. Seasonality exists in all Indian states for male and female workers for agricultural activities, also there is wide inter-state variation in wages. The intervention analysis revealed that the lockdown did not have any significant impact on agricultural wages. Implementation of MGNREGS led to a significant increase in real wages and its impact increased over time. Labour demand found to be inelastic, hence any change in wages (rise or fall) have direct implications on labour cost, which explains the increase in labour cost despite the consistent decline in labour use. In recent years (2017-18 to 2021-22), the labour cost is declining on account of almost stagnant real wages. The share of labour in costA_1 declines, while the share of machine use increases in the recent years, which indicates the substitution between both. The elasticity of substitution between labour and machine was found to be inelastic for paddy cultivation. Further, it was found that labor and machine substitution is not only endogenously determined but influenced by some exogenous factors such promotion of farm machineries for realizing higher yield, improving efficiency and convenience to the farmers.

List of contributing students and Chairperson of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Shubho Paul (21568)	M.Sc.	Performance analysis of e-NAM and its impact on price realization in Rajasthan and Haryana	Dr. P. Venkatesh	ICAR-IARI, New Delhi
2.	Ankit (21569)	M.Sc.	Impact of blending of edible vegetable oils on rapeseed and mustard crop in Bharatpur district of Rajasthan-An economic investigation	Dr. P. Anbukkani	ICAR-IARI, New Delhi
3.	Pavan Kumar Kumawat (21570)	M.Sc.	A study of determinants of performance of agribusiness start-ups in India	Dr. Akriti Sharma	ICAR-IARI, New Delhi
4.	Sneha S B (21571)	M.Sc.	Changing rural employment pattern and its implications on farm economy	Dr. Shivendra Kumar Srivastava	ICAR-IARI, New Delhi
5.	Hitaishree M. (21572)	M.Sc.	Competitiveness, concentration and capacity utilization of oilseeds processing industry	Dr. Kingsly Immanuelraj	ICAR-IARI, New Delhi
6.	Swati Singh (21573)	M.Sc.	Study of determinants of performance of farmer producer organization in India	Dr. Akriti Sharma	ICAR-IARI, New Delhi
7.	Sudhan Bhusal (21731)	M.Sc.	Estimating the economic and environmental benefits of direct seeded rice in Karnal district of Haryana	Dr.Alka Singh	ICAR-IARI, New Delhi
8.	Jaiprakash Bisen (10562)	Ph.D.	A multi market, multi- regional analysis of important cereals in India: A partial equilibrium approach	Dr. Shiv Kumar	ICAR-IARI, New Delhi
9.	Ragavendra K.J. (10734)	Ph.D.	A multi-stakeholder analysis of e-marketing of agricultural commodities	Dr. Shiv Kumar	ICAR-IARI, New Delhi
10.	Sharath S Yeligar (10938)	Ph.D.	Impact of India and European Union FTA on Indian agriculture	Dr. Shiv Kumar	ICAR-IARI, New Delhi

11.	B. J. Giridhar (11163)	Ph.D.	Conjunctive use of farm pond and ground water and its implications on farm economy in semi-arid region of Karnataka	Dr. Dharam Raj Singh	ICAR-IARI, New Delhi
12.	Naveen Kumar Naik (11165)	Ph.D.	Economic assessment of human-wildlife conflicts in agriculture	Dr. P. Venkatesh	ICAR-IARI, New Delhi
13.	Nandini Saha (11380)	Ph.D.	Economic evaluation of seed production of field crops in north India: Institutions, technology and markets	Dr. Pramod Kumar	ICAR-IARI, New Delhi
14.	Athare Prakash Goraksha (11384)	Ph.D.	Climate change vulnerability and risk management in agriculture of Maharashtra	Dr. Dharam Raj Singh	ICAR-IARI, New Delhi
15.	Osman Nabay (11924)	Ph.D.	An economic analysis of food systems and food security in Sierra Leone	Dr. P. Venkatesh	ICAR-IARI, New Delhi
16	Priyanka Upreti (10731)	Ph.D.	Institutions and technologies for enhancing efficiency and equity of groundwater irrigation in India	Dr. Dharam Raj Singh	ICAR-IARI, New Delhi

Agricultural Extension

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Prof. Manjeet Singh Nain

The Division of Agricultural Extension has been playing a pioneering role in the growth and development of extension science with specific reference to research, education and training in extension education since inception in 1960. It has credit of developing effective paradigm and prototype for research, relevant curriculum and methods of teaching and training, models and framework for information and technology dissemination as well as service provision and generation of successful cases and methodologies of agricultural and rural transformation. For last sixty three years with its vision, action and notable attainments, it has been carrying out a flagship role for extension profession. Indian Council of Agricultural Research entrusted it with the coveted responsibility of serving as "Centre of Advanced Studies" since 1994; which was later rechristened as "Center of Advanced Faculty Training" in April, 2010; for playing a leadership role in undertaking capacity building of the extension professionals and development agents of different extension systems The mandates of the division are to carry out basic and strategic research In the area of extension education; to carry out post-institutes and other development departments; to Carry out training programme to impart knowledge; to render expertise support and advisory and consultancy services to extension activities of the institute. In addition the division is coordinating B.Sc. Community Science programme of the Institute. Significant research findings of the post graduate students are enlisted under the following themes:

Theme1: Assessment of Government Centric Programmes, Schemes and Practices

Access to extension and advisory service: Diversity and impact in India

Dispersed rural population, monitoring difficulties and lack of accountability limits the efficacy of traditional extension systems in India. A comprehensive study on access to EAS was carried out in India using the Situation Assessment Survey of NSSO (77th round), with a total sample of 45,698 agricultural households. For assessment of impact at the farm level, 2,853 farmers who cultivate cotton crops were chosen. The factors that determine the access to EAS and the sectoral heterogeneity were obtained using the binary logistic regression model. The impact of access to EAS at the farm level was estimated using the Inverse Probability Weighted Regression Adjustment (IPWRA) method. There were wide disparities in the access to EAS in India based on age, gender, caste, and operational holding. Access to EAS was more in developed states than in underdeveloped states.The significant determinants of access to EAS were age, gender, education, training, social category, household size, membership in farmer organizations, access to formal loans, non-farm income, irrigation, and operational landholding. Access to EAS had a significant positive impact on cotton productivity and the value of output. Source wise heterogeneity in impact was observed. The Study implies that efforts to increase access to EAS are needed as half of the farmers had not accessed any source. More gender-inclusive extension services are needed as females accessed less EAS when compared to males. Efforts are needed to improve the effectiveness of other sources apart from mass media and private sources. Inter-sectoral heterogeneity in access to EAS can be improved by providing target-specific information to farmers. As a heterogeneous impact of access to information from different sources was observed, targeted extension approaches are needed to reach farmers accessing different sources of EAS, necessitating the development of tailored EAS.

Gender evaluation of integrated farming system for enhancing livelihood of tribal farmers in manipur

both farm women and men must have equal access to, use, and control over different agricultural technologies, and resources, as these are critical in overcoming the hurdles that they encounter. The study made an effort to assess the livelihood of tribal farmers in Manipur, (Kangpokpi, Tamenlong, Senapati, and Chandel districts), with 320 respondents (160 male and female each). There was a significant difference in knowledge levels between male and female participants regarding the integrated framing system. The adoption mean for each component was higher for male than for female with an Overall Adoption Index Score of 79.14 for male respondents, and 59.29for female respondents. Substantial gender gap in access to resources, decision-making, ownership and control, and drudgery was observed. The female farmers performed most of the farming activities, from sowing to harvesting. Time allocation to different activities from house management, child care, and social activities to earning a living were substantial by women, but their access to resources, decision making, ownership, and control is less than their male counterparts. It also shows a considerable drudgery of the female farmers in operating the farm activities. With an Overall Empowerment index, it is evident that male respondents were more empowered in all aspects. The gender-based disparity in the perception of livelihood security, with a higher percentage of female respondents expressing lower levels of security compared to their male counterparts was found. There was a significant difference in the composite index, with males having a higher Livelihood Security Index score compared to female. Economic constraints appear to be the most significant challenge for genders; socio-personal, technical, situational, and marketing constraints also play pivotal roles in hindering the adoption of integrated farming practices. Female respondents typically report less situational and marketing-related issues, but they struggle more with the socio-personal and practical barriers to adopting integrated farming systems.

A study on effectiveness of public distribution system in Bihar

The study assessed the effectiveness of the Public Distribution System (PDS) in Bihar, focusing on individuals' perceptions, knowledge levels about PDS and nutrition, and identified constraints in implementation. Ex-post facto and explorative research designs were employed in two districts with high children stunting rates. Beneficiary populations showed significantly higher perceptions. Both beneficiary and non-beneficiary groups demonstrated a medium level of knowledge about nutrition and PDS. The PDS was found most effective in Bank village and among district in the Rohtas district. BMI and occupation positively correlated with PDS effectiveness. Major implementation constraints included population pressure, lack of supporting documents, and corruption. Availing benefits faced challenges like malpractice, irregular distribution, low quantity, and poor quality.

Analytical study of operation greens

The perishability of crops and price instability along with post-harvest losses posses challenges in maintaining food and nutritional security for increasing population. To overcome these obstacles Operation Greens scheme was luanched by Government of India in 2018-2019. Main objectives of the includes enhancing value realization of TOP crops, price stabilization and increase in food processing capacity. The research study was conducted purposively in Anand and Kheda districts of Gujarat, Ahmednagar and Nashik districts of Maharashtra, and Meerut and Hapur districts of Uttar Pradesh with270 farmer along with 30 retailers and 30 adhtiya. The post-harvest losses in tomato were 21.51% followed by onion (12.59 %) and potato (13.67 %). Education, farming experience, cost to reach market, total production of TOP crops, numbers of input applied, storage of TOP crops, number of post harvest activities, unavailability of skilled labour, market risk and uncertainty, lack of training on cultivation practices, post harvest management and lack of government support were found significantly effecting post-harvest losses of TOP crops. Producers and processors contributed value addition of 23.17% and 38.46% value addition in tomato, 20.58% and 35.33% in onion, 26.50 % and 49.52 %in onion. Education, purchase price, experience and distance to market were found to be statistically significant affecting value chain development. Lack of proper utlization of potential of processing facility followed by delay in payment of produce from middlemen and lack of obtaining quality produce suitable for processing were observed as top constraints in the value chain development. Operation greens was 69.5% effective on value realization of TOP crops in production clusters. *Vangi Foods* was effective in functional efficiency, increase in income and farmers share in consumer rupees, sustainability and empowerment, the *Khemananda Dudh and Krishi Product* FPC in farmers' satisfaction and *JCL Agro Product Limited* in inclusiveness of farmers' under operation greens. FPOs were working towards betterment of farming community in enhancing crop productivity, income of farmers, enhancing the marketing and negotiating skills, contributing in value addition of crops through processing.

Theme 2: Nutrition and Health

Bio fortified crops in India: Knowledge and behavioral intentions of stakeholders for adoption

The adoption of biofortified crops depends on the knowledge and behavioral intentions of stakeholders, including farmers, consumers, and policymakers. The investigation was carried out for the adoption of pearl millet and rice in Vijayapura and Guntur respectively. Total 300 respondents in each district involved for pearl millet (Iron rich-Dhanshakti) from Vijayapura district, Karnataka and for Rice (Zinc rich- DRR Dhan45) from Guntur district, Andhra Pradesh. Theory of planned behavior was considered to assess the behavioral intentions of farmers. Overall 29%, 17% and 54% respondents were consumers, dealers and farmers for pearl millets whereas 24%, 16% and 60% respondents were consumers, dealers and farmers for rice and awareness was observed to be 64% and 67% for biofortified pearl millet and rice respectively. Knowledge questionnaire revealed that there were 23%, 42% and 36% respondents for pearl millet belonged to low, average and high category respectively. 25%, 43% and 32% respondents for rice belonged to low, average and high category respectively. The attitude of the respondents towards biofortified crop adoption include; discouraged due to inputs unavailability, its less fertilizer requirement, better nutritious quality than the local variety, makes one feel socially relevant, preference for local variety to the improved variety, more capital outlay requirement, and more expensive than local variety. It was found that factors such as inaccessibility of the product, inaccessibility of nutritional information, high cost of the product, food safety issues, poor product awareness, poor nutrition knowledge, taste and preference of conventional crop, pricing issues, negative sensitivity about biotechnology, awful smell and colour were ranked as inhibiting factors for the adoption of biofortified crops.

Effectiveness of public distribution system on household nutritional security

One of the reasons for malnutrition is the lack of dietary diversity in beneficiary households, with little or no inclusion of pulses, vegetables, meat, fruit, or dairy products in their diets. This study examines the dietary pattern, nutritional status of households, the effectiveness of PDS, coping strategies adopted in stress conditions, and preferences for nutri-cereals of households in the Bundelkhand region. Significant differences were observed in the average intake of each nutrient among districts, except calcium (gm) intake. This compelling evidence of disparities in nutrient intake among beneficiaries of the Public Distribution System (PDS) was observed. The percentage of AAY was higher (22%) in "Less than five" category of HDD as compared to PHH beneficiaries. Respondents have a discernible preference for certain foods across the four meals. Foods high in "Oil/fat", "Cereals", "Roots/ tubers", and "Vegetables" were the most well-liked across the board. The majority of respondents were classified into "Healthy weight" category. The key factors contributing to the effectiveness of a Public Distribution System (PDS) in ensuring household nutrition security include accessibility, satisfaction, nutritional aspects, viability, and supply-management mechanisms. The proposed integrated weightage method (IWM) for the "Nutri-PDS Effectiveness Index" was deemed robust. Tikamgarh district was ranked first on the Nutri-PDS effectiveness index, indicating the proficiency and efficiency of PDS. The majority of respondents want nutri-cereals in the form of flour, which saves processing costs. The proposed mixed weightage method (MWM) for "Coping Strategy Index" was deemed robust. Chhatarpur district was ranked first on the Coping Strategy Index, indicating the adoption of various strategies to cope with the nutrition insecurity of households. Strategies such as consuming nutrient-rich foods like legumes, nuts, and seeds, relying on less preferred foods, consuming the same foods for consecutive days, etc. were practiced to meet their basic nutrient needs.

A study of identification and validation of indicators for model agri-nutri (A2N) smart village

The A2N model is a comprehensive framework designed to address malnutrition by integrating agriculture and nutrition. In select villages, various nutrition interventions were experimented as a part of Agri-Nutri Smart village initiative. A study on identification and validation of indicators for model Agri-Nutri (A2N) Smart Village focused on 360 farmers and 30 extension personnel selected from three model villages and three comparison villages in each state namely; Uttar Pradesh and Telangana. In Telangana, 36.11% had moderate knowledge, while in Uttar Pradesh, 33.33% were highly knowledgeable, 58.3% in Telangana and 53.3% in Uttar Pradesh had moderately favorable attitude. Nutritional practices were mainly acceptable in Telangana (45.0%) and borderline in Uttar Pradesh (41.7%),. Agri-nutrition practices showed medium frequency for the majority in both states (42.8% in Telangana and 46.1% in Uttar Pradesh). The PLS-SEM analysis confirmed good model fit and revealed significant relationships: knowledge and attitude ($\beta=0.325$, $p=0.02$), knowledge and practices ($\beta=0.211$, $p=0.005$), and attitude and practices ($\beta=0.016$, $p=0.03$). Using a mixed-method approach, yielded 61 indicators across, using the Q-sort technique narrowed it down to 40 indicators with a mean score of above 4.5. Then Principal Components Analysis (PCA) was run to reduce into 12 factors, including Production Diversity, Agri-Inputs Management, Good Farm Practices, Health and Nutrition Practices, Nutrition and Learning, Financial Resilience, Basic Infrastructure, Smart Technologies, Market and Logistics, Social Networking, Gender Empowerment, and Sustainability. 77% of Telangana and 72% of Uttar Pradesh model villages' farmers achieving Agri-Nutri smart status. The primary contributors to inadequacies in ANSVI were nutrition and learning, followed by smart technologies. ANOVA results showed significant differences between model and non-model villages in both Telangana ($F = 13.798$, $p < 0.01$) and Uttar Pradesh ($F = 7.097$, $p < 0.01$), with consistent ANSVI performance across model villages. Self-efficacy played a vital role in non-model villages in both states by Nutrition Health Belief Model (HBM). Perceived severity, susceptibility, benefits, socio-economic factors, and perceived barriers significantly affected ANSVI values. Gender influenced Body Mass Index (BMI) categories, with female were more in underweight and less in overweight category. Prioritization, policy and institutional ($W = 86.03$) development ranked highest, followed by nutrition, technology, agricultural practices, and community engagement reflecting a holistic approach for Agri-Nutri Smart Village success.

Postural ergonomic assessment of paddy cultivation practices in coastal region of Andhra Pradesh

Paddy cultivation practices are extremely labour intensive; throughout the activities, farmers adopt various postures such as bending, twisting, standing, and squatting which are directly associated with drudgery and occupational or work-related health problems. The present study focussed on the perceived hazards in existing paddy cultivation practices, and the adoption intention of the farmers towards the improved tools available for the paddy cultivation. The data were collected with the help of an interview schedule and Body Part Discomfort (BPD) scale. ERGO Fellow software was used to analyse data of RULA, and REBA method to identify the postural discomfort among the farmers those who were involved in paddy production system. The majority of farm workers experienced very severe discomfort during load carrying, threshing, harvesting, transplanting operations in paddy production system. Postural discomfort was found to be more during transplanting, weeding operations as farm workers adopted squatting and bending postures with the repetitive movement of the hands. The majority of respondents were found to be fall in the category fourth, which indicates that further investigation and immediate change is required, whereas in REBA method respondents were found to be fall in the third category, which indicate high risk and implement change in their working posture. Long working hours, uncomfortable body postures, repeated effort, and physical stress all contribute to musculoskeletal discomforts in the paddy production system. All the improved tools found to be significant for the adoption intention with in which drum seeder got the highest mean rank.

Theme 3 : Entrepreneurship Development

An analytical study of linkages in selected agrienterprises

Ascertaining effective linkages for an agribusiness is believed to be a significant factor contributing to the growth of the agriculture sector. Government initiatives have encouraged the consolidation of farmers into cooperatives or producer companies. The study aimed Social Network Analysis to delineate and analyze the backward and forward agribusiness linkages of farmers in selected agri-enterprises. 240 farmers from two FPOs each (Crop Produce and Dairy) were selected from M.P. and Bihar states. Backward and forward agribusiness linkage actors were identified through focused group discussion using ‘One step modified reputational sampling’. Nature of connections among farmers and actors was examined through ‘Tie Strength’ and ‘Tie Direction’. Across all FPOs, farmers mostly relied on Strong ties for information and resources. Most of the farmers believed ties to be One way, suggesting top-down approach from agri institutions. Crop produce FPOs in M.P. and Bihar listed equal number of linkage actors but Dairy FPO in M.P. listed more number of linkage actors than dairy FPO of Bihar, signifying greater access to information and resources. Government institutions such as KVK, ATMA, NABARD, and state agri-officials were highly connected actors in the social network of all FPOs. Additionally, IFFCO and Dairy Cooperatives had strong linkages among the present cooperatives. FPOs had few farmers at the central position having ties with every major and minor linkage actors. Rest majority farmers were situated at periphery of their networks, having contacts with few actors. Farmers’ age, sex, education and income attributes had significant relation to their centrality measures. Correlation analysis between farmers perception score and degree centrality was either non-significant or negative, signifying that other factors than centrality measure were into play to effect the farmers’ perception. Major constraints perceived towards establishing agribusiness linkages were inflation, shortage of labour, lack of basic rural infrastructures, multiple intermediaries, not easy access to information and technology, lack of access to raw material or inputs, less or no government support, company/ cooperative registration procedure and lack of training facilities.

Value chain analysis of IARI wheat varieties in central and north-western plain zones of India

To analyse the value chain of wheat in NWPZ and CZ, two villages from each zone selected randomly by using multistage random sampling method. Primary data were collected from 160 farmers and 40 other stakeholders using interview schedule. Input-output ratio of wheat cultivation for marginal, small and medium farmers in NWPZ was 1:1.29, 1:1.313 and 1:1.314 respectively and in CZ it was 1:1.360,1:1.347 and 1:1.344 respectively. Value chain analysis of wheat in both zones showed that, the degree of value addition was highest in case of millers, followed by retailers and wholesalers. Furthermore, it denoted that fame's share in consumer rupee was increasing with decreasing number of middlemen and value chain was also becoming efficient with lesser middlemen. The most preferred traits revealed by farmers of NWPZ and CZ for IARI wheat variety was grain yield followed by straw yield, grain size, market rate and number of irrigation required. It was found that mean Livelihood Security Index (LSI) and Livelihood Asset Index (LAI) increased for farmers growing IARI wheat varieties, in NWPZ to the extent of 16 per cent and 11 per cent respectively, whereas in CZ it was 18 per cent and 9 per cent respectively. The barriers faced by farmers in NWPZ and CZ were variability in the amount of rainfall and low wheat prices respectively. Barriers faced by millers, retailers and wholesalers were related to quality, scarcity of grain & labor, market competition selling on credit, attracting & retaining customers, supply and demand imbalances and the increasing impact of e-commerce on their business.

Evaluation of the mango value chain of farmers' producer organizations

Farmer Producer Organizations (FPOs) are one of the solutions to reap the benefits of economies of scale, collective post-harvest operations, and collective marketing. A comprehensive study on ten FPOs and 300 farmers was carried out in Andhra Pradesh and Telangana states and data were collected using a structured interview schedule and open-ended interviews; analyzed using porters' value chain model, regression adjustment, Pro-WEAI, and mixed method analysis. The porter's value chain analysis identified ripening, storage, spoilage and handling and freight expenses as the major areas of cost minimization and the marketing channel with FPOs fetched higher prices to the farmers. FPOs involved in export gained higher prices compared to all other channels. Regression adjustment results indicated that nearly 35.8 percent increase in productivity, 21.9 percent increase in price, and 67.7 percent increase in the value of the output of members compared to nonmembers. The women who were empowered at the household level were also empowered at the value chain level. A gender-sensitive approach in extension services, such as hiring women extension agents and placing more emphasis on developing and supporting women-led FPOs, will have a multiplier effect on agriculture, farm families, and the rural economy. Farmers should be made aware of the importance of connecting FPOs to digital platforms like Kisan rath, Kisan rail, and Krishi udaan, which offer organised services with negotiable prices. Collaborating with ATMA, KVK, or research institutes to provide training, knowledge, and information on numerous issues as well as engaging the FPOs in secondary value addition activities helps to overcome the constraints. Better prices for produce, a large number of shareholders, adequate EAS, etc. were the major success factors identified.

Theme 4: Innovations in Extension Systems

Community managed extension system for sustainable agriculture: A multidimensional study

The emergence of Zero Budget Natural Farming in India represents a transformative shift in the realm of alternative agriculture. As the adoption of ZBNF continues to grow, it provides a new way of farming for the small and marginal farmers in India towards economic sustainability and ecological resilience. The perception of ZBNF and Non-ZBNF farmers in Andhra Pradesh and Maharashtra states were studied and found that majority of the ZBNF farmers (61.25%) and Non-ZBNF farmers (52.50%) had positive perception. The Core competency needs of community resource persons (CRPs) were studied and found deficient in majority of the core areas. The major significant determinants of adoption were ; integrated soil fertility management practices, adoption of ZBNF practices, integrated pest management practices, livestock ownership and use of waste decomposer, use of live mulching and drip irrigation. In Andhra Pradesh & Maharashtra farmers become 16 %& 15 %more likely to proper use of natural fertilizer, 14 % each use of new varieties, 13 %& 10 % to use of proper sowing method and 11 % to use manure/compost and practicing field preparation. In Andhra Pradesh, the average treatment effects for the treated (ATT) along with the KBM and NNM for crop yield found the positive and highly significant. The participants of FFS were getting higher yields in the range of 25-40 kg/acre whereas in Maharashtra, it ranged between 33-45 kg/acre. It was found that ZBNF farmers of Maharashtra (86.67%) had trust in strong ties for agricultural information about ZBNF practices and services in the community, compared to a lower percentage (73.33%) of farmers in Andhra Pradesh. In Andhra Pradesh, ZBNF trained farmers had the highest degree centrality (22.0) whereas in Maharashtra; Cooperatives & NGO had the highest degree centrality (23.0). In case of Andhra Pradesh betweenness centrality of ZBNF trained farmers (108.031) were more likely to influence people from different groups, whereas in Maharashtra, member of SHG (117.388) were more likely to influence people from different groups. In case of Closeness centrality, in Andhra Pradesh, of ZBNF trained farmers had the highest closeness centrality (0.813) whereas Maharashtra member of SHG had the highest closeness centrality (0.867). The average sustainability measurement index of ZBNF practices for both states was found under high category. ZBNF produce should be certified before going into value chain, and encouragement for establishing farmer selling societies/FPOs need to be encouraged.

An analytical study on livelihood and climate change adaptation among the communities of biosphere reserves and heritage zones

To understand the vulnerability, socioeconomic and ecological concerns as well as the adaptation and livelihood strategies taken up in the biodiversity management and sustainable livelihood in the context of climate change in Nilgiri *Biosphere Reserve* (NBR) and *Agasthyamalai Biosphere Reserve* (ABR), and sample size of 1656 were chosen purposively. Location specific time series data from 1901-2022 were extracted to analyse the occurrence of climate change. Communities in NBR and ABR were able to perceive that there were changes in rainfall quantum, decline in number of rainy days, shift in monsoon, increase in temperature and natural calamities. Vulnerability Index developed using the Shannon’s Entropy Method showed that NBR was more vulnerable to climate change than ABR. ‘Adjustment in Crop Calendar’ and ‘Crop Diversification’ were ranked first in NBR and ABR respectively among the crop-based, livestock based, fisheries based and other adaptation strategies. Crop-based, livestock-based, forest-based, business-based and diversified livelihood was the major strategies identified using the PCA and Agglomerative Hierarchical Clustering Method. The communities depending on the forest-based strategy were food insecure, in contrast to, the business-based and crop-based strategies. Education, dependency ratio, land size, credit use, membership of social groups, annual household income, landownership title, social cohesiveness and duration of living in/near BR were the major determinants affecting the choice of livelihood strategy. The perceived severity, response efficacy, perceived vulnerability and self-efficacy affected positively and significantly the conservation behaviour whereas response cost affected conservation behaviour negatively. The overall participation score of communities of NBR and ABR in biosphere reserve management was found to be moderate. The overall management effectiveness of NBR was found to be high compared to ABR. The stakeholder groups identified were indigenous communities, non tribes, government departments, tourism sector, NGO, local media, religious and political groups, tourists and researchers. The major success factors governing the effective management of biosphere reserve were found to be equity, efficiency, ecological sustainability, decentralization, interests and incentives.

Theme 4: Media and ICT

Utilization of information and communication technologies in the National Agricultural Research System for enhanced efficiency

In India, agriculture has become a knowledge-driven sector, emphasizing the crucial role of Information and Communication Technology (ICT) and its Management (ICM) in effectively harnessing and disseminating knowledge. The study was carried out with 660 scientists in ICAR system as it is mainly focused on ARD and many ICT interventions developed under this system. 52.19 percent of the respondents had undergone ICT training for less than 10 days duration, and had medium level time devoted to use ICTs in a day, extent of use of ICT tools and social media use respectively. 38.48% had medium strategy e-readiness, 43.33% had medium technology e-readiness, 37.42% had medium organizational support e-readiness, 36.97% had medium people/HR support e-readiness and 44.09% had highly e-culture readiness. In the digital competencies of NARS scientists; digital communication ranked highest, followed by information management. Using CB-SEM it was found that system quality, information quality and service quality exerts a significant influence on system usage, and in turn, system usage significantly impacts net benefits. This study extended the TAM by incorporating perceived effectiveness to assess the impact of information systems. The model reliability and validity was tested using PLS-SEM. Organizational support, training, and computer self-efficacy emerged as significant drivers. Concerning ICT developed under NARS, the need for multiple login IDs and passwords and the repetition of work were notable constraints and to address these issues, respondents recommend integrating all systems into a common platform and adopting a single-entry system to eliminate redundancy. ICT status in NARS stands at a medium level and the strengths exist in strategy, technology, and human resources support, room for improvement, particularly in organizational support and aspects of e-culture readiness was observed. Scientists excel in data management, information management, and digital communication but need enhancement in technical proficiency, digital content creation, safety, and troubleshooting skills. The intricate interplay of system quality, information quality, service quality, use, user satisfaction, and net benefits in determining information system success was revealed.

Critical analysis of *Pusa Samachar*: Multimedia based extension model for enhanced information delivery and usage

Public extension services in India are facing challenges due to limited out-reach, ineffective and imprecise targeting, high administrative costs, and a shortage of extension personnel which results in an ineffective information delivery to farmers. In this context, multimedia platforms are valuable tools for delivering information to farmers by providing interactive and visual content, two-way communication, language customization, instant updating of information, knowledge sharing, and networking opportunities, ultimately improving the accessibility and effectiveness of agricultural information dissemination. So, in this regard, this study attempted to identify the information need, multimedia use behaviour of farmers as well as their perception towards multimedia based agro-advisory services and its effectiveness in information delivery. It was observed that majority of the farmers had high information need and low information seeking behaviour using multimedia. Effort expectancy, self-efficacy, trust towards information source affects positively towards perceived benefit of using multimedia and perceived benefit of multimedia use affects positively towards their behavioural intention to use multimedia. Seventy percent of farmers had neutral perception towards *Pusa Samachar* model. There is a need to improve the timely delivery of information according to their disease pest infestation for different regions. *Pusa Samachar* model had positive effect on information utility of farmers, their knowledge acquisition level and higher adoption of improved technologies. Digital literacy affects positively towards higher multimedia channel perception of farmers. Multimedia channel characteristics affects positively towards viewership pattern of *Pusa Samachar*. The study reported that better selection of multimedia was most effective strategy to enhance viewership of *Pusa Samachar* regarding effective information delivery. Developing a mobile application for advisory followed by broadcasting *Pusa Samachar* in television were also identified as most suitable channel for information delivery.

Effectiveness of social media in enhancing knowledge and adoption of improved cultivation practices of finger millet in Karnataka

The study aimed at assessing the effectiveness of social media on attitude of farmers towards finger millet farming and their knowledge level and adoption level of improved cultivation practices of finger millet in Karnataka state. The study found that, among the users of social media, 71.67 percent were medium users of social media, both users and non-users of social media majority of the farmers were having moderately favourable attitude towards finger millet farming and it is found that social media has a significant and positive effect on farmers' attitude. From knowledge test it was found that in both users and non-users of social media majority of the farmers were having medium level of knowledge and adoption of improved cultivation practices of finger millet. Farmers' knowledge was poor on seed treatment, crop protection and fertilizer dosage and have poor adoption of irrigation, seed rate and crop protection practices. Social media has a significant and positive effect on farmers' knowledge and adoption of improved cultivation practices of finger millet. Low knowledge on services available in social media, age factor was restricting to use social media and insufficient skills in using social media by farmers were major constraints in using social media by the farmers.

Effectiveness of agricultural programs of DD Kisan channel : A multidimensional study

DD Kisan channel has emerged as a game-changer, catering exclusively to the diverse needs of the farming community and bridging the gap between agricultural knowledge and its beneficiaries. The study focused on 320 respondents of Lucknow & Baghpat of Uttar Pradesh and Pune & Aurangabad of Maharashtra. A significant percentage of viewers watched DD Kisan frequently, paid moderate attention demonstrating a regular interest in the channel. Discussions about DD Kisan programs were not very common among viewers. About 51.65 per cent of viewers preferred watching DD Kisan programs in the afternoon, 66.56 per cent of viewers reported moderate comprehension, 21.56 per cent understood the content completely and 11.87 per cent had the least understanding. Evening (37.5%) was the second most popular time slot. About 56.87 per cent of viewers did not take any notes. Education, farm size, mass media exposure, innovativeness, and viewers' attitudes towards DD Kisan had a significant relationship with television viewing behavior. Coverage varied across states, with Uttar Pradesh (9%), Rajasthan (8%), and Madhya Pradesh (6%) receiving substantial attention. Cereal crops (24%) received the most coverage, followed by millets (19%) and pulses (16%). "Phone-in program" was preferred over other presentation styles. Most viewers preferred programs lasting between 30-60 minutes. Programs with anchor-farmer interaction and crop protection-related content were appealing. Program presentation played a crucial role in determining the effectiveness of the program. Technical terms usage and formal production style were identified as major constraints. A dedicated marketing division, collaborative partnerships, specialist recruitment, and capacity building were crucial for program policy enhancement. Technical constraints faced by the viewers included the use of technical terms and a formal production style. Personal constraints encompassed a lack of information about experts and the need for reinforced program impact. Presentation-related constraints included incomplete content coverage and speaker orientation. Information-related constraints involved low coverage of success stories and marketing-related information.

Theme: 5. Contemporary Issues

Innovations for adaptation to climate change and natural disasters

The study aimed at analyzing household-level resilience and it's determinants, understanding adaptation behavior of farmers and exploring the extent of convergence among different institutions and its effectiveness against climate change in Odisha and Assam. The Household Resilience Index (HRI) was developed to assess the resilience capacities of households in the states of Odisha and Assam. The PCA results suggest that livelihood strategies, access to basic services, social capital and income and food access were the four main determinants of resilience. Risk evaluation, adaptation evaluation and maladaptation had a significant influence on farmer's adaptation decision. The study proposed that another structural construct social discourse should be given greater emphasis to promote adaptation. Odisha demonstrated a higher level of perceived convergence among institutions across different activities like planning, communication, teamwork and decision-making compared to Assam. In both states, the majority of respondents perceived convergence efforts as moderately effective, but the result shows statistically significant difference between the perceived effectiveness of extension services in Odisha and Assam. Institutional convergence programs had a positive impact on increasing the employment opportunities, income of farmers and improving agricultural productivity in both states. Addressing organizational and infrastructure constraints was paramount in both states emphasizing the importance of improving communication facilities and ensuring equitable resource allocation. Targeted interventions, such as training, access to quality inputs and market linkages should be continued and possibly enhanced to sustain these positive impacts. Continued monitoring and evaluation of convergence programs are essential to assess their long-term sustainability and adapt them to changing agricultural and environmental conditions. By understanding the factors which affect farmers' adaptation decision, researchers and policymakers can design efficient interventions and communication strategies for stimulating successful adaptation actions among farmers.

Farmer-led conservation and improvement of crop genetic resources in Odisha and Uttarakhand

The study was conducted in two states; *Odisha* and *Uttarakhand* of India. In total 420 farmers, divided into custodian and non-custodian categories, with 300 from *Odisha* and 120 from *Uttarakhand* and, 60 farmers from each state for validation of the e-module were sampled. The western *Odisha* farmers practiced organic and mixed farming for landraces, with significant income from landrace cultivation whereas, eastern *Odisha* farmers had a stronger focus on organic farming. In *Dehradun*, and *Bageshwar* districts of *Uttarakhand,* farmers with smaller landholdings also relied solely on organic farming. Extension services and seed banks played a vital role in these regions. In western *Odisha*, paddy landraces dominated due to their adaptability to local agro-climatic conditions and their resistance to pest attacks. Economic value was significantly boosted through the utilization of these landraces in the market and extensive promotional efforts by organized groups. In Eastern *Odisha*, the cultivation of paddy landraces was due the food and culinary preferences of the local population. The economic potential of these landraces was realized through their utilization in the market and multiplication facilitated by consortia, seed companies, and public bodies. In Dehradun cluster, cultural significance was guiding the cultivation of paddy and millet landraces. The intrinsic nutritional properties of millet landraces also played a pivotal role in their cultivation, and economic value of landraces was magnified through large-scale cultivation, extensive promotion driven by organized groups, multiplication efforts led by NGOs, formal seed banks, and the implementation of formal cultivation plans. In the *Bageshwar* cluster of *Uttarakhand*, the cultivation of both paddy and wheat landraces was influenced by cultural significance and alignment with their local food and culinary preferences. The farmers' conservation behavior towards landraces was influenced by their environmental values, awareness of consequences, self-efficacy, and personal norms, with custodian farmers showing stronger associations between these factors.

Critical analysis of migration behaviour of agricultural households in northern India

The migration pattern of North Indian agricultural households revealed the increase in rural-to-urban migration. The emergence of the feminization of agriculture and limited job diversity in farming has reshaped migration choices for these households. The research area was purposefully conducted in Uttar Pradesh (UP) and Rajasthan with a sample size of 1000 respondents, comprising 480 migrant farmers, 480 non-migrant farmers, and 40 professionals from KVK professionals. The farmers' developed their perception towards migration on the five key dimensions *viz.,* social pressure, standard of living, resource constraints, employment opportunities, and seasonal uncertainty in agriculture. The theory of planned behaviour with the engagement of women in agriculture and household decision-making constructs has significant effect on the migration behaviour & household decision-making pattern. The significant factors of migration were farming experience, *rabi* yield, livestock revenue, and age which were having more probability of migration among farmers. Thus, when farmers gain more experience, achieve higher *rabi* crop yields, generate increased revenue from livestock, and grow older, they are less likely to migrate. The migrants encountered livelihood insecurity at the origin whereas at destination they faced resource unavailability issues. The study predicted that to earn a monthly 28000/- of farm income, the migrant farmers must aim for a milk yield of at least 1600 liters per animal in a year along with a *rabi* yield of at least 22 quintals per hectare, and a kharif yield of at least 16 quintals per hectare to reach the afore mentioned income target. Therefore, the study highlighted the complexity of the migration phenomenon and its wide-ranging implications. By understanding the factors driving migration, its consequences on agricultural households along with its broader policy implications, the stakeholders can develop evidence-based strategies to promote sustainable rural development and harness the potential benefits of migration.

List of contributing students and chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Pasupulti Sahithi (21589)	M.Sc.	Evaluation of the mango value chain of farmers' producer organizations	Dr. Vinayak Nikam	ICAR-IARI, New Delhi
2.	Anirban Jana (21590)	M.Sc.	Value chain analysis of IARI wheat varieties in central and north-western plain zones of India	Dr. Nishi Sharma	ICAR-IARI, New Delhi
3.	Mathi Girishma (21591)	M.Sc.	Access to extension and advisory service: diversity and impact in India	Dr. Vinayak Nikam	ICAR-IARI, New Delhi
4.	Naveen Kumar H N (21594)	M.Sc.	Effectiveness of social media in enhancing knowledge and adoption of improved cultivation practices of finger millet in Karnataka	Dr. Lenin Venu	ICAR-IARI, New Delhi
5.	Amit Sinha (60094)	M.Sc.	A study on effectiveness of public distribution system in Bihar	Dr. Sangeetha Vellaichamy	#ICAR-IARI, Jharkhand

6.	Nuthaki Venkata Leela Krishna Chaitanya (60095)	M.Sc.	Postural ergonomic assessment of paddy cultivation practices in coastal region of Andhra Pradesh	Dr. Sukanaya Barua	#ICAR-IARI, Jharkhand
7.	Ashish Singh (10718)	Ph.D.	An analytical study of linkages in selected agrienterprises	Dr. Rashmi Singh	ICAR-IARI, New Delhi
8.	Channaveeresh Revappa Motagi (10757)	Ph. D	Biofortified crops in india: knowledge and behavioural intentions of stakeholders for adoption	Dr. Satyapriya	ICAR-IARI, New Delhi
9.	Sunil Kumar (10758)	Ph.D.	Community managed extension system for sustainable agriculture: A multidimensional study	Dr. Manjeet Singh Nain	ICAR-IARI, New Delhi
10.	Sondarva Yagnesh Mansukhbhai (10967)	Ph.D.	Utilization of information and communication technologies in the National Agricultural Research System for enhanced efficiency	Dr. Manjeet Singh Nain	ICAR-IARI, New Delhi
11.	Aiswarya S. (11195)	Ph.D.	An analytical study on livelihood and climate change adaptation among the communities of biosphere reserves and heritage zones	Dr. R. N. Padaria	ICAR-IARI, New Delhi
12.	Gangubai Shivappa Managuli (11197)	Ph.D.	Effectiveness of agricultural programs of DD Kisan Channel : A multidimensional study	Dr. N. V. Kumbhare	ICAR-IARI, New Delhi
13.	Surjay Kant Roy (11430)	Ph. D.	Effectiveness of public distribution system on household nutritional security	Dr. Satyapriya	ICAR-IARI, New Delhi
14.	Praveen Kumar (11700)	Ph.D.	Analytical study of Operation Greens	Dr. N. V. Kumbhare	ICAR-IARI, New Delhi
15.	Pagadala Sai Priyanka (11701)	Ph.D.	A study of identification and validation of indicators for model agri-nutri (A2N) smart village	Dr. V. Sangeetha	ICAR-IARI, New Delhi
16.	Sudip Kumar Gorai (11694)	Ph.D.	Innovations for adaptation to climate change and natural disasters	Dr. R. N. Padaria	ICAR-IARI, New Delhi
17.	Preeti Yadav (11695)	Ph.D.	Farmer-led conservation and improvement of crop genetic resources in Odisha and Uttarakhand	Dr. R. N. Padaria	ICAR-IARI, New Delhi
18.	Sonali Mallick (11697)	Ph.D.	Critical analysis of *Pusa Samachar*: multimedia based extension model for enhanced information delivery and usage	Dr. R. R. Burman	ICAR-IARI, New Delhi
19.	Sushmitha Saini (11699)	Ph.D.	Critical analysis of migration behaviour of agricultural households in northern India	Dr. R. R. Burman	ICAR-IARI, New Delhi
20.	TH.D Grace Chiru (11701)	Ph.D.	Gender evaluation of integrated farming system for enhancing livelihood of tribal farmers in Manipur	Dr. Monika Wason	ICAR-IARI, New Delhi

#IARI off campus

Agricultural Statistics

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Prof. Cini Varghese

The Division conducts post graduate teaching and in-service courses in Agricultural Statistics for human resource development. Division is conducting M.Sc. and Ph.D. programmes in Agricultural Statistics, in collaboration with the Graduate School of Indian Agricultural Research Institute, New Delhi which has the status of a Deemed University. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Design of Experiments

On some aspects of asymmetrical response surface designs

Response surface methodology is useful when multiple input variables affect a performance metric or quality attribute in a product or process. Although factors with mixed levels have more useful applications, the majority of rotatable response surface designs are symmetrical. In this study, methods have been developed for creating rotatable, asymmetrical third-order designs as well as a strategy for creating them with fewer design points when time and resources are the main limitations. A comparison of the designs developed is also made using efficiency criterion, Fraction of Design Space (FDS) plots and Variance Dispersion Graphs (VDGs). This study constructs third-order rotatable designs, symmetric and asymmetric, using unequal set sizes in t-designs. The resulting design has fewer runs than existing third-order designs, and proposed classes with G-efficiency are provided. There are numerous instances in agricultural experiments where both qualitative and quantitative factors are important. A method is introduced to design response surfaces that capture both symmetric and asymmetric factors in qualitative and quantitative terms for second and third-order models. List of designs for 3 to 10 factors along with G- and D-efficiencies are also presented. If a second-order model falls short in representing the relationship between input and response variables, sequential third-order response surface designs can help. The first-stage design, used for fitting the second-order model, can still be retained while additional runs may be employed to fit the third-order model more effectively.Proposed strategies for sequential third-order designs address symmetric and asymmetric factors, ensuring necessary moment matrix requirements and rotatability. These designs, available in smaller sizes, offer cost-effective ways to achieve optimal responses. For every design that was obtained, R package named “MixedLevelRSDs” has been prepared for the users to generate the designs together with its efficiencies.

PBIB designs based on higher association schemes and their applications

PBIB designs based on 2-, 3-, or higher-associate classes have been extensively studied in the literature. For some parameters, neither a BIB design nor a 2-associate-class PBIB design are available. The best alternative for such situations is a higher-class PBIB design, if such a design exists. Hence, this investigation provides three new association schemes: the icosahedral association scheme, the octahedral association scheme, the pentagonal prism association scheme, and the construction of related PBIB designs. These schemes produce resolvable and two-replicate PBIB designs. A list of these PBIB designs for treatments (v) ≤300 and replications (r) ≤6 has been tabulated. The nested block designs (nested balanced incomplete block (NBIB) designs and nested partially balanced incomplete block (NPBIB) designs) are available in literature for inferring on all possible elementary treatment contrasts. In agricultural and related sciences, many experimentations involve the comparison of multiple tests with control(s). While nested balanced treatment incomplete block (NBTIB) designs and 2-class nested partially balanced treatment incomplete block (NPBTIB) designs are available in literature, they might not cover all parameter combinations or may necessitate numerous replications. To address this, the study introduces higher-associate-class NPBTIB designs. Efficient catalogues of NPBTIB designs are provided for treatments (v) ≤16, test replications (r_1) ≤30, and control replications (r_2) ≤60. Furthermore, in experiments where researchers seek to compare tests with multiple controls, nested balanced bipartite block (NBBPB) designs are available but might not obtainable for all parameter combinations or may demand excessive replications. To tackle this challenge, the inquiry introduces nested partially balanced bipartite block (NPBBB) designs. An efficient catalogue of NPBBB designs is outlined for test treatments (v_1) ≤16, control treatments (v_2) =2, r_1 ≤30, r_2 ≤60. Some new methods of 3-class NPBIB and partially balanced bipartite block (PBBB) designs have also been given for constructing 3-class NPBTIB and NPBBB designs, respectively.

Experimental designs involving doubly nested blocking factors

The popular Incomplete Block Designs (IBDs) like balanced and partially balanced incomplete block designs (BIBDs and PBIBDs) work well for many agricultural trials, they might prove inappropriate under particular circumstances. Doubly Nested Incomplete Block (DNIB) designs, which are also called Tri-Hierarchical Incomplete Block (Tri-HIB) designs, form a sub-class of IBDs, capable of eliminating three sources of variation present in the experimental material, where one source of variation is nested within the second and the second nested within the third. In this study, some new methods of constructing Tri-HIB designs have been developed that yield four series of Tri-HIB designs. These designs are easy to construct and cover a wide range of parametric combinations. Each design gives rise to six component designs, three nested block designs and three block designs. A list of parameters of Tri-HIB designs for number of treatments up to 30 is presented along with efficiency factors. Further, for easy accessibility and wider adaptability of proposed Tri-HIB designs, an R package 'Tri.Hierarchical.IBDs' has been developed. Tri-HIB designs, besides being useful as block designs can find excellent application potential in obtaining Mating-environmental (ME) designs for breeding trials involving diallel/ partial diallel/ partial triallel/ partial tetra-allele crosses. The designs with sub-sub-block size 2, 3 and 4, with contents treated as lines, can be directly used to get desired types of crosses with high efficiency and low degree of fractionation. SAS programs have been written to study the characteristic properties of ME designs. Tri-HIB designs have also been studied by considering a mixed-effects model, with blocks, sub-blocks, and sub-sub-blocks treated as random and treatments treated as fixed effects. Variance components have been derived. Tri-HIB designs for equal block sizes were compared with those for unequal block sizes and it was observed that designs with equal block sizes performed better.

Algorithmic approach for construction of uniform designs

Uniform designs play an important role in various fields, including experimental design and optimization. Uniform design aims to distribute the experimental points evenly across the design space, which reduces the risk of over- or under-sampling areas of the design space. Adopting this design minimizes biases and promotes data reliability and accuracy. Two algorithms for construction of uniform designs have been developed, one for the rectangular regions and another for the irregular regions. Discrepancies criteria RMSD (Root mean square distance), AD (Average distance) and MD (Maximum distance) have been used for selecting the best design points that efficiently cover experimental region of interest. Both algorithms offer enhanced flexibility and applicability. The algorithms have been implemented using R codes. The implementation of the algorithms developed has also been demonstrated through examples. The algorithm developed for constructing uniform designs in rectangular region is an improvement over the existing algorithm for obtaining NT-Nets (Number-Theoretic Nets) and is capable of generating uniform designs in higher dimensions as well. The second algorithm has been developed for construction of uniform designs in the irregular region. Proposed algorithm for construction of uniform designs in the irregular region have many advantages over existing algorithms in terms of time efficiency. It also provides more efficient in certain situations. R Codes developed are general in nature and may be used for generation of uniform design for given parameters.

A study on cyclic minimal balanced crossover designs

Crossover designs form an important class of designs that has been advantageously used in dairy feeding trials, long-term experiments, clinical trials, etc. These designs are also known as change-over designs, repeated measurement designs and switch over designs. In these designs, each experimental unit receives a sequence of treatments over a number of periods with observations recorded in each period. In this study, two new methods of construction have been proposed. For all of them, only the presence of first order residuals effects of treatments have been assumed. Crossover designs have long been recognized for their efficiency in experimental research, allowing researchers to compare multiple treatments within the same group of units or subjects. Two new methods of construction for cyclic minimal balanced crossover designs (Cyclic MBCOD) and cyclic minimal strongly balanced crossover designs (Cyclic MSBCOD) have been given along with the illustration. Necessary condition for parameters (v, p, n) for existence of such designs has also been derived. Efficiency in crossover designs is assessed using relative efficiency for estimating direct and residual treatment effects in comparison to corresponding row-column designs. These designs are catalogued within a restricted parameter range ($n \leq 30$, $p \leq 7$, ≤ 20). These designs are meticulously constructed using methodological approach developed in previous chapters, offering a ready reckoner for researchers seeking innovative and efficient design solutions for their experiments. Furthermore, this study hints at the future potential of crossover designs, including the development of non-cyclical designs and designs with unequal period sizes. In a rapidly evolving landscape of experimental research, the findings of this study provide a valuable reference for researchers, practitioners, and decision-makers, guiding them towards making innovative experimental design choices.

Theme 2: Sample Surveys

Development of geographically weighted regression estimator for multi-collinear survey data

The primary objective of a sample survey is to gather information about a population and obtain a valid estimate of parameter using auxiliary information. In the existing literature, various approaches are available for parameter estimation in survey data. One of the popular approach is model assisted approach, where population values are considered realizations of a random process. Using this approach, parameter predictions are made by fitting a linear model between study variables and auxiliary variables, assuming independence among observations. The inclusion of auxiliary variables enables precise estimation of finite population parameters. However, in agricultural surveys, observations are spatially correlated, meaning that nearby observations are more closely related, with correlation diminishing as distance between units increases. This spatial correlation fails to be explained by the classical linear model used in parameter estimation, leading to an oversight in understanding the relationship between variables.

To address this limitation, Geographical Weighted Regression (GWR) emerges as a spatial technique for modelling spatial data. In the realm of model-assisted survey sampling, employing fitting model-assisted estimation can be susceptible to multicollinearity, potentially compromising the accuracy of the estimates. Nevertheless, this challenge can be effectively addressed through the implementation of advanced techniques such as ridge regression and LASSO. In this work ridge regression and LASSO has been used to address the multicollinearity. This study proposes three estimators - GWridge, GWRR, and GWLASSO - to address the multicollinearity issue in model assisted survey sampling. Among these, GWridge performs the best in comparison to other proposed estimator and traditional estimator. Detailed investigation of the GWridge estimator reveals its asymptotic properties under specific assumptions, showing that it estimator satisfies asymptotic model unbiasedness and is asymptotically consistent.

Geographically weighted logistic regression based model-calibration estimator of finite population proportion

In various real-world sample survey scenarios, collected data often involves binary variables. This research addresses the challenge of estimating population proportions in complex sample surveys involving binary variables. These binary variables exhibit two possible values, such as presence/absence or success/failure. When dealing with binary response variables and aiming to estimate population proportions, conventional linear regression models struggle to capture non-linear response functions. In such cases, logistic models offer more suitable alternative. The research explores the calibration approach, a widely-used method in survey analysis. It enhances estimation by adjusting original design weights based on known population characteristics. The model-calibration approach extends this concept to incorporate more complex models, resulting in improved model-assisted estimators. Surveys often encounter varying relationships between variables across locations, known as spatial non-stationarity. Geographically Weighted Regression (GWR) models address this by capturing these spatially diverse connections. In this study, we develop two Geographically Weighted Logistic Regression based model calibration (GWLRMC) estimators for population proportion using complete auxiliary information. The proposed GWLRMC estimators are proven to be asymptotically design unbiased and approximately model unbiased under specific regularity assumptions. We derive approximate variances and estimators of variances for these estimators using the same set of assumptions. Through a spatial simulation study conducted in R software, we compare the performance of the developed estimators with existing ones like the NHT estimator, regression, and SLGREG estimators across various scenarios. Simulation results demonstrate that the proposed GWLRMC estimators for population proportion under SRSWOR are asymptotically design unbiased based on percentage relative bias (%RB). Additionally, the proposed estimators exhibit greater efficiency compared to existing estimators in terms of percentage relative root mean square error (%RRMSE). Ultimately, this research provides an effective methodology for estimating finite population parameters within complex surveys, incorporating complete auxiliary information while considering spatial non-stationarity.

To develop a two auxiliary calibration estimator of the population total under two stage sampling design when the variance function of the study variable is known

The primary goal of sample surveys is to draw conclusions about a population using information obtained from a selected sample. To achieve this, sampling weights, also known as design weights, are used in analyzing survey data. To enhance the accuracy of estimations in survey sampling, auxiliary variables are often employed. The calibration method is a popular technique in survey estimation, which adjusts the sampling design weights using additional information to create more efficient estimators for population parameters. In practical surveys, data collection occasionally provides information on multiple auxiliary variables, which can further enhance estimation precision. One such technique is multiauxiliary calibration estimation. This method employs multiple auxiliary variables to estimate population totals while incorporating linear constraints, a concept introduced by Alam*et al*., in 2023, resulting in highly efficient estimators. However, the proposed approach is limited to single-stage sampling designs, while real-world surveys often employ more complex multistage designs. To address this, the present thesis introduces a new multi-auxiliary calibration estimator for population totals under a two-stage sampling design when the variance function of the study variable was known. This development takes into account, the study variable and the two auxiliary variables generated from the multivariate normal population and also various combinations of values of correlation between study and auxiliary variables were taken into consideration for the comparative study of the performance of proposed estimator through simulation studies in R software with existing estimators of the population total under two stage sampling design developed by Aditya*et al*., (2016) and Pathi (2022). The empirical findings indicate that proposed estimator outperform existing estimators and validate its effectiveness in enhancing accuracy and precision for estimating population total using auxiliary information within a two-stage sampling setup.

Estimation of crop yield at gram panchayat level using remote sensing and small area estimation techniques

PradhanMantriFasalBimaYojana (PMFBY), which is yield based insurance scheme has increased the number of Crop Cutting Experiments (CCEs) significantly. To reduce this number, crop yield estimation procedures are developed using small area estimation (SAE) technique using Geo-spatial variables as auxiliary variable, to obtain more efficient and reliable estimates of crop yield at gram panchayat (GP) level. The study was conducted for Fatehpur tehsil of Barabanki district in UP, using Sentinel-2 multispectral data and CCE data on yield obtained from the "Integrated Sampling Methodology for Crop Yield Estimation using Remote Sensing, Field Surveys and Weather Parameters for Crop Insurance" project. Three strata of low, medium and high vegetation were made using NDVI, NDWI, SAVI and the combination i.e., NDVI+NDWI+SAVI. The area under wheat crop has been obtained from each strata using crop mask of wheat developed by classifying satellite data using MXL classification, for developing weights to generate small area estimates at gram panchayat level. Estimates of crop yield were obtained based on Synthetic and Composite small area estimators and were compared with the usual estimator on the basis of %CV and %RE. The Synthetic and Composite estimators were found to more efficient than the usual estimator. Synthetic estimator is found to be more efficient than the Composite estimators based on percent relative efficiency (%RE) in most of the GPs. Based on %CV, among all the Synthetic estimates and Composite estimates, the estimates based on the stratification using the combination of NDVI+NDWI+SAVI exhibiting low %CV values. This study shows that more reliable estimates of crop yield can be obtained using SAE techniques and is an initial step in the direction of applying small area estimation techniques using RS and GIS as auxiliary variable which can be scalable at higher level future.

Theme 3: Statistical Modeling

Singular spectrum analysis (SSA) based decomposition models for agricultural price forecasting

Due to the biological nature of agricultural commodity production, forecasting their prices becomes a challenging task. To address this challenge and to predict agricultural prices accurately, decomposition techniques have been employed to decompose price data into distinct components. One such technique is Singular Spectrum Analysis (SSA), which offers a non-parametric approach with few data assumptions. In this study, SSA-based TDNN (SSA-

TDNN) model for agricultural price forecasting has been proposed. To evaluate the forecasting performance of the proposed SSA-TDNN model, we used the Potato price series and the forecasting performance of the SSA-TDNN model is compared with SSA-ARIMA, TDNN, SSA, and ARIMA models using evaluation criteria such as RMSE, MAPE, and MAE. After that, a hybrid model is introduced, combining Empirical Mode Decomposition (EMD) and SSA for improved forecasting. EMD decompose the initial time series into Intrinsic Mode Functions (IMFs), with the first IMF subjected to further SSA decomposition. Ultimately, all the decomposed subseries will undergo forecasting using TDNN. We also investigated different trend rates (TR) for SSA, and it is observed that TR values of 85% and 90% performed well in one and multi-step forecasting scenarios. At last, we extended the application of SSA for multivariate agricultural price series. Accordingly, we proposed a hybrid model by combining Multivariate Singular Spectrum Analysis (MSSA) and Multivariate GARCH (MGARCH) models. For this, MSSA is first employed on the multivariate agricultural price series and obtained the residuals. After testing the MARCH effects through the MARCH LM test, we modelled the residuals using the DDC GARCH model. We assessed different window lengths (*L*) and combined MSSA-MGARCH model consistently outperformed separate MSSA and SSA models, with 50% of *L*. This study showcases decomposition techniques' effectiveness and application in enhancing agricultural price forecasting accuracy and interrelationship analysis.

A study on wavelet-based nonlinear time series models for capturing volatility in agriculture

This study explores the use of wavelet-based models for capturing volatility in the agricultural domain. It develops and evaluates wavelet-based artificial neural network (ANN) and support vector regression (SVR) models to improve the accuracy of capturing volatility in agriculture. The research discusses traditional statistical methods and newer approaches utilizing wavelet-based and complete ensemble empirical mode decomposition with adaptive noise (CEEMDAN) methods. It also explores the potential of artificial intelligence and machine learning algorithms, including ANN and SVR. The study prepares the data by ensuring its suitability for modeling through tests for stationarity, normality, non-linearity, and autoregressive conditional heteroscedasticity-Lagrange multiplier (ARCH-LM). It employs feature selection using multivariate adaptive regression splines (MARS) before fitting the wavelet and CEEMDAN decomposed subseries into ANN and SVR models. To optimize the combination of predicted subseries and improve the final prediction of the original series, optimization technique such as particle swarm optimization (PSO) is employed. The proposed wavelet-based models are evaluated using different error functions and model confidence set (MCS)-based tests to assess their accuracy in capturing volatility. The simulation study, utilizing Monte Carlo technique, provides insights into the relationship between degree of volatility and the optimal filter-level combination. To facilitate practical implementation and enhance reproducibility, three R packages have been developed: 'WaveletML', 'CEEMDANML', and 'WaveletMLbestFL'. The developed models demonstrated the effectiveness in capturing underlying patterns, nonlinear relationships and precisely representing volatility. Feature selection technique like MARS and optimization technique like PSO further enhance the accuracy of volatility capture. The findings also emphasize the importance of selecting appropriate wavelet filters and levels of decomposition based on dataset characteristics and provide a more objective and generalized approach to use the technique. The availability of the developed R packages facilitates wavelet and CEEMDAN-based analysis in various domains, supporting decision-making in the agriculture sector and promoting sustainable practices.

Study of time series models for non-linear intervention effects

Time series data is the sequence of observations collected for a variable for an equal interval of times. Any sudden man-made or natural event which significantly affects the behaviour of time series is known as an intervention. In this study, the ban on blending in Mustard has been taken as an intervention effect. The Ban on the blending of mustard oil for the production of Multi-Sourced Edible Vegetable Oils (MSEVOs) come into force in October 2020 by the Food Safety and Standards Authority of India (FSSAI). In the past, researchers attempted to study the effect of intervention in a time series with the help of time series models like ARIMA-X (Autoregressive Integrated Moving Average with Exogenous Variable) and ANN-X (Artificial Neural Network with Exogenous Variable), where the exogenous variable was the linear function like the step function, ramp function or their combination. In this study, a new algorithm has been proposed to study the time series with intervention with the help of ARIMAX and ANNX where the exogenous variable is a non-linear model rather than the linear function. Also, this is the first attempt made on the intervention of a ban on blending Mustard. Our proposed model has been developed by fitting the ARIMA /ANN at the pre-intervention period and fitting the non-linear model at the residual of the ARIMA/ANN forecast for the post-intervention period. By combining these two results our proposed model has been developed. Three major Mustard producing districts of Rajasthan namely Alwar, Tonk and Sriganganagar have been considered to study the effectiveness of the proposed model. In all the selected markets Hoerl model fits best to the residual. Our proposed models ARIMAX and ANNX both perform better than traditional models. Comparison study has been made based on MAPE (Mean Absolute Parentage Error) and MSE (Mean Squared Error).

Modeling agricultural price volatility using Garch-Itô models

Time series modeling and forecasting have gathered increased attention in recent years due to the necessity of improving prediction accuracy, especially in volatile environments. Due to the inherent volatility of agricultural commodities, prices are quite unpredictable. Historical data that is classified into high-frequency and low-frequency data is used in volatility modeling. Although the GARCH model is frequently used to model volatility, it is not particularly efficient at capturing high-frequency characteristics. To overcome this limitation, the Unified GARCH-Itô model incorporates both characteristics. However, it struggles to accurately capture and model jump variations in volatility, leading to the development of the Realized GARCH-Itô model. This model combines both characteristics as well as jump variations to reflect volatility dynamics more realistically. This research investigates the application of these models in weekly price series data for onions across several marketplaces. It has been found that jump variations improve the GARCH-Itô models' efficiency. Conventional methods of determining jump points frequently result in fewer jumps or none at all. In order to improve computation robustness, this research presents an approach that uses the Discrete Wavelet Transform to identify the ideal number of jump points. The algorithm's steps are explained in detail, showing how well it works to overcome the drawbacks of earlier jump point computation methods. The results indicate that the GARCH-Itô model with the proposed algorithm performs better than other conventional models in assessing volatility in agricultural price data. This study makes a substantial contribution to increasing the precision of volatility modeling and forecasting in the agricultural commodities market. The combination of the novel jump point calculation technique with the Realized GARCH-Itô model offers a more thorough and dependable method for capturing the complex dynamics of agricultural commodity pricing. Consequently, this improves understanding and forecasting of market behaviors marked by inherent volatility and jump fluctuations.

A study on EXPAR and EXPARMA models to capture cyclical nature of the data

When modelling real-world processes where data is collected at successive time intervals and exhibits behaviour like aperiodic cycles with variable peaks and troughs, non-linear time-series models are crucial. A major drawback of standard time-series models is that if fluctuations are not synchronous with calendar, they are often attributed to random error and hence omitted by the models. However, repeating patterns may not always be seasonal. Such is the case with data containing significant cyclical behavious. Disregarding the standard autoregressive integrated moving average models, two families of models which have previously been used in literature and show considerable promise for capturing the cyclical nature of data are the Exponential Autoregressive and Exponential Autoregressive Moving Average models, where the former has been devised by adding an exponential term to each lag of the commonly used autoregressive model and the latter is a simple modification of the former in the sense that it also contains the error terms in a similar fashion. This study offers a straightforward method for estimating the parameters of these aforementioned models, which can be significantly higher in number than the standard models, though a minimization algorithm being applied on the residual sum of squares. Further, codes have been developed and distributed for implementing the algorithm in R, which have also been utilized for analyzing 8 datasets in this study. To test the applicability of the developed codes, a simulated EXPARMA(2,2) process has been used. Once the codes were validated; fitting was done on real-world data and the fits were compared with ARIMA model on the basis of various accuracy measures. One of the datasets was also split into training and testing sets to demonstrate the superiority of the models under study in forecasting the cycles for out-ofsample observations.

Theme 4: Statistical Genetics

Statistical model based prediction of discrete and continuous trait response in evolutionarily distant species using genome wide variants

Genomic Selection (GS) is a cutting-edge approach with transformative potential in plant and animal sciences. The primary goal of genomic selection is to enhance prediction accuracy, enable more precise forecast of performance or risk, etc. A main challenge in GS is to predict the Genomic Estimated Breeding Values (GEBV) of individuals with high accuracy for selection in breeding. Therefore, a study on “Statistical model based prediction of discrete and continuous trait response in evolutionarily distant species using genome-wide variants,” has been considered to achieve the objectives: (i) to identify suitable combination(s) of variable selection and GS model(s) for prediction of discrete and continuous trait responses through simulated data, (ii) to identify genome wide significant variants and their interactions to develop GS model for breeding value prediction, and (iii) to develop GS model for prediction of multi-trait mixture response. The investigation explores interactions between feature selection techniques and various GS models, including elasticnet, LARS, random forest, support vector machine-recursive feature elimination, and without feature selection. These are combined with eleven GS models categorized under BLUP-based, Bayesian, and machine learning approaches. The study considers different sample sizes, marker densities, heritability levels, and addresses challenges such as additive x additive interaction effects and multi-trait-mixture response predictions. Results indicate that integrating feature selection methods with GS models consistently outperforms using GS models alone. Notably, the combination of LARS feature selection and SVM-lin GS model demonstrates high prediction. In the presence of additive x additive interaction effects, GS models like RKHS and EGBLUP, combined with LARS feature selection, show higher prediction accuracy. Additionally, two different encoding schemes; (a) level encoding, and (b) multiple correspondence analysis were considered for multi-trait-mixture response and the BayesA multi-trait GS model shows higher prediction accuracy. These findings contribute to advancing genomics, facilitating more informed and precise predictions in breeding programs.

List of contributing students and Chairperson of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D	Title of the thesis	Chairperson	Institute
1.	Akarsh Singh (21599)	M.Sc.	Geographically weighted logistic regression based model-calibration estimator of finite population proportion	Dr. Ankur Biswas	*ICAR-IASRI, New Delhi
2.	Saikath Das (21600)	M.Sc.	A study on EXPAR and EXPARMA models to capture cyclical nature of the data	Dr. Bishal Gurang	*ICAR-IASRI, New Delhi
3.	Surya Prakash Tripathi (21601)	M.Sc.	To develop a two auxiliary calibration estimator of the population total under two stage sampling design when the variance function of the study variable is known	Dr. Kaustav Aditya	*ICAR-IASRI, New Delhi
4.	Rakesh Chhalotre (21602)	M.Sc.	Algorithmic approach for construction of uniform designs	Dr. Rajender Parsad	*ICAR-IASRI, New Delhi
5.	Subhankar Biswas (21603)	M.Sc.	Study of time series models for non-linear intervention effects	Dr. Amrit Kumar Paul	*ICAR-IASRI, New Delhi
6.	Banavath Samuel Naik (21604)	M.Sc.	Estimation of crop yield at gram panchayat level using remote sensing and small area estimation techniques	Dr. Prachi Misra Sahoo	*ICAR-IASRI, New Delhi
7.	Sbhradip Roy (21605)	M.Sc.	Modeling agricultural price volatility using Garch-Itô models	Dr. Ranjit Kumar Paul	*ICAR-IASRI, New Delhi
8.	Ashish Gupta (21606)	M.Sc.	A study on cyclic minimal balanced crossover designs	Dr. B.N. Mandal	*ICAR-IASRI, New Delhi
9.	Subhrajit Satpathy (10766)	Ph.D.	Statistical model based prediction of discrete and continuous trait response in evolutionarily distant species using genome wide variants	Dr. A.R. Rao	*ICAR-IASRI, New Delhi
10.	Ashis Ranjan Udgata (10975)	Ph.D.	Development of geographically weighted regression estimator for multi-collinear survey data	Dr. Anil Rai	*ICAR-IASRI, New Delhi
11.	Ankita Verma (11439)	Ph.D.	On some aspects of asymmetrical response surface designs	Dr. Seema Jaggi	*ICAR-IASRI, New Delhi
12.	Vinayaka (11442)	Ph.D.	PBIB designs based on higher association schemes and their applications	Dr. Rajender Parsad	*ICAR-IASRI, New Delhi
13.	Prabhat Kumar (11443)	Ph.D.	Singular spectrum analysis (SSA) based decomposition models for agricultural price forecasting	Dr. Girish Kumar Jha	*ICAR-IASRI, New Delhi
14.	Sandip Garai (11710)	Ph.D.	A study on wavelet-based nonlinear time series models for capturing volatility in agriculture	Dr. Ranjit Kumar Paul	*ICAR-IASRI, New Delhi
15.	Nehatai Wamanrao Agashe (11713)	Ph.D.	Experimental designs involving doubly nested blocking factors	Dr. Cini Varghese	*ICAR-IASRI, New Delhi

*Sister Institute

BIOINFORMATICS

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Prof. Girish Kumar Jha

The Division conducts post graduate teaching and in-service courses in Bioinformatics for human resource development. Division is conducting M.Sc. and Ph.D. programmes in Bioinformatics in collaboration with the Graduate School of Indian Agricultural Research Institute (IARI), New Delhi which has the status of a Deemed University. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Whole Genome/ Proteome/Metagenome Analysis

Discovery of molecular markers and development of database for rice bean

Ricebean (V. umbellata) is a valuable annual legume cultivated during the Kharif season, primarily in Northern India, especially in Uttarakhand and Assam. Despite its designation as a minor legume, Ricebeans play a crucial role in enhancing crop diversity, serving as an intercrop with maize and sorghum to optimize land use. The seeds, rich in protein and essential nutrients, contribute significantly to the nutritional needs of communities, particularly in regions where protein-rich food sources are essential. Out of 511010 transcripts, there are a total of 61905 SSRs, 79359 Primers for those sequences and 172749 amplicons. Dinucleotide repeats were predominant with an absolute proportion of 76.5%, followed by trinucleotides (20.8%). Out of the dinucleotide motif, AT accounted for 17.5%, followed by TA (16.9%) and others. The group motifs AT/TA accounted for 17.5% of the total, followed by TA/AT (16.9%). The 10-bp-long SSR motif accounted for 33.1%, followed by the 15-bp-long SSR motif (12.3%). A total of 196222 SNPs were identified, and the highest quality was 999. There are total of 196221 SNPs present in the Ricebean leaf and seed transcriptome. The present study introduces the first whole genome- based molecular marker database for Ricebean, known as RbMmDb, which includes data on SSRs, primers, amplicons, and SNPs. The database, accessible online and developed using a three-tier architecture, provides motif-wise SSR and location-wise SNP information, offering a valuable resource for researchers and the public interested in Ricebean genetics and cultivation.

Comparative genomic studies for domestication related traits in Vigna species

In the realm of plant domestication, the transition from nomadic lifestyles to settled agricultural communities is intricately linked to evolutionary changes. While many crop species have undergone domestication, some, like the Vigna species (cowpea, mung bean, adzuki bean, and rice bean), still harbor wild traits such as pod shattering and photo-period sensitivity, limiting their cultivation and causing yield loss. To unravel the genetic basis of these traits in Vigna, a comparative genomic study was undertaken. The research identified candidate orthologs and gene families related to shattering and photoperiod response traits in Vigna through comparative analysis and synteny studies. Cis-regulatory element enrichment analysis shed light on the conservation of regulatory elements across crop plants. For overcoming shattering and photosensitivity, specific genes were proposed as targets. For instance, VungMSL23.1 in cowpea, VangMSL23.1 in adzuki bean, VumbMSL23.1 in rice bean, and VradMSL12 in mung bean were suggested for non-shattering traits. In the context of photoperiod sensitivity, five groups of potential genes were identified across the four Vigna crops. Genome editing tools were proposed to be applied to these target genes to gain insights into their role in non-shattering and photo-insensitive phenotypes, thus accelerating the domestication process. To facilitate further research and access to the generated data, a database was developed. This comprehensive resource contains detailed information about genes related to shattering/non-shattering and photoperiod response traits in Vigna species. Additionally, a novel cis-regulatory enrichment analysis tool tailored for the Vigna genomic background was created. The database and tool are accessible through http://www.nbpgr.ernet.in:9093/, providing a valuable platform for researchers and enthusiasts in the field of crop improvement and domestication.

Development of genome-phenome browser for rice cultivars

The integration of advanced bioinformatics tools has played a pivotal role in deciphering the intricate biological complexities of Rice, enabling researchers worldwide to deepen their understanding of this vital crop. As the pursuit to unravel the biology of Rice continues, there is a pressing need to extract biological experimental information more accurately and precisely. This study acknowledges this necessity and takes up the task of conducting a comprehensive analysis of functionally validated and characterized rice genes, which exert significant effects on the phenotypes of this staple grain. valuable information on these genes has been meticulously gathered and categorized for further annotation. The compilation of phenotypes caused by these genes has been instrumental in creating a robust and valuable database. Leveraging the power of MySQL and extending the capabilities of GBrowse genome browser, a state-of-the-art Genome-phenome browser has been developed. This browser serves as a comprehensive repository, facilitating easy access to genotype and phenotype information of rice genes that have undergone functional characterization during the course of this study. By harnessing the potential of this genome-phenome browser, researchers can now dive into a wealth of information available across literature, enabling them to identify and explore genes responsible for influencing a diverse range of morphological, physiological, and resistance or tolerance traits in Rice. The detailed analysis offered by this resource also extends to the annotation of genes that have undergone functional characterization, contributing to a deeper understanding of their roles and implications in Rice breeding efforts. Ultimately, this research is poised to significantly impact the realm of Rice breeding and crop improvement. By shedding light on how these functionally characterized genes influence various traits that are of utmost importance to Rice cultivation, this study will guide and inform breeding strategies aimed at enhancing crop yield, disease resistance, and overall resilience in the face of changing environmental conditions.

Theme 2: Artificial Intelligence/ Machine Learning/Statistical Techniques in Bioinformatics

A semi-supervised approach for binning of metagenomics data

Microorganisms, diverse in their habitats and characteristics, have been traditionally studied through culture-based methods, limiting our understanding of microbial life. Metagenomics, a culture-independent approach, has revolutionized microbial research by directly analyzing genetic material from environmental samples. This enables the comprehensive study of entire microbial communities, shedding light on genetic diversity, functional potential, and ecological interactions. Despite its power, metagenomic data analysis faces challenges, particularly in clustering and assembling genomes from the multitude of organisms present. In this study, a novel approach is introduced, leveraging deep learning for clustering metagenomic data using the Kmeans algorithm. Recognizing the need for more robust methods in binning, the study explores the use of single-copy phylogenetic marker genes for accurate delineation of prokaryotic species. The research conducted a comprehensive investigation on a 10s metagenome dataset, employing a semi-supervised clustering approach. The process involved reducing the high-dimension feature matrix to 512 dimensions using autoencoder, followed by clustering and analysis using marker genes data identified in the contigs. The K-Means clustering phase revealed 8 clusters with a rand index of 0.85 and an F1 score of 0.61. Subsequent correction of clusters increased the count to 10 clusters, significantly enhancing clustering quality with a rand index of 0.68 and an overall accuracy of 0.62. The study emphasizes the importance of rigorous cluster correction in metagenomic analysis, showcasing its impact on precision and the significance of final cluster outcomes. By combining deep learning, single-copy phylogenetic marker genes, and cluster correction, this study contributes to the refinement of metagenomic data analysis, offering a more accurate and insightful understanding of microbial communities and their dynamics.

Web tool for CRISPR/Cas9 off target prediction in plants

Gene editing allows us to modify organism at genome level enabling us to control their phenotypic traits. CRISPR-Cas9 is one such technology which has surpassed all the existing technology for gene editing. It is a RNA mediated nuclease genome editing system. Its mechanism replicates naturally occurring immune defense system of bacteria but same technology can be adopted to modify eukaryotic gene as well. However, off-target cleavage is one of its major challenges preventing its application in real world because of its detrimental effect on the target organism. Off-target effects can be reduced by designing a suitable and exactly precise gRNA but for that complete data on off-target phenomena is needed. Several techniques have been developed to predict off-target in CRISPR-Cas9 like in-vivo, in-vitro and in-silico techniques. But due to cost and time factors in-vivo and in-vitro cannot be performed all the times. In in-silico mode of off-target predictions data obtained from previously conducted in-vivo and in-vitro techniques of off-target prediction are used to study statistical and mathematical relations between them, then using this data and their relations, different insilico tools have been developed such as web tools for off-target predictions, etc. In recent past tools developed based on Artificial Intelligence (Machine learning and Deep learning) have become more popular. They have over shadowed the tools based on traditional alignment approach in terms of accuracy in predicting CRISPR-Cas9 off-targets. Recently plant based, machine learning model were developed by Das et al., 2023 and deep learning models were developed by Chandini et al., 2022. Using these two developed models IASRI-CRISPR (i-CRISPR) have been developed to predict off-targets in plants. The current study showed how machine learning and deep learning approach might be better used for off-target prediction in the CRISPR-Cas9 system of gene editing and genome editing, exclusively for plant genomes.

Development of tool for selective sweep analysis using artificial intelligence

Natural selection is the key process of evolution. Natural selection especially directional selection plays pivotal role behind genetic hitchhiking mechanism which induces the occurrence of selective sweep. Selective sweep is a biological phenomenon which increases the frequency of the alleles closely linked to the beneficial alleles and non-linked alleles shows decrement in their frequency. From evolutionary aspects to adaptation of newly developed varieties in the environment selective sweep plays crucial role and so analysis of selective sweep has wide importance in evolutionary and population genomics. But most of the existing tools do not provide satisfactory results due to lack of applied approaches as well as lack of implementation of advanced technologies. So, in this research work artificial intelligencebased machine learning algorithms have been implemented as classifier starting with simulated population genomic dataset. Among all machine learning classifiers Random Forest has performed best by ranking through TOPSIS analysis based on evaluation measures like Accuracy, Precision, Recall, Sensitivity etc. and it has performed better than the already existing tools like Sweep Finder, Omega Plus, SweeD, diploS/HIC also. Utilizing this as best model an interactive selective sweep analysis tool has been developed namely “Sweep Discovery Tool” and it had been deployed to the hosting platform “http://cabgrid.res.in:5599/”. This tool has the ability to predict selective sweep status among three classes viz. Hard Selective Sweep, Soft Selective Sweep and No Selective Sweep through VCF files as input and this is a user-friendly tool where user can choose the chromosome and region of interest in the specific chromosome to obtain the selective sweep status. The Sweep Discovery Tool will enlighten a new pavement of selective sweep analysis as well as genomic research with optimistic future prospects.

Novel and efficient pipeline for metagenomics binning

Metagenomics, an essential aspect of microorganism examination, faces the challenge of reconstructing distinct organisms’ genetic makeup from fragmented sequences obtained through shotgun sequencing. Genome assembly, a key step in this process, encounters difficulties due to the mingling of genomic reads from various microorganisms. The abundance and interweaving of these reads necessitate effective binning techniques for segregating and reassembling genomes. Binning, clustering techniques like k-means, k-medoids, Hidden Markov Model (HMM), and hierarchical clustering have been widely employed, but each has its limitations. This study introduces a novel approach to metagenomic binning by constructing a frequency table of motifs or segments through local alignment with gaps. The segments, crucially, should not overlap during alignment. K-means clustering is then applied to categorize contigs based on these segments and motifs. Notably, this motif-based binning approach demonstrates a Rand Index tending towards 1, indicating its effectiveness. It outperforms existing tools like MaxBin and MetaBat, showcasing its potential in metagenomic binning. The proposed approach opens avenues for further improvement. Advanced clustering methods, incorporation of GC content and tetra-nucleotide frequency, hold promise for enhancing performance. Beyond binning, the approach sheds light on mutation concepts and conserved regions, offering insights into evolutionary biology. This comprehensive methodology not only addresses current limitations in metagenomic binning but also provides a platform for future advancements and a deeper understanding of microbial evolution.

Development of an approach for identification of core microbiome

The “core microbiome” concept, crucial for understanding consistent microbial communities in specific hosts or environments, has been addressed in this study. While existing core identification methods have value, they come with limitations such as sampling bias and arbitrary cutoffs. To overcome these challenges, the study introduces an innovative approach and develops the “CoreMicrobiomeR” R package for implementation. Arabidopsis thaliana core root microbiome data was used for investigation. The proposed approach involves distinct phases, including filtering, normalization, core microbiome determination, diversity analysis, significance testing, and visualization. The unique aspect of designating the most abundant taxa as the core, based on total abundance, presents a straightforward yet effective strategy. Various filtering and normalization methods were explored, and the default top ten percent of total abundance was adopted to determine the core microbiome. F-test analysis was applied for significance testing, and both alpha and beta diversity measures were computed. The culmination of this study is the “CoreMicrobiomeR” R package, representing a significant advancement in microbial community analysis. The package offers adaptability by allowing customization of core inclusion thresholds. Incorporating diversity analysis and significance testing enhances its analytical capabilities, ensuring only relevant taxa are retained as part of the core microbiome. The statistical tests conducted by the package act as a supplementary validation step, establishing the authenticity of the identified core taxa. In essence, this research provides a comprehensive methodology for core microbiome identification, accompanied by a user-friendly package that empowers researchers in the field.

Development of database of genes and gene families responsible for nutritional traits in field crops

Nutritional insecurity is a major challenge in developing countries which are largely dependent on cereal based diets. Soil and plant scientists have accumulated much information on the concentration of minerals in the leaves of food crops. Nutritionally dense crops offer an inexpensive and sustainable solution to the problem of malnutrition. A comprehensive search strategy was a followed to obtain the genes responsible for nutritional traits in plants. The genes for mineral transportation, vitamin biosynthesis and essential amino acid biosynthesis were retrieved using advanced searches with gene ontology keyword for specific nutrients, plants, crops and their nutrient-related role in conjunction with the BOOLEANS like OR/AND), from 4 databases viz. GenBank, EnsemblPlants, Gramene, and UniProt. A total of no. of 7695 sequences for mineral transportation, 1480 sequences for vitamin biosynthesis and 2583 sequences for essential amino acid were obtained. This study was oriented towards the application and comparison of different machine learning techniques (namely, support vector machine, random forest, Naïve Bayes and K nearest neighbour) for development of classification models for nutritional trait (mineral transportation, vitamin biosynthesis and essential amino acid biosynthesis) related gene sequences in flowering plants. Firstly the machine learning techniques were applied for developing three binary classification models binary classification for mineral transportation, vitamin biosynthesis and essential amino acid biosynthesis genes. Afterwards, three multiclass classification models mineral transportation, vitamin biosynthesis and essential amino acid biosynthesis genes were developed using each of the four classifiers. 5-fold cross validation was performed to compare the performances four classifiers independently and the results suggested that Random forest, SVM and KNN performed best for both binary as well as multiclass classification. The performance of naïve Bayes was comparatively lower. Finally, a database nutritional trait (mineral transportation, vitamin biosynthesis and essential amino acid biosynthesis) related gene sequences in flowering plants has been developed.

Development of advanced learning based classification approach for fungal metagenomic data

Microorganisms are an inevitable part of the ecosystem playing various beneficial roles as well as harmful effects. Rapid advancement in NGS technologies has given rise to the new scientific field, "Metagenomics" for understanding the microbial community composition and functions directly from any environmental sample such as human gut, skin, soil, ocean, crop rhizosphere *etc*. Accurate binning and taxonomic annotation of raw metagenomic reads is an essential step before the subsequent functional analysis. Computational approaches, especially machine learning and deep learning algorithms, have been found efficient to classify prokayotic microorganisms from metagenomic datasets as compared to the reference-based method. However, identification of eukaryotic fungi species from metagenomic data is a highly challenging task. Internal Transcribed Spacer (ITS) region is the universal DNA marker for the taxonomic annotation of a majority of fungal species. In this present study, a convolutional neural network based approach, *CNN_Funbar* has been developed using UNITE+INSDC reference ITS datasets for classifying fungi ITS sequences at all the six taxonomic levels, *viz*., species, genus, family, order, class and phylum. The proposed *CNN_FunBar* models have produced > 93% average accuracy for classifying ITS sequences from balanced datasets with 500 sequences per category and 6-mer frequency features at all the taxonomic levels. Species and genus level *CNN_FunBar* models, *viz*., *Species_Model.h5* and *Genus_Model.h5* could identify 62 species and 41 genera from the simulated fungal metagenomic dataset with a classification accuracy of 91.93% and 95.16% respectively. *CNN_FunBar* has been found to outperform existing fungal taxonomy prediction tools (funbarRF, Mothur, RDP Classifier, and SINTAX) as well as competitive machine learning-based algorithms (SVM, KNN, Naive-Bayes, and Random Forest). A web application, *CNN_FunBar* has been developed for extracting oligonucleotide frequency features from input ITS sequences followed by their classification using proposed *CNN_FunBar* models at various taxonomic levels. The developed tool is freely available at https://github.com/ritwika1993/CNN_FunBar_ITS.

Development of computational approaches to understand plant-pathogen interactions

The investigation of protein-protein interactions (PPIs) in plant-pathogen systems is a complex and essential field to unravel the intricate molecular mechanisms underlying plant defense and pathogen virulence. Traditional experimental methods for identifying these interactions are time-consuming, prompting the emergence of computational techniques as valuable complements. In this study, the accuracy of established computational approaches, particularly the interolog-based method relying on similarity searches, was investigated. Due to the low sensitivity of the interolog technique, a machine learning-based ensemble model was employed to construct a multi-species plant-pathogen PPI predictor. This model incorporated diverse sequence encodings and multiple learning algorithms, including Auto-covariance (AC), Conjoint Triad (CT), and Local Descriptor (LD) schemes. Evaluation metrics such as accuracy, sensitivity, precision, recall, and F1-score guided the selection of these encoding schemes. AC and CT exhibited high accuracy with Support Vector Machine, while LD performed optimally with Random Forest. Combining the predictions of these individual models yielded an ensemble model with enhanced accuracy (~97%). This newly developed ensemble model was compared with existing tools for PPI prediction using an independent test dataset. The result of the comparative assessment exhibited the promising potential of the classifier in this domain. Hence, the developed model is proposed as an efficient tool for the prediction of multispecies plant-pathogen PPIs. To illustrate its utility, the model was applied to predict PPIs involved in wheat blast, a severe fungal disease threatening global wheat production. The study revealed the involvement of wheat proteins in energy production mechanisms in response to fungal attacks, while fungal effector proteins supported pathogen growth. To enhance accessibility, a web-based prediction server named PlantPathoPPI (freely accessible at http://login1.cabgrid.res.in:5080/) was developed, allowing diverse end-users to benefit from the proposed model. Taken together, PlantPathoPPI can serve as a valuable tool accelerate the investigation of plant-pathogen interactions.

Development of advanced learning model for prediction of epigenetic modifications in crops

In the context of the vast DNA sequencing data available today, there is a pressing need for a robust and precise DNA methylation prediction tool to facilitate the study of epigenetic behaviour in crop plants. The prevalent epigenetic modifications, N6-methyladenine (6mA) and 5-methylcytosine (5mC), play crucial roles in various biological processes. Traditional in vitro methods, though highly accurate in detecting epigenetic alterations, are resource-intensive and time-consuming. Overcoming these challenges, this study introduces an ensemble-based machine learning model for predicting 6mA and 5mC sites in crops. The novel machine learning framework integrates four techniques: ensemble machine learning, a hybrid approach for feature selection, incorporation of features like Average Mutual Information Profile (AMIP), and the use of bootstrap samples. Five distinct feature sets—Di-Nucleotide Frequency, GC content, AMIP, Mono-nucleotide Binary Encoding, and Nucleotide Chemical Properties—are chosen for the vectorization of DNA sequences. Nine machine learning models, including Support Vector Machine, Random Forest, k-Nearest Neighbour, Artificial Neural Network, Multiple Logistic Regression, Decision Tree, Naïve Bayes, AdaBoost, and Gradient Boosting, along with two deep learning models, Long Short Term Memory (LSTM) and Bidirectional-LSTM, are tested with relevant features extracted through the feature selection module. The top three performing models are selected to form a robust ensemble model named EpiSemble, designed for predicting 6mA and 5mC methylation sites. EpiSemble demonstrates significant accuracy improvements over existing models for various datasets related to crops. Notably, the model introduces the novel feature AMIP, integrates feature selection modules, incorporates bootstrapping of samples, and utilizes ensemble techniques to enhance the accuracy of predicting 6mA sites in plants. The developed R package, EpiSemble, is the first of its kind for predicting epigenetic sites in crop plant genomes, providing valuable support to plant researchers. The package is accessible at https://cran.rproject.org/web/packages/EpiSemble/index.html.

Deep learning based algorithm for identification of copy number variation

Copy number variations (CNVs) are a significant class of variants having role in the etiology of numerous disease manifestations. It is still challenging to find CNVs in genomic data, and the approaches used currently have an unacceptably high false positive rate. Before moving to downstream analysis or experimental validation, interventions of human specialists to carefully check the original CNV calls for weeding out false positives is required. Here, we present a deep learning-based tool designed uptake this human intervention while validating CNV calls, with emphasis on the calls made by PennCNV tool, which is one of the most reliable CNV callers reported in literature. An ensemble model was developed that outperformed traditional machine learning techniques, with improved accuracy of 0.9807 in CNV calls and an ideal area under the receiver operating characteristic curve of 0.9985. The model's improvement resulted in reducing the false positives and instances when the CNV association results couldn't be replicated. This study also presents a CNV prediction server (http://backlin.cabgrid.res.in/eqcnvdb/index.php) based on ensemble deep learning technique with minimum false discovery rate (FDR) which can be used in other related species. This work is the first genome-wide, chromosome-wise, breedwise CNV Atlas of Indian Equine breeds, EqCNVDb, available at http://backlin.cabgrid.res.in/eqcnvdb/index.php. The output of this study can be further evaluated for horse breed signature, evolutionary studies including adaptive response of equine germplasm against biotic and abiotic stresses. Keywords: copy number variation, equine, PennCNV, machine learning, deep learning, prediction server, EqCNVDb.

Computational intelligence in the discovery of natural products from agriculturally important metagenomics data

This study delves into the transformative realm of metagenomics, leveraging high-throughput sequencing technologies to explore the vast microbial diversity crucial to biosphere processes and agricultural challenges. Focusing on agriculturally significant metagenomics, the research employs direct DNA sequencing from soil, plants, and livestock, revealing hidden genetic elements. The challenge of reconstructing individual genomes from complex DNA mixtures is addressed through innovative binning strategies, with Deep Embedded Clustering (DEC) and Variational Autoencoders (VAE) outperforming existing methods. The study emphasizes the pivotal role of binning in laying the foundation for identifying Natural Products (NPs) by clustering genomes or taxonomically related groups. NPs, organic compounds synthesized by living organisms, hold immense potential in fields ranging from medicine to agriculture. The research introduces a novel approach to NP identification, integrating physicochemical properties and Natural Language Processing (NLP) techniques like CountVec, TFIDF, and Word2Vec. The study targets five NP classes, including Polyketide synthase (PKS), Non-Ribosomal Polyketide Synthase (NRPS), Ribosomally synthesized and post-translationally modified Peptides (RiPP), Terpenes, and Hybrid PKS-NRPS. In the realm of machine learning, the study trains and tests nine models on a comprehensive feature matrix, with Logistic Regression (LR) employing TFIDF and SMOTE emerging as the most potent. The culmination of these methodologies results in an AI-based tool called NaturePred, offering NP class prediction and protein physicochemical property calculation. Applied to an Agriculturally Important Metagenomics dataset from Mustard soil Rhizosphere, the study unveils a rich presence of over 40% RiPPs, indicating robust plant-microbiome interactions and soil health. By amalgamating innovative binning strategies, advanced NLP techniques, and machine learning, this study lays a robust foundation for future advancements in agriculture and microbial research. The proposed AI tool, NaturePred, holds promise in unlocking untapped agricultural potential, propelling microbial research into uncharted territories and uncovering hidden treasures within microbial genomes.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Abhik Sarkar (21621)	M.Sc.	Development of tool for selective sweep analysis using artificial intelligence	Dr. D.C. Mishra	*ICAR-IASRI, New Delhii
2.	Ravi (21622)	M.Sc.	Discovery of molecular markers and development of database for rice bean	Dr. Monendra Grover	*ICAR-IASRI, New Delhi
3.	Deeksha P.M. (21623)	M.Sc.	A semi-supervised approach for binning of metagenomics data	Dr. S.B. Lal	*ICAR-IASRI, New Delhi
4.	Abhishek Anand (21624)	M.Sc.	Web tool for CRISPR/Cas9 off target prediction in plants	Sh. Sanjeev Kumar	*ICAR-IASRI, New Delhi
5.	Subham Ghosh (21625)	M.Sc.	Novel and efficient pipeline for metagenomics binning	Dr. U.B. Angadi	*ICAR-IASRI, New Delhi
6.	Sorna A.M. (21626)	M.Sc.	Development of an approach for identification of core microbiome	Dr. Md. Sameer Farooqi	*ICAR-IASRI, New Delhi
7.	Soumya Sharma (10778)	Ph.D.	Development of database of genes and gene families responsible for nutritional traits in field crops	Dr. Sunil Archak	*ICAR-IASRI, New Delhi
8.	Anubhav Roy (10781)	Ph.D.	Development of genome-phenome browser for rice cultivars	Dr. Sudeep Marwaha	*ICAR-IASRI, New Delhi
9.	Ritwika Das (11005)	Ph.D.	Development of advanced learning based classification approach for fungal metagenomic data	Dr. Anil Rai	*ICAR-IASRI, New Delhi
10.	Sneha Murmu (11006)	Ph.D.	Development of computational approaches to understand plant-pathogen interactions	Dr. Sunil Archak	*ICAR-IASRI, New Delhi
11.	Shweta Kumari (11007)	Ph.D.	Comparative genomic studies for domestication related traits in Vigna species	Dr. Sunil Archak	*ICAR-IASRI, New Delhi
12.	Dipro Sinha (11227)	Ph.D.	Development of advanced learning model for prediction of epigenetic modifications in crops	Dr. Sunil Archak	*ICAR-IASRI, New Delhi
13.	Nitesh Kumar Sharma (11466)	Ph.D.	Deep learning based algorithm for identification of copy number variation	Dr. Sarika	*ICAR-IASRI, New Delhi
14.	Sharanbasappa (11739)	Ph.D.	Computational intelligence in the discovery of natural products from agriculturally important metagenomics data	Dr. D.C. Mishra	*ICAR-IASRI, New Delhi

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Computer Application

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Prof. Alka Arora

The Division of Computer Application at ICAR-Indian Agricultural Statistics Research Institute has the mandates to undertake research and application software development using emerging Information Technologies in Agriculture and allied sectors; to conduct post-graduate and ad-hoc training courses in Computer applications; to provide advisory, IT infrastructure services and consultancy in the field of Agricultural Informatics. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Decision Support System/ Machine Learning/Web-Mobile Based Application in Agriculture

Development of web based bibliometric analysis tool for agriculture

The global adoption of digital technology has accelerated the daily data gathering, which has an impact on academic research through rising paper submissions to online databases. Scholars, organizations, and politicians must prioritize identifying and assessing influential research. To manage extensive scholarly data, we employ a technique that originated in library sciences but has now carved out its own distinct place in the realm of research: bibliometric analysis. Bibliometric analysis involves examining and assessing scientific literature through the extraction of vital information, primarily emphasizing quantitative evaluation of publications, citations, and co-authorship networks. This approach aims to pinpoint emerging research domains and trends within articles, while also evaluating journal performance, studying collaboration patterns among research components, and uncovering gaps within the chosen subject domain. However, bibliometric analysis specific to agricultural studies lacks comprehensive coverage. Many major scholarly databases do not encompass most Indian agriculture journals, and a performance indicator that incorporates The National Academy of Agricultural Sciences (NAAS) journal score is absent.In this study, we developed the Author Performance Indicator (AuthorPerIndic), a score that evaluates an ICAR scientist's productivity based on journal NAAS scores and their authorship. Additionally, we created a novel web tool using Django framework facilitating bibliometric analysis at the author level for ICAR-IASRI scientists. Data is sourced from the ICAR-initiated KRISHI publication repository and processed to meet analysis requirements. The tool employs AuthorPerIndic for performance analysis alongside collaboration and keyword analyses. This tool provides researchers with a systematic way for tracking and evaluating their progress, as well as a chronological picture of their accomplishments. A culture of increasing publication in high-impact journals is also fostered by the tool.

Decision support system for energy budgeting of crop production

The Decision Support System for Energy Budgeting of Crop Production is a comprehensive solution aimed at optimizing energy budgeting in crop production. Leveraging Android Studio, Java programming, and the

Android SDK, the app empowers developers to create a user-friendly interface for various stakeholders, including agronomists, farmers, policymakers, researchers, and extension workers. Key features include intuitive UIs, cropping pattern comparison and recommendation, use of advanced energy budgeting algorithms, efficient data management and graphical data visualization. By facilitating informed decisions through data-driven insights, this system contributes to sustainable and efficient agricultural practices. The Decision Support System stands as a transformative tool that modernizes agricultural practices, making them more sustainable, data-informed, and resource-efficient. The App is a critical tool that aligns modern agricultural practices with the principles of sustainability, data-driven decision-making, and resource efficiency. It empowers agricultural professionals to navigate the intricacies of energy management, ultimately leading to more resilient, productive, and environmentally conscious farming practices.

Development of web application for feature selection and crop yield prediction of landscape diagnostic survey data using machine learning technique

Agriculture is considered to be the backbone of Indian economy. More than 70% of Indian population depends on agriculture for their livelihood. Crop yield prediction is of great importance to global food production.Policy makers rely on accurate predictions to make timely decision to strengthen food security. Farmers and growers can also make informed financial and management decisions depending on crop yield prediction. To address such importance, a web-based tool has been developed for feature selection and crop yield prediction of Landscape Diagnostic Survey data (under CSISA) for rice and wheat crop in Bihar and Eastern Uttar Pradesh. The web-based application has been developed using Flask framework written in Python. This application requires a .csv file from user as input and performs feature selection and crop yield prediction using Machine Learning techniques for that dataset. Methods such as Stepwise Regression, Random Forest Regression, Ridge Regression and LAASO have been used for feature selection and models viz. Multiple Linear Regression, Random Forest Regression, Ridge Regression and Support Vector Regression have been employed for crop yield prediction based on the features selected. The performance of the models was evaluated using statistical diagnostic measures and best model was identified for feature selection and yield prediction. In this work, for the chosen datasets, it was found that Random Forest Regression produced better prediction results compared to other models.

Development of mobile application for beneficial insects in crops

In modern agricultural practices, the significance of beneficial insects in promoting sustainable pest management and enhancing crop yields has gained widespread recognition. This research endeavours to address the need for an innovative approach to leverage technology for maximizing the beneficial insects' positive impact on agricultural ecosystems. The study presents to design and develop mobile application that facilitates in effective utilization and conserving beneficial insects within agricultural landscapes. The proposed mobile app serves as a comprehensive tool for extension professionals, progressive farmers, entomologists, and agriculture practitioners by enabling them to identify and protect these beneficial insect species relevant to specific crops and geographic regions. The development process involves discussion and collaboration with entomologists and extension professionals to ensure scientific accuracy and practicality of the collected information. The beneficial insects are categorized into various categories such as pollinators (honey bee, digger bee, carpenter bee, bumble bee, squash bee etc.), predators (ladybird beetle, crickets, damsel bug, lace wing etc.), parasitoid (tachnid fly, minute polyphagous wasp, *Encarsiaspp*, *Tetrastichussppetc.*), scavengers (dung beetle, carrion beetle, darkling beetle, fungus gnat), decomposers (termites, cockroach, carrion beetle) and soil builders (ants, wasp, beetle, cutworm) for these beneficial insects morphological appearance, special characters, behaviour, mechanism and interaction against pest are discussed. App testing is conducted to validate the app's effectiveness and user-friendliness through students of Graduate School, IARI. The anticipated outcomes of this research include the democratization of knowledge regarding beneficial insects, leading to improve pest management practices, reduced reliance on chemical pesticides, and enhanced ecological balance within agricultural ecosystems. By seamlessly integrating technological innovation with sustainable agriculture, this research signifies a crucial step towards harnessing the potential of beneficial insects for resilient and productive farming systems.

Development of mobile app for pest surveillance and management of tomato crop

PestSurv Tomato, an innovative mobile application designed and developed to revolutionize pest management in agriculture. This comprehensive mobile tool addresses the persistent challenges faced by farmers, particularly in the surveillance and management of pests that threaten crop productivity, food security, and environmental sustainability.The app's objectives, including the creation of a user-friendly interface for pest surveillance and the provision of real-time pest management advisories, have been successfully realized. PestSurv Tomato empowers farmers with the ability to independently conduct pest surveillance on their fields. This innovative approach ensures early detection of pest incidents, reducing crop damage, and financial losses. One of the app's most significant advantages lies in its ability to generate timely and customized pest management recommendations. By processing surveillance data instantly, PestSurv Tomato provides farmers with tailored guidance for pest control measures. This timely intervention is crucial in preventing extensive crop losses and reducing the need for aggressive control methods.The research emphasizes the significance of sustainable pest management, including integrated pest management (IPM), and underscores visual inspection as a cost-effective tool. This research delineates the critical role of mobile applications in revolutionizing pest surveillance and management in agriculture, ultimately contributing to improved crop health, higher yields, and enhanced food security. The research's objectives, focused on designing and developing a mobile application for pest surveillance and advisory, have been successfully achieved. PestSurv Tomato represents a significant advancement in empowering farmers to effectively manage pest-related challenges, bridging the gap between detection and response. This research serves as a testament to the transformative potential of technology in modern agriculture, offering a promising path towards sustainable and resilient farming practices.

Theme 2: Artificial Intelligence/Deep Learning/ Natural Language Processing/Machine Learning Application in Agriculture

Development of deep learning model for identification of major wheat diseases

Wheat is a main staple food crop globally and one significant factor that negatively impacts Wheat yield is fungal diseases such as rust.Wheat rusts, caused by pathogenic fungi, are responsible for substantial losses in Wheat production. One of the effective control methods is early automated disease identification based on the analysis of digital images, with the possibility of obtaining them in field conditions using mobile devices. Thus, thisthesis proposes a novel in-field automatic Wheat disease identification and severity stage estimation system based on Deep Learning architectures, which can be deployed on mobile devices to perform real-time diagnosis at farmer’s fields. An image dataset for three major fungal diseases of Wheat (stripe rust, leaf rust and stem rust) and healthy leaves were prepared from the experimental fields of ICAR-Indian Agricultural Research Institute, New Delhi and its regional centre at Madhya Pradesh, during 2019 to 2021. The image dataset is referred to as WheatRust21, consisting of 6556 images of healthy and diseased leaves from natural field conditions. An image repository is created for the systematic storage of images along with their corresponding metadata. A EfficientNet architecture-based model for Wheat disease identification is proposed for automatically detecting major Wheat rusts. Several classical CNN-based models were attempted such as VGG19, ResNet152, DenseNet169, InceptionNetV3, and MobileNetV2 for Wheat rust disease identification and obtained accuracy ranging from 91.2 to 97.8 per cent. To further improve accuracy, we experimented with eight variants of EfficientNet architecture and discovered that our fine-tuned EfficientNet B4 model achieved a testing accuracy of 99.35 per cent, a result that has not been reported in the literature so far to the best of our knowledge. Another disease severity stage estimation model for Wheat rusts is also proposed in this study. It utilizes EfficientNet architecture and convolutional block attention mechanism (CBAM) to classify disease symptoms into early, middle, and end stages based on their severity level. The proposed severity estimation model achieved an overall testing accuracy of 96.8 % and an average F1 score of 96.2 %. Lastly, the proposed models are deployed in a mobile application for facilitating the real-time image-based Wheat disease detection and severity level by farmers in the field.

Study of text mining approaches for topic discovery in agriculture

Organizing and exploring enormous amount of documents, papers and other text information is a challenging task for researchers and publishers. Researchers from different disciplines are conducting research and number of articles related to their domains are being published. The research articles related to agriculture are continuously being published in the form of research papers, popular articles, blogs, surveys, short stories etc. These possess useful information and this information can be processed to infer important valuable knowledge by applying text mining techniques. Topic discovery is the innovation towards extracting the underlying semantic structure from large collection of unstructured text. It is a convenient way to analyze unclassified text into topic clusters that can be utilized in classification of documents. Topic discovery can group words with similar meaning and distinguish between uses of words with multiple meaning. In this study, a novel approach was developed, for topic recognition based on Latent Dirichlet Allocation (LDA) technique with various combinations of text pre-processing methods. Agricultural text corpus was extracted from Google Scholar (https://scholar.google.com) and Krishi Portal (https://krishi.icar.gov.in) using customized search by using web scraping script for collection of required data. Three combinations of preprocessing methods were used, before training of the models for topic discovery and the models were evaluated on the performance metrics. The study demonstrated the effectiveness of the LDA topic model in clustering and finding similar documents. A novel approach was proposed, to determine the number of topics in a document, enabling users to organize and explore documents by topic for easier access. Additionally, a topic discovery model was developed. The results indicated that LDA successfully identified topics from agricultural research articles. The number and quality of topics were found to be influenced by the text pre-processing method. The relevance of the identified topics was further confirmed by domain experts. The study emphasized the impact of pre-processing on the number and quality of topics. These findings can be used to enhance the information retrieval mechanism by identifying topics in agricultural research articles and recommending related research articles to the researchers.

Natural language processing based interactive system for integrated pest management in rice and wheat

The agricultural sector faces significant challenges, with pest management being of paramount importance for sustaining crop productivity and ensuring global food security. This research focuses on addressing these challenges by harnessing the power of Natural Language Processing (NLP) to enhance Integrated Pest Management (IPM) in the context of rice and wheat crops. The study explores the integration of NLP techniques to facilitate communication between farmers and digital systems, enabling real-time access to vital information like pest management. Traditional methods, such as Kisan Call Centers (KCC), offer human-based advice but come with limitations. To overcome these limitations and provide an instant solution for pest management, the study aims to achieve three objectives: the establishment of a Named Entity Recognition (NER) pipeline for the KCC dataset, the development of a model for intent classification using machine learning techniques, and the creation of a response generation system for interactive query answering. To accomplish these goals, an extensive dataset of 3.6 million queries was collected for the UP State of India from 2017 to 2021 by developing a web scraping interface. For NER, the open-source library 'SpaCy' was utilized, and an algorithm for automatic annotation of text data was developed, resulting in a high-performing NER model. The intent classification model was created using an ensemble approach of naïve Bayes and decision tree algorithms and deep learning methods like LSTM and BiLSTM, achieving remarkable accuracy. Furthermore, an interactive response generation system was developed by integrating NER and intent models, offering contextually relevant responses for IPM-related queries. The results demonstrate the effectiveness of the proposed NLP-based system in providing prompt and accurate information for pest management in rice and wheat crops. By bridging the gap between information seekers and relevant knowledge, it empowers farmers, researchers, and agricultural experts with valuable insights, ultimately contributing to sustainable pest management practices and improved crop productivity.

List of contributing students and Chairpersons of their advisory committee

Sl. No	Name of the student & Roll No.	M.Sc./ Ph.D.	Title of the thesis	Chairperson	Institute
1.	Sakshi Rawat (21558)	M.Sc.	Development of web based bibliometric analysis tool for agriculture	Dr. K. K. Chaturvedi	*ICAR-IASRI, New Delhi
2.	RohitVanshraj (21628)	M.Sc.	Decision support system for energy budgeting of crop production	Dr. (Ms.) Shashi Dahiya	*ICAR-IASRI, New Delhi
3.	Sasikumaran S (21630)	M.Sc.	Development of web application for feature selection and crop yield prediction of landscape diagnostic survey data using machine learning technique	Dr. Soumen Pal	*ICAR-IASRI, New Delhi
4.	Bhavya Shree V (21746)	M.Sc.	Development of mobile application for beneficial insects in crops	Dr. K. K. Chaturvedi	*ICAR-IASRI, New Delhi
5.	GouravMaitra (21748)	M.Sc.	Development of mobile app for pest surveillance and management of tomato crop	Dr. Mohammad Samir Farooqi	*ICAR-IASRI, New Delhi
6.	Sapna Nigam (11008)	Ph.D.	Development of deep learning model for identification of major wheat diseases.	Dr. Rajni Jain	*ICAR-IASRI, New Delhi
7.	Lakshmi Sonkusale (11232)	Ph.D.	Study of text mining approaches for topic discovery in agriculture	Dr. K. K. Chaturvedi	*ICAR-IASRI, New Delhi
8.	Murari Kumar (11475)	Ph.D.	Natural language processing based interactive system for integrated pest management in rice and wheat	Dr. K. K. Chaturvedi	*ICAR-IASRI, New Delhi

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