TB-ICN: 366/2025

67 YEARS
THE GRADUATE SCHOOL
1958-2025

63rd Convocation

Significant Research Achievements of Post Graduate Students 2024

Presented by

Professors of The Graduate School

March 19-20, 2025

Convenor
Dr. Monika A. Joshi
Professor
Seed Science & Technology

Co-Convenor
Dr. Shruti Sethi
Principal Scientist
Food Science & Postharvest Technology

The Graduate School
ICAR-Indian Agricultural Research Institute
New Delhi - 110012

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Compiled and Edited by

Monika A. Joshi and Shruti Sethi (2025) Significant Research Achievements of Post Graduate Students (2024) Book of Abstracts; Presented by Professors of The Graduate School; March 19-20, 2025. pp 280.

Published by

Joint Director (Education) & Dean, ICAR-IARI on behalf of the **Director**, ICAR-Indian Agricultural Research Institute, New Delhi 110 012

Printed at

M. S. Printers, C-108/1 Back Side, Naraina Industrial Area, Phase-1, New Delhi-110028,
Tel.: 011-45104606, 7838075335, E-mail: msprinter1991@gmail.com

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School of Crop Protection

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Venue : A.P. Shinde Symposium Hall, NASC Complex, New Delhi
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Time : 14.00-15.30 h
Farewell to Degree Recipients in the Divisions

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March 17-22, 2025

67 YEARS
THE GRADUATE SCHOOL
1958-2025

Venue
AP Shinde Symposium Hall
NASC Complex, New Delhi
&
Bharat Ratna C. Subramaniam Auditorium
NASC Complex, New Delhi

ICAR

The Graduate School
ICAR-Indian Agricultural Research Institute
New Delhi - 110012

MONDAY, MARCH 17, 2025

Time : 09.00 - 17.30 h

Presentation of "Significant Post Graduate Students' Research" by M.Sc./M.Tech. students for "Merit Medals" and "NABARD-Professor VL Chopra Gold Medal & Best Student of the Year" awards

Chairman : Dr. B.M. Prasanna, Distinguished Scientist CIMMYT and Director, CIMMYT-Asia, New Delhi
Convenor : Dr. Anil Dahuja, Professor, Division of Biochemistry
Co-Convenor : Dr. Atul Kumar, Associate Dean (PG), The Graduate School
Chairperson's Remarks

TUESDAY, MARCH 18, 2025

Time : 09.00 - 17.30 h

Presentation of "Significant Post Graduate Students' Research" by Ph.D. students for "Merit Medals" and "NABARD-Professor VL Chopra Gold Medal & Best Student of the Year" awards

Chairman : Dr. B.M. Prasanna, Distinguished Scientist CIMMYT and Director, CIMMYT-Asia, New Delhi
Convenor : Dr. Anil Dahuja, Professor, Division of Biochemistry
Co-Convenor : Dr. Atul Kumar, Associate Dean (PG), The Graduate School
Chairperson's Remarks

WEDNESDAY, MARCH 19, 2025

Presentation of Significant Educational Achievements for the year 2024 by the Professors representing different Schools of the teaching disciplines

Convenor : Dr. Monika Atul Joshi, Professor, Seed Science & Technology
Co-Convenor : Dr. Shruti Sethi, Principal Scientist, FS&PHT

Session I - Crop Improvement

Time : 09.00-10.30 h
Chairman : Dr. R.M. Sundaram, Director, ICAR-IIRR, Hyderabad

Dr. H.K. Dikshit	Genetics and Plant Breeding
Dr. Sunil Archak	Plant Genetic Resources
Dr. Monika A. Joshi	Seed Science & Technology
	Chairperson's Remarks

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Time : 11.00-12.35 h
Chairman : Dr. H.C. Sharma, Former Vice Chancellor, YSPUHF, Nauni, Solan (HP)

Dr. Suman Gupta	Agricultural Chemicals
Dr. Subramanian S.	Entomology
Dr. Anil Sirohi	Nematology
Dr. Aundy Kumar	Plant Pathology
	Chairperson's Remarks

Session III – Natural Resource Management

Time : 14.00-16.20 h
Chairman : Dr. B. Venkateswarlu, Former Vice Chancellor, VNMKV, Parbhani & Former Director, ICAR-CRIDA, Hyderabad

Dr. A.K. Mishra	Agricultural Engineering
Dr. P. Krishnan	Agricultural Physics
Dr. Y.S. Shivay	Agronomy
Dr. D.K. Sharma	Environmental Sciences
Dr. Rajeev Kaushik	Microbiology
Dr. T.J. Purakayastha	Soil Science & Agricultural Chemistry
Dr. Susama Sudhishri	Water Science & Technology
	Chairperson's Remarks

Session IV – Basic Sciences

Time : 16.50-18.05 h
Chairman : Dr. P Ananda Kumar, Former Director, ICAR-NIPB, New Delhi

Dr. Anil Dahuja	Biochemistry
Dr. Jasdeep C. Padaria	Molecular Biology & Biotechnology
Dr. Anjali Anand	Plant Physiology
	Chairperson's Remarks

THURSDAY, MARCH 20, 2025

Presentation of Significant Educational Achievements for the year 2024 by the Professors representing different Schools of the teaching disciplines

Convenor : Dr. Monika Atul Joshi, Professor, Seed Science & Technology
Co-Convenor : Dr. Shruti Sethi, Principal Scientist, FS&PHT

Session V – Horticultural Sciences

Time : 09.00-10.35 h
Chairman : Dr. S. Uma, Former Director, ICAR-NRC for Banana, Tiruchirapalli (TN)

Dr. K.P. Singh	Floriculture & Landscaping
Dr. R.M. Sharma	Fruit Science
Dr. Ram Asrey	Post Harvest Management
Dr. R.K. Yadav	Vegetable Science
	Chairperson's Remarks

Session VI – Social Sciences

Time : 11.05 -12.50 h
Chairman : Dr. N.P. Singh, Former Member (Official), CACP, Ministry of Agriculture & Farmers Welfare, Govt. of India, New Delhi

Dr. Pramod Kumar	Agricultural Economics
Dr. M.S. Nain	Agricultural Extension
Dr. Cini Varghese	Agricultural Statistics
Dr. Sarika	Bioinformatics
Dr. Alka Arora	Computer Application
	Chairperson's Remarks

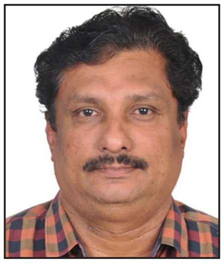
Session I: School of Crop Improvement

Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Genetics and Plant Breeding	20	16
Plant Genetic Resources	05	02
Seed Science and Technology	09	02
Total	**34**	**20**

SCHOOL OF CROP IMPROVEMENT

Chairperson: Dr. Raman M. Sundaram, Director, ICAR-IIRR, Hyderabad, Telangana



Dr. Sundaram completed his B.Sc. (Agri) from TNAU, Coimbatore, M.Sc. (Agri) in Molecular Biology and Biotechnology from the G.B. Pant University of Agriculture and Technology, Pantnagar as a DBT Research Fellow and Ph.D. in Plant Sciences from University of Hyderabad, Hyderabad as a CSIR-JRF. He joined ICAR-Indian Institute of Rice Research (IIRR), Hyderabad as a Scientist in the Biotechnology Section in 1998 and his studies focused on biotic stress resistance, hybrid rice applications of biotechnology and product development through transgenic breeding. Dr. Sundaram was appointed as Director of ICAR-IIRR, Hyderabad in April 2021. As Director of the Institute, he is serving as the Coordinator of All India Coordinated Research Project on Rice (AICRPR) and also as the Coordinator of ICAR-Consortia Research Platform on Crop Biofortification (CRP-Biofortification). He is very well known for his work in trait characterization, molecular studies and molecular breeding in rice, which has culminated in identification of few novel genes, development of several products, high-impact publications and National awards and laurels. In collaboration with CSIR-CCMB, Hyderabad, his research team was instrumental in development and release of one of the first biotech products in rice, which is a high yielding, bacterial blight resistant, fine-grain type rice variety possessing low glycemic index (50.9), named Improved Samba Mahsuri (RPBio-226). It is one of the first marker-assisted selection (MAS) products in the country and is being cultivated in >7 lakh hectares across the country. His team has developed four other MAS derived varieties, besides contributing towards development and release of >10 rice varieties and has made significant contribution towards application of biotechnological tools in hybrid rice. He has undergone intensive training on rice biotechnology at International Rice Research Institute, Philippines, Cornell University and Iowa State University, USA. He has also handled and coordinated several externally funded research projects, published his works in many International (>140) and National (> 30) journals and has authored >40 books/book chapters, technical bulletins and popular articles related to biotechnology and rice. He is the recipient of several awards and recognitions which include Lal Bahadur Shastri Outstanding Young Scientist Award of ICAR in 2011, Indo-US Research Fellowship in 2011, Hari Om Ashram Trust Award of ICAR in 2012, CSIR Innovation Award for Rural Development in 2013, PN Behl Award for Excellence in Crop Sciences (2012-13), DBT Award for Biotechnology Product and Process Development and commercialization (2015), etc. Besides these, he is a Fellow of National Academy of Agricultural Sciences (2019), Fellow of National Academy of Sciences, India (2020), Fellow of Indian Society of Genetics and Plant Breeding (2017), Associate of NAAS (2013) and has received USAID fellowship (2005), IUSSTF Fellowship (2011) and DST-Alexander Von Humboldt Foundation Travel Grant (2014). He served as the Editor-in-Chief of Journal of Rice Research, Academic Editor of PLOS One Journal, Journal of Plant Biochemistry and Biotechnology, Indian Journal of Genetics and Plant Breeding and is also serving as a member of several National and International Committees.

GENETICS

1

Prof. H. K. Dikshit

The Division of Genetics at IARI, the "Seat of Green Revolution" in India, deals with the genetic improvement of crops contributing immensely to basic, strategic and applied research in genetics and plant breeding of various crops and model genetic organisms. The teaching and research activities of the division integrate both conventional and modern biotechnological tools and align well with the farmer's needs to achieve the food and nutritional security of the country. The achievements of the students have been presented in four major themes, as below:

Theme 1: Breeding for Higher Productivity

Mapping genomic regions() governing uppermost internode length in rice

The wild abortive (WA) cytoplasm is widely used in hybrid rice seed production but is associated with incomplete panicle exsertion, reducing the outcrossing rate and seed set. The uppermost internode length (UIL1) plays a crucial role in panicle exsertion. The present study evaluated 201 recombinant inbred lines (RILs) derived from RTN10B and IRG213 across three locations-Delhi, Karnal, and Aduthurai—to identify quantitative trait loci (QTLs) for UIL1, panicle exsertion ratio (PER), plant height (PH), tiller number (TN), second and third internode length (UIL2, UIL3), panicle length (PL), and the length from flag leaf to panicle tip (PFL). A microsatellite-based linkage map (2077.1 cM, 104 markers) was used for QTL mapping, identifying 22 QTLs, with 19 clustering into four hotspots. A major QTL hotspot on chromosome 1 (RM12055-RM320) spanning 1.4 Mb contained seven QTLs for PER, PFL, PH, PL, UIL, SIL, and TIL. In-silico analysis identified 15 candidate genes linked to internode and panicle exsertion traits. QTL validation using markers RM12055, RM6696, and RM302 confirmed significant R^2 values and additive effects, with IRG213 alleles contributing positively. Ten QTLs were validated in an F2:3 population from IRG213 and Pusa 6B, with markers RM12055 and RM6696 consistently associated with UIL, PFL, and PER. Testcross hybrids (A-lines × IRG213, B-lines × IRG213) exhibited significant trait variations across locations, with Group B showing superior UIL1, PFL, and PER due to nuclear-cytoplasmic interactions. These results highlight the role of maternal cytoplasm in hybrid performance. The identified QTLs require fine mapping for marker-assisted selection, aiding the introgression of superior traits into male sterile lines to enhance pollination and hybrid seed production in rice.

Exploring the genetic and adaptive diversity of *Oryza* species naturized in Jharkhand, India

This study focuses on the adaptive and genetic diversity of *Oryza* species naturalized in Jharkhand, with a focus on *Oryza nivara*, *O. rufipogon*, and *O. sativa*. A total of 75 samples, including 5 checks, were collected from 24 districts across various altitudinal gradients (100–1000 msl) and habitat niches. Morphological characterization revealed significant variation among the species. *O. nivara* showed the strongest adaptation to higher altitudes (500-1000 msl), whereas *O, rufipogon* was restricted to high altitudes (500-1000 msl). *O. sativa* exhibited broad adaptability, spanning all altitudinal ranges. ANOVA results indicated highly significant genetic variability for plant height, leaf length, and grain yield. Correlation analysis indicated that grains per panicle were positively correlated with leaf width and leaf length, while traits such as tiller number showed a negative correlation with panicle width. This analysis suggests a complex interplay between traits that influence yield potential in these species. PCA explained *O. rufipogon* exhibited greater genetic diversity compared to the other species. Molecular analysis using GBS identified 26,267 high-quality SNPs. Population structure analysis revealed moderate genetic differentiation between *O. nivara* and *O. rufipogon*, while *O. sativa* displayed significant genetic divergence. These findings highlight the significant genetic and morphological diversity within the *Oryza* species in Jharkhand, particularly in the wild species *O. rufipogon*, which may serve as a valuable genetic resource for rice breeding programs. The study underscores the importance of conserving these native genetic resources to ensure the sustainability of rice agriculture in this region.

Genetic diversity and marker-trait association analysis for morpho-biochemical traits in colored rice (*Oryza sativa*) collected from Chhotanagpur Plateau

The colored rice varieties (red, black, and brown) gaining recognition due to their rich nutritional profiles and bioactive compounds. These varieties are abundant in phenolics, flavonoids, and anthocyanins, known for their antioxidant, anti-inflammatory, and anticancer properties. To study the genetic diversity and biochemical potential of colored rice landraces from the Chhotanagpur plateau, 50 rice landraces, including 33 with colored grains, were evaluated for 21 agro-morphological (height, panicle number, grain dimensions, and yield per plant) and biochemical (total phenolic content (TPC), total flavonoid content (TFC), and total anthocyanin content (TAC)). Antioxidant activities were measured through DPPH and FRAP assays. Significant genetic variability was observed among landraces, with high phenotypic and genotypic coefficients of variation for traits like plant height, grain length, and yield. Heritability estimates were moderate to high, indicating strong genetic control. Correlation analysis revealed strong positive associations, particularly between grain length and test weight ($r = 0.98$). Traits like panicle number and grain width exhibited substantial direct effects on yield. Cluster analysis grouped genotypes into 10 clusters, with grain test weight contributing the most to genetic diversity (40.86%). PCA showed that the first three components explained over 50% of phenotypic variance. The biochemical analysis identified Karihini-1 (black rice) with the highest TPC and TAC, while Kirka Kochi (red rice) had the highest TFC. Black rice consistently showed superior biochemical values. Marker-trait analysis revealed five significant SNPs for TFC, with two on chromosome 5, highlighting it as a hotspot for flavonoid regulation.

Genetic mapping of root system architecture in rice (*Oryza sativa* L.)

Rice production faces challenges from climate change and soil degradation, with abiotic stresses affecting root system architecture and overall plant health. RSA traits are vital for nutrient uptake, anchorage, and stress tolerance, yet their genetic mechanisms remain largely unexplored. This study mapped RSA diversity and identified key genetic factors influencing these traits. A total of 281 Indian rice germplasm lines were screened under hydroponic and pot culture conditions, revealing significant variations in traits like total root length, root dry weight, and root volume. Correlation analysis showed strong associations among RSA traits, suggesting coordinated regulation. PCA highlighted major contributors to root trait variation. Cluster analysis grouped genotypes based on root morphology and anatomy, identifying high-performing genotypes such as IRG 184, IRG 256, and IRG 141 under hydroponics, and IRG 174, IRG 212, and IRG 293 under pot culture. GWAS using SNP markers on an admixed rice population revealed haplotype structures shaped by recombination events, with LD block sizes averaging 180.7 kb and three genetic subpopulations with 21 significant MTAs linked to RSA traits. Novel candidate genes, including *Os06g0296200, Os04g0625100, WRKY54*, and *MYB-TF*, were identified as potential regulators of root architecture and stress resilience. A recombinant inbred line population from a cross Kalinga III/Salumpikit validated four MTAs, emphasizing Salumpikit's potential as a donor for RSA improvement. SSR markers RM6100, RM11, RM122, and RM8085 were identified for marker-assisted selection, facilitating the introgression of desirable root traits into elite rice cultivars. These findings offer valuable genetic insights into RSA regulation, aiding the development of climate-resilient rice varieties through precision breeding strategies.

Genetic analysis and marker-traits association study for physiological traits in bread wheat (*Triticum aestivum* L.)

This study focuses on advanced wheat breeding material in India, particularly evaluating genotype-environment interactions and identifying genomic regions responsible for agro-physiological traits. The analysis of general combining ability revealed that parents P2 (35th ESWYT-147) and P8 (HDCSW-18) exhibited strong combining ability to enhance genetic gains through physiological traits. The study also estimated heterosis in 56 hybrids, with several showing significant and desirable heterosis for traits like crop growth rate, canopy temperature depression, grain yield, leaf area index, and chlorophyll content. The experiment involved 260 genotypes, including four checks (HD 3226, HDCSW 18, HD 3117, HD 2967), grown in four different environments with varying sowing times and locations in New Delhi and Karnal, Haryana. The highest grain yield was recorded at KLTS, while the lowest was at KLLS. The DLLS environment was found to be most suitable for selecting broadly adaptable genotypes, as it is both discriminative and representative. For marker-trait association, 220 genotypes were analyzed using 10,193 SNP markers from an initial 35,153. The study identified 219 QTLs related to various agro-physiological traits across the four environments. Additionally, several candidate genes (e.g., TraesCS1A02G390200, TraesCS3A02G377300) were linked to developmental pathways influencing these traits, providing valuable insights for future wheat breeding programs.

Morpho-physiological and molecular characterisation of elite wheat varieties carrying alternative dwarfing genes

Semi-dwarf lines demonstrate significant yield advantages over their taller counterparts. In this study alternative dwarfing genes, *Rht 18* and *Rht 14* introgressed in the background of elite wheat varieties HD3086, HD2967, HI1544, and HI1500 were evaluated in BC$_2$F$_6$ and BC$_1$F$_6$ generations. A total of 77 lines for *Rht 18* gene and 39 for *Rht 14* gene were evaluated for their performance for various morpho-physiological and agronomic traits. Mean plant height decreased in improved lines carrying *Rht 18* and *Rht 14* genes compared to *Rht B1b* lines. ANOVA showed significant variation for traits under all three irrigated, restricted irrigation, and stubble retained conditions. The presence of alternative genes was confirmed using SSR and gene-specific markers suggesting the presence of both major (*RhtB1b*) and alternate genes in the evaluated lines. The background recovery using SNP genotyping in improved HD3086 and HI1544 carrying *Rht 18* gene was 90% and, 70% respectively and in improved HD3086, HD2967 and HI1500 carrying *Rht 14* gene was 92%, 75% and 70%, respectively. 12 lines carrying *Rht 18* and *Rht 18* +*Rht B1b* gene and 13 lines carrying *Rht 14* gene solely or in combination with *Rht B1b* gene were superior in performance in more than one condition. There were many lines identified to be superior in restricted irrigation condition probably due to the presence of alternative dwarfing genes. A cup experiment showed that *Rht 18* and

14 genes did not affect germination at a depth of 8cm and had better root and coleoptile length elongation leading to better early establishment.

Identification of genomic regions for kernel row number in maize (*Zea mays* L.)

Kernel Row Number (KRN) is a critical yield component trait in maize that has been extensively found to correlate positively with overall grain yield. In the present investigation, morphological characterization of the F_2 population from a cross between two contrasting parents, 2345Y with 8-10 KRN and DH18/11 with 16-22 KRN, was done. Seven phenotypic classes of KRN were found in the 354 F_2 individuals with 8-20 KRN. Broad sense heritability was estimated at 56.69%. Inheritance pattern through the Wright-Castle estimator revealed three factors with six alleles, and East's hypothesis (lowest KRN class frequency in $F_2 = 1/4^n$) supported the results. Twenty-two SSR markers out of 161 were found to be polymorphic through the parental polymorphism survey, which was used to determine the allelic status of the F_2 population. Fourteen Meta-QTLs were found from 131 successfully projected initial QTLs (out of 326 from the literature survey), distributed in chromosomes 1, 3, 5, 9 and 10. Six putative genes, out of 1028 candidate genes from the MQTL region showing considerable expression in maize ear primordium were selected, which can be used for future expression analysis studies.

Genome wide association studies for harvest index and associated traits in chickpea (*Cicer arietinum* L.)

This study aimed to assess genetic variability and identify traits contributing to seed yield, harvest index (HI), and related traits in chickpea, focusing on long-season environments in northern India. A diverse germplasm of 182 genotypes, including varieties, trait-specific genotypes, and advanced breeding lines, was evaluated across three contrasting environments. Analysis of variance (ANOVA) revealed significant differences among genotypes for seed yield/plant, HI, seeds/plant, and 100-seed weight. Positive correlations were observed between seed yield/plant and pod yield/plant, HI, and biomass/plant. Genotyping by sequencing 178 germplasm lines identified 35,795 high-throughput SNPs, enabling the identification of genomic regions associated with various traits. Population structure analysis revealed two subpopulations with extensive linkage disequilibrium (LD) and low LD decay. The FarmCPU model identified 172 marker-trait associations (MTAs), with significant associations for Days to 50% flowering (DAF), HI, and shelling percentage (Sh.%). Notable pleiotropic MTAs were found on chromosomes 6 and 5, linked to traits such as biomass, pod yield, seed yield, and seed number/plant. Most MTAs for seed yield and related traits were located within a 25kb region on chromosome 6. In silico analysis of selected MTAs revealed candidate genes involved in flowering, pollen maturation, and fertilization. Validation in recombinant inbred line (RIL) populations confirmed the reliability of the MTAs. The combined approach of genome-wide association studies and RIL validation enhances the credibility of the findings and offers valuable insights for chickpea breeding aimed at improving yield and HI.

Genome-wide association studies on plant architectural traits in chickpea (*Cicer arietinum* L.)

Crop plant architecture plays an important role in plant breeding for yield optimization, regulating photosynthetic rate and efficiency, utilization of resources, occurrence of pests and diseases, effective mechanical harvesting, space optimization, and improving the quality of plant produce. A set of 280 diverse genotypes, which included the core collection of chickpea was evaluated during the *rabi* season of 2021 and 2022. A total of 10 plant architecture-related traits, including plant height, first pod height, canopy width, inter-nodal length, and days to flowering were studied and significant variability was observed as per the analysis of variance (ANOVA) and phenotypic descriptors. Diversity based on π and θ estimates suggests the presence of substantial diversity, while Tajim's D reflects balancing selection due to the abundance of shared alleles. Significant marker-trait associations (MTAs) for traits like plant height (PH), first pod height (FDPH), and days to flowering were observed using trait-based or BLUP estimates. In total, 97 and 51 MTAs were identified using trait-based and BLUP-based multi-model GWAS analysis, respectively. Among these 17 were consistent MTAs being present either across the year or were identified using more than one GWAS model. Likewise, 9 consistent MTAs were identified using the BLUP estimates. Interestingly, two genomic regions present on chromosomes 5 and 7 were found to harbor multiple MTAs for PH and FPDH. The linkage disequilibrium (LD) block analysis reflects the prevalence of multiple LD blocks in these regions. The allelic effects of the MTAs reflect their additive nature in determining the phenotype. Overall, the MTAs identified in the current study are highly useful for the chickpea breeder in modulating the plant architecture, mainly PH and FPDH.

Mapping of loci governing extra-earliness and multi-flowering traits in lentil (*Lens culinaris* Medik.) using QTL Seq approach

Developing early-maturing lentil genotypes under changing climatic conditions can reduce yield losses caused by terminal drought or heat stress. Whole-genome resequencing (WGRS) and QTL-seq identified loci associated with earliness using a RIL population (F4:5; Globe Mutant × L4775). Earliness was confirmed as a recessive trait through genetic analysis, and QTL-seq revealed three key QTLs (*LcqDTF3.1, LcqDTF3.2*, and *LcqDTF3*.3) on chromosome 3, having 246,244 SNPs and 15,577 insertions/deletions (InDels). Candidate genes such as *LcELF3a* and *LcFRI* showed significant differential expression, indicating their roles in regulating earliness. An A-to-G transition in the *LcELF3a* gene was identified, causing alternative splicing in early-flowering genotype L4775. Cloning and sequencing of *LcELF3a* cDNA confirmed exon 3 skipping, resulting in a 52 bp deletion, a premature termination codon, and a truncated *LcELF3a* protein. Two validated InDel markers, I-SP-356.6 and I-SP-383.9, linked to *LcFRI* and *LcELF3a* respectively, explained 47.7% and 82.35% phenotypic variance (PVE) for the earliness trait. These markers, validated across lentil genotypes, are promising tools for marker-assisted selection (MAS) to transfer earliness traits into elite cultivars. Additionally, loci influencing multi-flowering (MF) traits were identified using an RIL population (F3:4; ILL7663 × MFX). Genetic analysis for the MF trait revealed inhibitory gene action and QTL-seq uncovered two QTLs (LcqMF3.1 and LcqMF3.2) with significant differential expression of *LcSPL13a* and *LcELF3a* genes. An InDel marker, I-SP-361.57, linked to *LcSPL13a* gene, explained 51.23% PVE, underscoring its role in MF regulation. These findings offer valuable genetic markers for breeding lentil varieties with enhanced earliness and multi-flowering traits, critical for getting stable yields under changing climate challenges.

Inheritance studies and mapping of early maturity in soybean [*Glycine max* (L.) Merr.]

Early-maturing soybean varieties are critical to mitigate terminal drought and high temperatures. In this study, an attempt was made to understand the inheritance of days to flowering and maturity and map the genetic factors controlling these traits. SKAF148, an extra early maturing photoperiod insensitive soybean germplasm line was crossed with late maturing highly photoperiod sensitive varieties DS9712 and PUSA12-13. The F_2 populations of SKAF148 × DS9712 and SKAF148 × Pusa 12-13 indicated polygenic inheritance of the days to flowering and maturity traits. However, the predominance of early flowering under short-day conditions and intermediate flowering under long-day conditions suggested a complex genetic interaction with the environment. The F_2 populations also demonstrated transgressive segregations. The segregated plants exhibited higher variability for pods/plant, seeds/plant, and 100-seed weight across different growth conditions. The study employed 519 SSR markers, of which 258 were polymorphic (49.71%). Mapping with 250 F_2 plants from the SKAF148 × DS9712 cross revealed five QTLs for days to flowering on chromosomes 10, 11, and 19, explaining 44.34% of phenotypic variance, and five QTLs for days to maturity on chromosomes 1, 4, 5, and 11, contributing 34.89%. Additionally, nine QTLs for yield-related traits were identified, five of which were novel. Eleven novel QTLs for reproductive phase duration were mapped which collectively explained 33.64% of the variance. The output will help in breeding for early maturing high-yielding soybean varieties.

Genetic analysis and mapping for seed weight in *Brassica juncea* (L.) Czern & Coss.

Most of the released high-yielding hybrids of *B. juncea* have a low 1000-seed weight (TSW) with no increment in oil content (OC), and, therefore, have poor acceptance among the farmers in India. It is, thus, imperative to understand the genetic basis of these traits and deploy them in commercial hybrid breeding programs. Further, identifying underlying genes and associated markers will help deploy them in marker-assisted selection. For this purpose, a set of 15 diverse *B. juncea* genotypes with TSW ranging from 1.32 to 8.26 g was used to generate 210 hybrids following a full diallel mating scheme. These hybrids, along with their parents, were evaluated in three different environments. Inheritance of TSW suggests the predominance of additive gene action, whereas non-additive gene action was observed to regulate OC. Further, TSW and OC were reported to be influenced by maternal and non-maternal effects, respectively. Parents with bold seeds were identified as good general combiners for both traits. Hybrid NPJ 253 x NPJ 161, with both parents having high seed weight, exhibited the highest mean (8.43g) and heterobeltiosis (17.2%) for TSW. A Genome-Wide Association Study was conducted using 152 *B. juncea* genotypes, leading to the identification of 16 stable MTAs for TSW. *In-silico* analysis revealed their association with candidate genes involved in different seed development pathways. Further, two Indel markers are associated with the *Bju.CKX2* gene has been successfully developed and validated in a set of genotypes and a F_2 population. Overall, the material and insights from the study unveiled new opportunities for researchers to deploy these markers in MAS for developing high-yielding hybrids and cultivars with bold seeds and higher OC.

Characterization of the M_2 population of winged bean (*Psophocarpus tetragonolobus*) through agro-morphological traits and molecular markers

Winged bean is an underutilized crop, it is known as the ‘one species supermarket’ because all its parts are edible. Genetic variation within the population is important for selection of desirable traits. In our study promising variety of winged bean AKWB1 was irradiated with 4 dosages of gamma rays at BARC, to create variation. A total of 147 families which comprise 873 M_2 plants of winged bean exhibited significant variation in qualitative (18) and quantitative traits (12) compared to the parental line (AKWB-1). Seed yield/plant exhibited a strong, positive correlation with the total number of seeds/plant (0.98), green pod yield/plant (0.95), and pod numbers/plant (0.91). Mutant genotyped using 22 polymorphic SSR markers which produced a total of 85 alleles. The number of alleles ranged from 2 to 6, with an average of 3.86 alleles per locus. The average PIC value was found to be 0.4727 and it ranged from 0.1886 to 0.7382. A total of 31 unique alleles were found across 21 marker loci. According to Neighbor-joining dendrogram based on Neis (1983) genetic distance, 2 major clusters were identified. The SSR data analysis using STRUCTURE v.2.3.4 software revealed the maximal ΔK at K = 2, indicating that two groups existed among the two populations. These results suggest that gamma radiation effectively generated significant genetic diversity in the winged bean.

Identification of the gene for seed coat colour in winged bean (*Psophocarpus tetragonolobus* L.) DC)

Minimal information on the genetics and genomics of the winged bean has been reported. Quantitative trait loci (QTLs) for pod, flower, and seed-related traits of the winged bean have been discovered. However, the candidate gene responsible for seed coat colour has not been identified yet. Identifying the gene for seed coat colour is crucial for molecular breeding, as it can serve as a phenotypic marker. Seed colour is also valued for its antioxidant properties and flavours. We collected seeds from pods at different maturity stages from distinct genotypes of winged beans with contrasting seed colours, such as purple (Purple-13), semi-purple (Purple-1), brown (IC-41980), and white (CR-1) in Kharif 2023 at the ICAR-IIAB, Ranchi to investigate the gene(s) responsible for seed coat colour. ICAR-IIAB, Ranchi has developed a chromosome-level reference genome sequence of winged bean (unpublished data). We analyzed seed coat colour-related QTLs qSdc1.1 and qsdc3.1 using flanking marker information reported by Chankaew et al. (2022) to identify genes responsible for seed coat colour. Gene prediction from these QTL regions identified 127 genes for qSdc1.1 and 24 for qsdc3.1. In-silico annotation of these genes using the NCBI database with literature review highlighted four key seed coat colour-related genes with their different paralogs: *qSdc1.1-9, qSdc1.1- 12, qSdc1.1-15, qSdc1.1-16, qSdc1.1-17, qSdc1.1-18, qSdc1.1-25, qSdc1.1-28* (UDP glycosyltransferase 83A1), *qSdc1.1-74, qSdc1.1-78, qSdc1.1-79* (Transcription factor MYB113), from QTL qSdc1.1. Similarly, from QTL Qsdc3.1 the selected genes were qSdc3.1- 3 (G-box-binding factor 4), qSdc3.1-12, qSdc3.1-13, qSdc3.1-16, qSdc3.1-18 (WAT1-related protein). The expression analysis of the identified genes was carried out using qRT-PCR with our designed primer, and Actin was used for internal control. The upregulation of qSdc1.1-78 (MYB113) and qSdc3.1-13 (WAT1-related protein) in Purple-13 and Purple-1, but not in CR-1, suggests their potential role in controlling seed coat colouration in the winged bean.

Theme 2: Breeding for Resistance to Biotic Stresses

Molecular mapping of QTL(s) governing sheath blight resistance in rice

Rice sheath blight is one of the most important fungal disease-causing yield losses of up to 50%. An *Oryza rufipogon*-derived introgression line, Pusa 1908-13-12-5 developed at ICAR- IARI, New Delhi was identified as resistant. Three different populations such as rice landraces for association mapping (GWAS), RIL population (PB 1 / Pusa 1908-13-12-5) for linkage mapping, and an independent backcross population for validation of the mapped QTLs were used. Among the rice landraces, one genotype was identified to be resistant while 18 genotypes were moderately resistant, 117 were moderately susceptible, 85 were susceptible, and 40 exhibited highly susceptible. Genotyping was carried out with 80K Rice pan Genome Array (RPGA), GWAS identified three marker-trait associations, *qLH3*.1 and *qLH5*.1 on chromosomes 3 and 5, respectively for lesion height (LH), and *qRLH10*.1 in chromosome 10 for relative lesion height (RLH). The RIL population was evaluated for disease response along with the two parents and checks. A linkage map spanning 2508.59 cM with an average adjacent marker distance of 0.82 cM was constructed with 3074 SNPs using IciMapping. A total of six QTLs were mapped, and four QTLs were major QTLs. The major QTLs, *qShB1*.2, *qShB1*.3, and *qShB1*.4 collocated within 1.29 Mb regions on Chromosome 1. Kompetitive Allele Specific PCR (KASP™) assay was developed for the linked SNPs and used for validation in independent BC$_1$F$_{2:3}$ families (PB 1121//PB 1121/ Pusa 1908-13-12-5). One SNP (AX-182186537) on chromosome 1 was validated; The QTL validated in the genetic background of Basmati rice could be used in molecular marker-assisted breeding.

Fine mapping of a major QTL *qBK1.2* imparting tolerance against bakanae disease caused by *Fusarium fujikuroi* in rice (*Oryza sativa* L.)

Bakanae disease caused by *Fusarium fujikuroi* is an emerging disease of rice causing losses in all rice-growing regions around the world. A BC_2F_2 mapping population was developed by backcrossing the recurrent parent Pusa Basmati 1121 with the recombinant inbred line RIL28, which harbors a major quantitative trait locus (QTL) governing resistance to bakanae, *qBK1.2*. Genotyping of the BC_2F_2 population using flanking markers RM10153 and RM5336 identified 24 recombinants. Further, MassARRAY-based single-nucleotide polymorphism assays were designed to identify markers polymorphic between the parental lines. This led to fine mapping of *qBK1.2* to 130 kb between the SNP markers rs3164311 and rs3295562. In-silico mining of the fine-mapped region identified 11 putative candidate genes with functions related to defense. The expression analysis identified two significantly differentially expressed genes, that is, *LOC_Os01g06750* and *LOC_Os01g06870*, between the susceptible genotype PB1121 and the resistant genotypes Pusa1342 and R-NIL4. Furthermore, the SNPs identified in *LOC_Os01g06750* produced minor substitutions of amino acids with no major effect on the resistance-related functional motifs. However, *LOC_Os01g06870* had 21 amino acid substitutions, which led to the creation of the leucine-rich repeat (LRR) domain in the resistant genotype Pusa1342, thereby making it a potential candidate underlying the major bakanae-resistant QTL, *qBK1.2*. The markers used in the fine mapping program are of immense utility in marker-assisted breeding for bakanae resistance in rice.

Inheritance and mapping of genomic regions for brown spot resistance in rice (*Oryza sativa* L.)

Climate change poses a significant threat to agriculture, with the potential to alter disease dynamics and pest populations, thereby exacerbating the challenges of maintaining crop yields. Brown spot disease in rice, historically linked to the Bengal famine of 1943, is becoming a growing concern due to shifting cultivation practices and changing climatic conditions. This research work leveraged the power of BSA-seq to identify genomic regions associated with brown spot resistance in rice, working on an early segregating population derived from the cross, Bala X NIL-7. This study also focussed on investigating the inheritance patterns of resistance and evaluating the impact of the disease on the performance of rice crops under both direct-seeded and transplanted conditions. The research revealed that brown spot disease significantly impairs crop performance, affecting yield-contributing traits in susceptible plants. The top two SNPs with the highest Δ SNP index were located within coding regions of genes encoding a chitinase-like protein and a pentatricopeptide repeat-containing protein on chromosome number 4 and 6 respectively, known to play crucial roles in disease resistance in various crop models. Inheritance studies suggested that major genes with supplementary interactions confer resistance to brown spot disease. The identification of specific SNPs associated with resistance provides a strong foundation for map-based cloning and marker-assisted selection to improve brown spot resistance in rice. This research offers valuable insights for breeding resistant rice varieties and developing effective disease screening strategies to mitigate the impact of brown spot disease on rice production.

Identification of genomic loci associated with yellow rust resistance derived from *Triticum turgidum* and *T. spelta* and their utilization in wheat improvement aided by speed breeding

Bread wheat (*Triticum aestivum* L.) is the world's second most cultivated staple crop, contributing 20% to global protein and calorie intake. Yellow rust, a significant threat to wheat production, can cause yield losses of 50–90%, necessitating resistance breeding for sustainable cultivation. Landraces and wild relatives of wheat harbour novel resistance genes. This study explores resistance introgressed from *T. turgidum* and *T. spelta* into wheat. The introgression line TTD533 (*T. aestivum* cv NI5439//*T. turgidum* acc. IARI183) carries a recessive resistance gene, with F_4 progeny (HD2932 × TTD533) segregating as 104 resistant, 43 segregating, and 103 susceptible plants (χ^2=5.064, *p*=0.0795). Similarly, TSD858 (*T. aestivum* cv Agra Local/T. *spelta* acc. IARI276) harbours a dominant resistance gene, with F_5 progeny (AL × TSD858) showing 105 resistant, 13 segregating, and 119 susceptible plants (χ^2=1.117, *p*=0.572). Both lines resisted yellow rust pathotypes 110S119 and 238S119, unlike their susceptible parents. Bulked segregant analysis identified resistance loci of TTD533 on chromosome 1DL (484–493 Mb) and TSD858 on 1BL (651–677 Mb), novel regions for *Yr* genes. Furthermore, combining yellow rust resistance in TTD533 and TSD858 with leaf and stem rust resistance from T250-20-20-16, and T250-20-20-6 (*Aegilops speltoides*-derived lines) was achieved using speed breeding technology. With optimized growth conditions (22 hours light/2 hours dark, 21/17°C, 60–80% RH), the wheat cycle was shortened to 77–78 days, advancing generations (F_1 to F_3) in just five months. This highlights speed breeding as a transformative approach for rapid wheat improvement.

Identification of heterotic restorers and improvement of maintainer and restorer lines for yellow rust resistance in wheat (*Triticum aestivum* L.)

Hybrid has the potential to break the yield plateau of wheat by exploiting the heterosis phenomenon. Ten cytoplasmic lines and four restorer lines developed at ICAR-IARI, New Delhi, were crossed in Line × Tester fashion to develop hybrids and evaluated for combining ability and heterotic potential. Forty F_1s, their parents along with six commercial checks were evaluated in Randomized Complete Block Designs with two replications at ICAR-IARI, New Delhi, and Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, during 2019-2020. A 2851 and A 2733+*Lr24* were the best general combiners for grain yield. A3083×902R, A 2851 × 955R and A2687×955R exhibited higher grain yield with significant SCA effects. These hybrids also showed the highest better parent heterosis (50.23-91.29%) and Standard Heterosis (11-24.2%) against commercial checks HD 2967, HD 3086, and HI 1544. The restorers 955R and 902R were found to be desirable for heterotic combinations for grain yield. Additionally, the maintainer line, 365B, and restorer line, 1752R susceptible to yellow rust, were improved with the stripe rust resistance genes *Yr10* from donor parent Avocet+*Yr10* and *Yr15* from donor parent HD2967 + *Yr15*. The F_1 and backcross generations were screened with linked and validated SSR markers *Xpsp3000* for *Yr10* in the B line and *Xgwm273* for *Yr15* in R line. The marker-assisted backcross breeding was used to identify the superior plats with *Yr10* and *Yr15* genes into the maintainer and restorer line.

Genetic studies on tolerance to fall armyworm (*Spodoptera frugiperda* (J.E. Smith)) in tropical field corn (*Zea mays L.*)

Corn is one of the important cereal crops, having wide utility in the form of food, feed, and fodder, and possesses high genetic yield potential. However, infestation of fall armyworm (FAW) causes a severe reduction in yield followed by objectionable quality. In the present study, 21 experimental maize hybrids were evaluated which are developed through a Line × Tester approach, using seven susceptible lines and three testers with varying levels of tolerance to FAW; two tolerant (AI-542 and AI-125) and one moderately tolerant (PDM-24). The genetic component of variation suggested that both the yield component traits and studied biochemical parameters are under genetic control, and many of the traits were inherited through the male parents along with the resistance mechanism. On the other hand, ear and leaf damage was contributed by lines that are otherwise susceptible to FAW. General combining ability revealed that inbred lines, AI-542 and AI-125 appear to be a good combiner contributing to important yield component traits and biochemicals *vis-a-vis* resistance to the offspring. The analysis of biochemical parameters considering both constitutive and induced phytochemicals *viz.,* enzymatic activity, nonenzymatic antioxidant defense, and nutritional and antinutritional components revealed that protein content plays a major role in preference and total phenols, tannins, TAL and PAL offers anti-preference mechanism. The inbred lines AI-542, AI-125, and hybrids, AI-1116×AI-542, AI-1116×AI-125, PML-105×AI 542, PML-105×AI-125, AI-518×AI-125, PDM-4061×PDM-24, UMI-1210×AI-542 were found with greater constitutive and/or FAW damage induced defense phytochemicals. These could be further studied to understand the resistance mechanism to FAW in field corn.

Identification of novel alleles/genes against blast disease through genome wide association mapping in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

Foliar blast (FB) disease caused by the fungal pathogen *Magnaporthe grisea* has emerged as a major challenge to pearl millet cultivation, threatening forage and grain production. Despite the availability of diverse genetic resources potentially harbouring resistance to FB, there have been less systematic efforts to identify and map the resistance genes and genomic regions associated with blast. In the present study, 250 pearl millet accessions were evaluated across seven diverse environments under natural disease pressure and in glasshouse conditions with artificial inoculation. Heritability-adjusted-Genotype-plus-Genotype-by-Environment (HA-GGE) biplot analysis indicated “IP 11353” as an “ideal” genotype which showed stable resistance and genetic buffering against foliar blast (FB). Additionally, “IP 22423, IP 7910, and IP 7941” were classified as “desirable” genotypes due to their promising resistance performance. Further, a genome-wide association study (GWAS) using 3, 68,463 high-quality SNPs revealed 33 significant marker-trait associations across seven chromosomes. Notably, SNP S3_273713430 on Chr-3 exhibited a stable association with FB resistance, explaining phenotypic variance in the range of 14.48%–37.02%. Genomic analysis within a +4 kb window around the SNP loci identified candidate genes encoding Fbox-LRR proteins, which were further validated through RNA-seq and biparental mapping using KASP markers. This study represents the first attempt to elucidate the genetic basis of FB resistance in pearl millet, highlighting the interaction between host and pathogen.

Understanding the complex regulatory network of Fusarium wilt (*Fusarium oxysporum fsp. lentis*) resistance in lentil (*Lens culinaris* Medik.) using comparative RNA-seq analysis

Lentil (*Lens culinaris Medikus*), a crucial leguminous crop with high nutritional value for food and animal feed, is grown globally. Despite its nutritional benefits, lentil yields are often low due to various biotic and abiotic stress. Among the biotic challenges, diseases such as wilt, caused by *Fusarium oxysporum* lentis, particularly impact its growth and yield. This study aimed to explore the complex molecular mechanisms behind lentil’s resistance to wilt infection. Using advanced RNA sequencing technology, we analyzed two genotypes, L4147 (resistant) and Vidhokar (susceptible), both inoculated with Fusarium spores. The RNA sequencing provided insights by comparing resistant and susceptible plants under different conditions. We identified a total of differentially expressed genes (DEGs) involved in various biological processes, including defense responses. Key enriched pathways included secondary metabolite biosynthesis, metabolic processes, and plant-pathogen interactions. Several DEGs related to histones, ion activity, resistance genes, and metabolic functions showed differential expression, potentially enhancing the plant’s defense mechanisms. We narrowed down the DEGs to 15, focusing on those with significant roles in defense, such as LRR receptor-like kinases, transcription factors, and pathogenesis proteins. Protein-protein interaction analysis revealed complex relationships among these proteins, involving cell cycle regulation, MAPK signaling, and secondary metabolite biosynthesis. Validation of 36 genes through RNA sequencing and qRT-PCR confirmed their relevance to the defense mechanism. This study, employing cutting-edge technology, provides comprehensive insights into the molecular mechanisms of wilt resistance in lentils.

Diversity analysis in soybean with special reference to mung bean yellow mosaic virus (MYMV) resistance in soybean (*Glycine max* (L.) Merrill)

Soybean occupies first place in India as an edible oil seed crop with respect to area and production. The area of soybean is increasing year by year but the productivity remains low. The three major constraints in soybean production in India are drought; weed infestation and location-specific biotic stress (Lal and Sapra, 2013). A set of one hundred forty-two advanced breeding lines developed from several diverse crosses were screened for resistance against Mungbean Yellow Mosaic Virus (MYMV) at the hot spot. Out of one hundred forty-two lines 63 lines were found to be highly resistant and 23 lines were found to be resistant to the MYMV. These 142 advanced breeding lines along with the six checks were characterized for twelve qualitative and twelve quantitative traits. They were further grouped into five different clusters using the K-means clustering method. The genotypes in clusters IV and V were highly diverse and can be used for developing heterotic crosses. Two lines namely, DS 1961 (0.829%) and DS1988 (0.748%) with low phytic acid content were identified. The genotypes DS 1847, DS 1976, DS 1877, DS 1863, DS 1838, DS 1854, DS 1907, DS 1890, DS 1880, DS 1869, DS 1949, DS 1844 and DS 1856 were identified as distinct accessions. One CAPS marker developed at IARI was used to see if this marker can distinguish the resistant and susceptible genotypes. The results show that the CAPS marker failed to distinguish the resistant and susceptible genotypes.

Theme 3: Breeding for Tolerance to Abiotic Stresses

Estimation of genetic diversity for low phosphorus tolerance in paddy (*Oryza sativa* L.) landraces from Chhotanagpur plateau region

Phosphorus (P) deficiency is a significant constraint in rice (*Oryza sativa* L.) production, particularly in the Chhotanagpur plateau region. This study aimed to estimate the genetic diversity of 83 rice landraces from this region for low phosphorus tolerance by focusing on the presence of the *Pup1* locus, a major gene/QTL associated with P uptake efficiency. Molecular characterization was conducted using *Pup1*-specific markers (K1, K5, K20-1, K20-2, K29-1, K29-2, K29-3, K41, K42, K43, K46-1, K46-2, K48, K52, and K59). The results revealed that a significant proportion of genotypes possessed tolerant alleles, with markers like K5 and K20-1 showing a high frequency of tolerant genotypes. The *Pup1* locus was fully or partially present in most upland-adapted rice varieties but was absent in the sensitive check variety MTU 1010, indicating its role in agro-ecological adaptation. Cluster analysis further supported the genetic diversity of these landraces, identifying two main clusters based on the presence of the *Pup1* locus. The findings underscore the importance of *Pup1* in breeding programs aimed at improving phosphorus use efficiency in rice.

Exploring phosphorus starvation tolerance in aus rice (*Oryza sativa* L.) and deciphering the genetic basis of tolerance through genome-wide association studies

Phosphorus (P) deficiency is a major limitation to rice productivity in many regions with nutrient-poor soils, improving phosphorus use efficiency (PUE) in rice is critical for sustainable agriculture. This study aimed to evaluate the genetic variation in the aus rice (*Oryza sativa* L.) for low P tolerance and identify key genomic regions and genes associated with P-deficient conditions. A total of 181 aus rice accessions were evaluated, with 42% showing high performance under both stress and control conditions. Grain yield-based stress tolerance attributes, particularly stress tolerance index and mean productivity, were useful in identifying superior accessions like 'Kalabokari' and 'ARC-12021'. Genome-wide association studies (GWAS) identified 71 significant marker-trait associations related to P uptake and yield under stress, including key phosphate transporter genes such as OsPT11 and OsPHR2. Notably, several PSTOL1-negative accessions also showed low P tolerance, suggesting alternative mechanisms. Transcriptome analysis revealed distinct gene expression patterns between tolerant and sensitive genotypes, with genes related to stress responses upregulated in tolerant varieties. Several genes were commonly identified in GWAS and transcriptome analysis, offering scope for further research. This study highlights several promising accessions and genetic markers for low P tolerance, providing a basis for breeding P-efficient rice varieties. Future research should focus on validating key genes and exploring PSTOL1-independent pathways to develop rice varieties suited for nutrient-poor soils, contributing to sustainable agriculture.

Genome wide association mapping for combined drought and heat tolerance in wheat (*Triticum aestivum* L.)

Wheat (*Triticum aestivum L.*) feeds a third of the global population, but climate change and population growth threaten food security. Increased production with improved quality and stress resilience is essential. A genome-wide association study for tolerance to combined drought and heat stress was carried out using elite lines during the rabi seasons of 2022-23 and 2023-24. Multi-location phenotyping was conducted under irrigated, restricted irrigation, and late-sown conditions to simulate drought, heat, and combined stress, along with a control setup. Important Agronomical, physiological and grain nutrition traits such as Days to Heading (DH), Plant height (PH), Normalized Difference Vegetation Index (NDVI), Chlorophyll Content (SPAD), Chlorophyll fluorescence (Fv/Fm), Thousand Grain Weight (TGW), Grain Weight per Spike (GWPS), Yield (YLD), Biomass (BM), Harvest index (HI), Grain zinc (GZnC) and grain iron contents (GFeC) and Water use efficiency (WUE) were phenotyped. A significant correlation was observed among various yield-contributing traits in the study. The panel comprised two subpopulations, and genome-wide SNP data was generated using the 35K Axiom™ Wheat Breeder's Genotyping Array. The elite diversity panel showed sufficient genetic diversity. A total of 109 significant marker-trait associations were identified, including 8 under control conditions, 26 under drought stress, 19 under heat stress, and 56 under combined drought and heat stress conditions. An in-silico analysis of the identified markers against the IWGSC reference genome revealed that most SNPs were located within or near candidate genes involved in key plant metabolic processes. These identified genes and marker-trait associations (MTAs) hold significant potential for molecular breeding to develop climate-resilient crop varieties.

Studies on regulatory and functional response of root plasticity to abiotic stresses in maize (*Zea mays* L.)

Abiotic stresses in the current climate change era are hindering global maize production. The root system architecture (RSA) is critical for water and nutrient uptake, and plant stability under stress and non-stress conditions. Thus, RSA modulation is one of the effective strategies to mitigate the adverse effects of edaphic stresses. The current investigation explored the maize RSA plasticity in response to drought, low-nitrogen and salinity stresses. The study showed appreciable plasticity for RSA-traits among the target maize inbred lines and significant positive correlations among the total length, surface area, volume, linear length, number, fresh and dry weights of roots (0.47 to 0.99; $p<0.001$ to 0.05). Whereas average diameter showed significantly negative correlations with specific root length (-0.70 to -0.95; $p<0.001$) and root length distribution (-0.87 to -0.98; $p<0.001$). Further, the significance ($p<0.001$) of genotypes, stress and genotypes × stress interactions suggested the possibility of developing stress-specific maize cultivars. The inbreds SKV671 and CML597 exhibited superior performance for various RSA traits under drought and low-nitrogen conditions, while PML93 and MG42 excelled in salinity stress. The gene regulatory network analysis identified hub transcription factor genes, viz. *ZmKN1*, *ZmEREB147*, and *ZmAP2/ERF* are the major regulators of RSA. Additionally, the expression of *Zm00001eb212120* and *Zm00001eb414320*, and *GRMZM2G050939* are associated with direct and inverse relation with RSA traits under various stress conditions, respectively. The information generated on the complex regulatory and functional basis of RSA and the identified genotypes showing stress-specific RSA plasticity has immense utility in maize breeding towards the development of stress-resilient cultivars.

Genome wide association analysis for traits influencing terminal heat stress in lentil (*Lens culinaris* Medik. *culinaris*).

Terminal heat stress, which occurs during the critical reproductive stage, significantly limits lentil productivity. However, research on lentils' resilience to high temperatures, is still limited. To address these issues, we assessed 158 lentil genotypes under normal and late-sown conditions over two consecutive seasons using eleven heat stress indices. Analysis of variance revealed significant variations among the genotypes for all studied heat tolerance indices. Principal component analysis, correlation and biplot analysis indicated the presence of a significant positive correlation between Yp, Ys, and the following heat tolerance indices: YI, MP, HM, GMP, MRP and STI. Conversely, TOL, SSPI, and PYR were found to be associated with heat susceptibility. Furthermore, cluster analysis based on these indices successfully classified 158 genotypes into heat-tolerant and heat-sensitive groups. Ultimately, genotypes P13143, P13130, and P13135 were identified as the most heat-tolerant and high-yielding in both conditions. Subsequently, 140 out of the 158 total genotypes were selected for GWAS to identify the genomic regions associated with terminal heat tolerance. Using the GBS technique, 34,995 genome-wide SNPs were identified. In addition, our study revealed four distinct subpopulations among tested genotypes and an LD decay of 512 kb was observed. Association analysis using BLINK led to the identification of 28 significant MTAs. Furthermore, these 28 MTAs were found to be linked with 150 protein-coding and 7 uncharacterized genes. Several key candidate genes such as those coding for WRKY transcription factors, Heat shock proteins, Pentatricopeptide repeat proteins, Ulp1 protease family, Zinc finger family proteins, Myb transcription factor, Auxin response factor and F-box proteins were identified.

Genetic diversity analysis for low phosphorous tolerance in lentil germplasm

The present study aimed at screening 150 lentil accessions procured from ICAR-NBPGR, New Delhi representing acidic zones of Jharkhand, Bihar, Odisha, West Bengal, Andhra Pradesh, and North-Eastern states to identify genotypes with greater PUE. The experiment was conducted under two distinct soil phosphorus environments: low phosphorus (11.2 kg/ha) and optimum phosphorus (66.3 kg/ha) at the ICAR-Indian Agricultural Research Institute in Jharkhand during the *rabi,* 2023-24. Thirteen traits related to phosphorus use efficiency (PUE) and yield-attributing traits were assessed, revealing significant variations. The average PUE in optimum conditions was 0.52, which decreased by 46.87 under P stress with an average value of 0.35 in low P conditions. Analysis of variance (ANOVA) indicated significant genotype by environment interactions for all traits. Heritability values were generally lower under low P conditions, suggesting an environmental influence on trait expression. The study found a high genetic coefficient of variation (GCV) for most traits, indicating potential for selection. Principal component analysis (PCA) and cluster analysis demonstrated substantial genetic diversity among the genotypes, grouping them into distinct clusters based on PUE and yield attributing traits. Notably, genotype IC78455 exhibited higher PUE across both environments. This research provides valuable insights into the genetic diversity for low phosphorus tolerance and yield potential in a diverse set of lentil accessions, laying the foundation for targeted breeding efforts to enhance these critical traits and ensure sustainable agricultural productivity under low phosphorus conditions.

Theme 4: Breeding for Enhanced Nutritional Quality

Molecular mapping and characterization of neurotransmitter compound, gamma amino butyric acid (GABA) in the germinated brown rice (GBR)

Gamma-aminobutyric acid (GABA), a key inhibitory neurotransmitter in the central nervous system, is gaining recognition for its calming effects, particularly in addressing stress-related disorders, mental health issues, and lifestyle diseases. Because of these proven benefits, there is an increasing demand among health-conscious people for GABA-rich foods. Germinated Brown Rice (GBR), is one of the predominant sources of GABA and hence can be recommended as an alternative to white rice. The current study depicted the existence of significant genetic variation in GBR for GABA content, ranging from 7.19 to 75.04 mg/100g in a GWAS panel of 192 Indian rice accessions. The accessions with high GABA content can be used as donors for the genetic improvement of GABA in the high-yielding varieties. Further, the panel was genotyped with 50K SNP markers and genome-wide association analysis using the multi-locus models FarmCPU and Blink identified six significant marker-trait associations (MTAs) for GABA content, explaining 0.06 to 4.15% of the phenotypic variance. *In-silico* analysis identified 10 putative candidate genes spanning the MTA regions including those encoding Proline-rich proteins, Orn/DAP/Arg decarboxylase, and Aldehyde dehydrogenase, which play key roles in GABA biosynthesis. Furthermore, metabolite analysis identified 130 compounds, including amino acids and metabolites like spermidine and putrescine involved in GABA biosynthesis. This research provides valuable insights into the genetic mechanisms underlying GABA accumulation in rice and highlights the potential for utilizing this knowledge for accessions with high GABA content (Kew, HPR 2104) as donors, while identified MTAs and candidate genes can be deployed in breeding programs for enhancing GABA content in the GBR and developing biofortified rice varieties with nutraceutical properties.

Genome wide association study to identify marker trait associations for nutritional and glycemic quality traits in Indian dwarf wheat (*Triticum sphaerococcum Percival*)

Wheat (*Triticum aestivum L.*) is a staple crop, providing essential calories and protein globally. However, micronutrient deficiencies, particularly in developing countries, is a serious threat. Indian dwarf, a landrace, holds the potential to improve the nutritional quality of modern wheat. This study analyzed 116 *T. sphaerococcum* accessions and seven bread wheat varieties across two years. Seven traits viz., total starch (TS), amylose (AML), amylopectin (AMP), glycemic index (GI), zinc (ZN), iron (FE), and protein (PRO). Substantial genetic variation was observed among *T. sphaerococcum* accessions, for nutritional and glycemic traits. Specifically, 22 accessions had higher TS than DBW 327, 18 had higher AML than PBW RS1, 33 had higher AMP than DBW 327, 61 had higher ZN than PBW RS1, six had higher FE than PBW RS1, 91 had higher PRO than HD 3385, and six accessions exhibited lower GI than PBW RS1, indicating potential for developing wheat with reduced glycemic impact. ANOVA revealed significant differences among genotypes, years, and genotype-by-year interactions for all traits, except FE. Population structure identified five sub-populations, with linkage disequilibrium decay at 7.617 Mb genome-wide. Genome-wide association studies using MLMM, FarmCPU, and BLINK models identified 49 significant marker-trait associations across all traits, with 25 considerable gene annotations. Notable SNPs included AX94664110 (22.30-22.33% PVE) for TS, AX94441003 (9.8-12.39% PVE) for GI, AX94773766 (26.04-27.63% PVE) for ZN, AX94707847 (20.92-23.23% PVE) for FE, and AX94796135 (49.48% PVE) for PRO. These findings provide a foundation for marker-assisted selection and biofortification efforts, emphasizing *T. sphaerococcum* role in enhancing wheat's nutritional quality.

Analysis of genetic variability, molecular characterization and marker-aided enrichment of methionine in maize

Traditional maize endosperm protein lacks sulfur containing essential amino acid - methionine. Multi-location evaluation of 48 inbreds revealed significant variation for methionine (0.031-0.305%). Analysis using 7 × 7 half-diallel mating design revealed the predominance of additive gene action for methionine accumulation. Sequence characterization of *ask2, fl2, dzs10,* and *dzs18* genes revealed significant SNPs and InDels *viz*., (i) T to A in *ask2*, (ii) C to T in *fl2*, (iii) presence of *misfit Transposable Element* in *dzs10* and (iv) 4 bp, 9bp and 15 bp InDels in *dzs18.* Introgression of favorable alleles of *ask2*, *fl2,* and *dzr1* genes into elite parents (PMI-PV5 and PMI-PV6) of a released hybrid (Pusa HQPM5 Improved) led to 1.38-, 1.83- and 1.82-fold increase in methionine among *ask2*-, *fl2* and *dzr1*-introgressed inbreds over the original parents, respectively. The recovery of recurrent parent genome (RPG) among the introgressed progenies ranged from 84.3-93.8%. The mean methionine among reconstituted hybrids possessing favourable allele of *ask2*, *fl2* and *dzr1* genes were 0.261%, 0.352% and 0.344%, respectively while original hybrid had 0.188% methionine. Expression analysis of *ask2*, *fl2* and *TIDP2802* (putative gene in *dzr1* locus) genes across 20-, 30- and 40-days after pollination (DAP) revealed highest expression at 20-DAP. Methionine accumulation was also found to be highest at 20-DAP among the inbreds. The genotypes possessing *ask2*, *fl2* and *dzr1* also showed higher seedling vigour, root length and seminal roots, besides superoxide dismutase and peroxidase enzyme activity compared to original genotypes. This is first report on development of high methionine biofortified maize hybrids.

Genetic, physiological and molecular characterization of *lpa1*- and *lpa2*-based low phytate maize genotypes

Phytic acid (PA) reduces the nutritional value of maize by lowering zinc and iron bioavailability. Low phytate maize is key for addressing poor micronutrient bioavailability. Here, we developed low phytic acid double mutants (*lpa1/lpa2*) in maize by crossing *lpa1* and *lpa2*-based near-isogenic lines (NILs) in seven genetic backgrounds. We assessed the expression levels of *lpa1* and *lpa2* genes in foliage and seeds at various developmental stages and characterized double and single mutant lines for seed physiology and seedling vigor. The double mutants exhibited the highest reduction in phytic acid (PA) (41%), followed by *lpa1* (36%) and *lpa2* (30%) lines. Mean PA levels were 1.72 mg/g for double mutants, compared to 1.86 mg/g for *lpa1*, 2.05 mg/g for *lpa2*, and 2.92 mg/g for wild-type lines. Both mutant (*lpa1/lpa2*, *lpa1,* and *lpa2*) and wild-type lines had comparable agronomic performance and grain yield. The lowest PA concentrations were observed at 15 DAP in foliage and seeds. In seeds, double mutants showed a 4.05-fold and 2.90-fold reduction in expression of *lpa1* and *lpa2* genes, respectively at 15DAP. Overall, these results indicated that *lpa1* and *lpa2* genes had seed-specific expression. Also, the mutant lines displayed comparable germination and vigour to wild types with double mutants and *lpa2* lines displaying minimal reductions in germination and vigor. The double mutant lines showed the greatest reduction in PA, similar agronomic performance, grain yield, germination, and vigour along with lower expression of *lpa1* and *lpa2* genes, indicating their potential to enhance maize's nutritional quality.

Genetic variability and molecular analysis of folate accumulation in maize kernels

Folates (vitamin B9) are essential for normal growth and development of human beings. Folate deficiency leads to neural tube defects, along with other diseases including cancer. Biofortification of staple crops like maize for folates offers a sustainable and feasible approach. We evaluated 48 maize inbreds for folate and its major derivatives, at three stages of kernel development-15, 30, and 45 days after pollination (DAP). Significant variability found for 5-methyltetrahydrofolate, 5-formyltetrahydrofolate, and total folate content across the different stages indicated strong genetic control. Folate levels of genotypes exhibited a declining trend as the kernel matured. Characterization using 78 SSR markers based on candidate genes governing folate metabolism indicated a high conservation of genes. About 30 polymorphic SSRs had a mean polymorphism information content (PIC) of 0.36, ranging from 0.19 (Fo-SSR-62) to 0.59 (Fo-SSR-50). Identification of diverse high folate inbred lines and superior haplotypes offers potential for use in maize folate biofortification programs while contrasting inbreds can be used for mapping genomic regions. Expression patterns of 3 candidate genes viz., *GTPCHI, SAM* and *CTM* governing folate metabolism in contrasting inbreds at 12 DAP and 24 DAP stages showed *GTPCH1* plays a critical role in early folate biosynthesis, while *SAM* and *CTM* genes may contribute to folate metabolism and reduction during kernel maturation. High folate lines such as PMI-SWT016, PMI-PV7, MGU213wx, PMI-SWT020, and MGU203W can be used as donors for future biofortification programmes. This is the first research effort in the country dealing with the characterization of the maize genotypes for folate accumulation.

Identification of novel alleles/ genes for grain protein content and essential amino acids through genome-wide association mapping in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

Pearl millet a climate-resilient nutri-cereal holds the potential to address global malnutrition due to its rich nutritional profile. The present study aimed to identify alleles and genes associated with grain protein content and essential amino acids through genome-wide association studies (GWAS) and multi-environment trials. Field trials were conducted at ICAR-IARI, New Delhi (2022, 2023) and ICAR-IIMR, Hyderabad (2023) during *kharif* season using 248 inbred lines in an alpha-lattice design to assess genetic variability, genotype-by-environment (G×E) interactions, and marker-trait associations. Phenotypic analysis revealed significant variability in protein content (7–23 g/100 g) and amino acids. Non-essential amino acids were more abundant than essential ones, with glutamic acid and leucine being the most prevalent. Protein content negatively correlated with most amino acids, while amino acids showed positive inter-correlations. PCA and clustering identified genotypes from India, Nigeria, and Mali as biofortification candidates. G×E analysis using AMMI, GGE, BLUP, and WAASB identified G150, G211, and G143 for high protein content and G57, G209, and G101 for high grain yield. Multi-trait stability models (MTSI, MGIDI, MTMPS, FAI-BLUP) consistently selected G57 (IP 12298), G218 (IP 8767), G151 (IP 4542), and G139 (IP 3138) for high yield and stability.GWAS identified 653 significant marker-trait associations, with key associations predominantly located on chromosomes 1, 3, and 5. Functional annotation of 41 genes revealed role of these genes in amino acid metabolism and transcriptional regulation.

Introgression of *lox2* allele in vegetable soybean through rapid breeding approaches under controlled environmental conditions

Vegetable soybean [Glycine max (L.) Merr.], despite its nutritional value, suffers from low productivity.

To accelerate breeding progress, a modified "speed breeding" technique was applied to 16 vegetable soybean genotypes. Under controlled environments with extended light and dark periods [10 hours of light (30°C) and 14 hours of dark (25°C)] and with/without CO_2 supplementation (550 ppm), genotypes exhibited earlier flowering, increased pod and seed production, and improved seed weight. This method enabled 4-4.5 generations per year, significantly shortening the breeding cycle. One major challenge for vegetable soybean in India is its beany flavor, associated with the Lox2 gene. To address this, the Lox2 null allele i.e. lox2 was introgressed into the Swarna Vasundhara variety from PI596540, a germplasm line using marker-assisted backcross breeding under controlled environments. This accelerated generation advancement, achieving up to 98.74% recurrent parent genome recovery in BC_2F_3 lines. Foreground and background selection ensured precision, completing the process in 24 months. This study represents a significant step forward in vegetable soybean breeding in India, demonstrating the potential of speed breeding for rapid generation advancement and the development of improved, consumer-preferred varieties.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Kothalanka Victor Paul (21775)	M.Sc.	Genetic variability and molecular analysis of folate accumulation in maize kernels	Dr. Rajkumar Uttamrao Zunjare	ICAR-IARI, New Delhi
2.	Rohit Sarkar (21777)	M.Sc.	Genome wide association analysis for traits influencing terminal heat stress in lentil (*Lens culinaris* Medik. *culinaris*)	Dr. Muraleedhar S Aski	ICAR-IARI, New Delhi
3.	Malavika N Shal (21779)	M.Sc.	Identification of genomic loci associated with yellow rust resistance derived from *Triticum turgidum* and *T. spelta* and their utilization in wheat improvement aided by speed breeding	Dr. Niranjana M	ICAR-IARI, New Delhi
4.	Keerthi G M (21780)	M.Sc.	Studies on regulatory and functional response of root plasticity to abiotic stresses in maize (*Zea mays* L.)	Dr. Mallikarjuna MG	ICAR-IARI, New Delhi
5.	Monika Sahu (21781)	M.Sc.	Genetic studies on tolerance to fall armyworm (*Spodoptera frugiperda* (J.E. Smith)) in tropical field corn (*Zea mays* L.)	Dr. Ganapati Mukri	ICAR-IARI, New Delhi
6.	Shiwani Meena (21783)	M.Sc.	Genome-wide association mapping for combined drought and heat tolerance in wheat (*Triticum aestivum* L.)	Dr. Harikrishna	ICAR-IARI, New Delhi
7.	Prathibha K (21784)	M.Sc.	Genome-wide association study to identify marker trait associations for nutritional and glycaemic quality traits in indian dwarf wheat (*Triticum sphaerococcum Percival*)	Dr. Kiran B. Gaikwad	ICAR-IARI, New Delhi
8.	Rohit (21970)	M.Sc.	Morpho-physiological and molecular characterisation of elite wheat varieties carrying alternative dwarfing genes	Dr. Neelu Jain	ICAR-IARI, New Delhi
9.	Ankita Singh (50086)	M.Sc.	Understanding the complex regulatory network of Fusarium wilt (*Fusarium oxysporum* fsp. *lentis*) resistance in lentil (*Lens culinaris* Medik.) using comparative RNA-seq analysis	Dr. Muraleedhar S. Aski	#ICAR-IARI, Assam

10.	Hrudya Biji (50092)	M.Sc.	Diversity analysis in soybean with special reference to mung bean yellow mosaic virus (MYMV) resistance in soybean (*Glycine max* (L.) Merrill)	Dr. S.K. Lal	#ICAR-IARI, Assam
11.	Mamta (50095)	M.Sc.	Molecular mapping and characterization of neurotransmitter compound, gamma amino butyric acid (GABA) in the germinated brown rice (GBR)	Dr. Haritha Bollinedi	#ICAR-IARI, Assam
12.	Ayan Deb (60122)	M.Sc.	Genetic diversity and marker trait association analysis for morpho-biochemical traits in coloured rice (*Oryza sativa* L.) collected from chhotanagpur plateau	Dr. Shashibhushan Choudhary	#ICAR-IARI, Jharkhand
13.	Aiswarya V S (60129)	M.Sc.	Exploring phosphorus starvation tolerance in aus rice (*Oryza sativa* L.) and deciphering the genetic basis of tolerance through genome-wide association studies	Dr. Somnath Roy	#ICAR-IARI, Jharkhand
14.	Jyotsna Maurya (60134)	M.Sc.	Genetic diversity analysis for low phosphorous tolerance in lentil germplasm	Dr. Anima Mahato	#ICAR-IARI, Jharkhand
15.	Bhaskar Chodasani (60140)	M.Sc.	Exploring the genetic and adaptive diversity of *Oryza* species naturalised in Jharkhand, India	Dr. Shashibhushan Choudhary	#ICAR-IARI, Jharkhand
16.	Valipeta Samantha Reddy (90021)	M.Sc.	Inheritance and mapping of genomic regions for brown spot resistance in rice (*Oryza sativa* L.)	Dr. Vijai Pal Bhadana	**ICAR-IIAB, Ranchi
17.	Aritabha Kole (90022)	M.Sc.	Identification of genomic regions for kernel row number in maize (*Zea mays* L.)	Dr. Sujay Rakshit	**ICAR-IIAB, Ranchi
18.	Anand Maurya (90023)	M.Sc.	Characterization of the M2 population of winged bean (*Psophocarpus tetragonolobus*) through agromorphological traits and molecular markers	Dr. Sudhir Kumar	**ICAR-IIAB, Ranchi
19.	Pratap Ghosh (90024)	M.Sc.	Identification of the gene for seed coat colour in winged bean (*Psophocarpus tetragonolobus* L.)	Dr. Avinash Pandey	**ICAR-IIAB, Ranchi
20.	Kommula Uday (90031)	M.Sc.	Estimation of genetic diversity for low phosphorus tolerance in paddy (Oryza sativa L.) landraces from Chottanagpur plateau region	Dr. Shashibhushan Choudhary	**ICAR-IIAB, Ranchi
21.	Amar Kant Kushwaha (10611)	Ph.D.	Fine mapping of a major QTL *qBK1.2* imparting tolerance against bakanae disease caused by *Fusarium fujikuroi* in rice (*Oryza sativa* L.)	Dr. Ashok K. Singh	ICAR-IARI, New Delhi
22.	Nenavath Krishna Kumar Rathod (11050)	Ph.D.	Inheritance studies and mapping of early maturity in soybean [*Glycine max* (L.) Merr.]	Dr. Akshay Talukdar	ICAR-IARI, New Delhi

23.	Neethu Mohan (11053)	Ph.D.	Identification of heterotic restorers and improvement of maintainer and restorer lines for yellow rust resistance in wheat (*Triticum aestivum* L.)	Dr. Shailendra Kumar Jha	ICAR-IARI, New Delhi
24.	Mukesh Sankar S (11054)	Ph.D.	Identification of novel alleles/genes against blast disease through genome wide association mapping in pearl millet [*Pennisetum glaucum* (L.) R. Br.]	Dr. Sumer Pal Singh	ICAR-IARI, New Delhi
25.	Gangadhara K N (11280)	Ph.D.	Genetic mapping of root system architecture in rice (*Oryza sativa* L.)	Dr. K.K. Vinod	ICAR-IARI, New Delhi
26.	Rahul (11519)	Ph.D.	Genome wide association studies on plant architectural traits in chickpea (*Cicer arietinum* L.)	Dr. Shailesh Tripathi	ICAR-IARI, New Delhi
27.	Hriipulou Duo (11520)	Ph.D.	Analysis of genetic variability, molecular characterization and marker-aided enrichment of methionine in maize	Dr. Firoz Hossain	ICAR-IARI, New Delhi
28.	Meniari Taku (11529)	Ph.D.	Introgression of *lox2* allele in vegetable soybean through rapid breeding approach under controlled environmental conditions	Dr. Akshay Talukdar	ICAR-IARI, New Delhi
29.	Shivanagouda Patil N (11533)	Ph.D.	Genome wide association studies for harvest index and associated traits in chickpea (*Cicer arietinum* L)	Dr. V. S. Hegde	ICAR-IARI, New Delhi
30.	Shiv Kumar Singh (11538)	Ph.D.	Genetic analysis and marker-traits association study for physiological traits in bread wheat (*Triticum aestivum* L).	Dr. Rajbir Yadav	ICAR-IARI, New Delhi
31.	Shivaprasad K M (11794)	Ph.D.	Mapping of loci governing extra-earliness and multi-flowering traits in lentil (*Lens culinaris* Medik.) using QTL Seq approach	Dr. Gyan Prakash Mishra	ICAR-IARI, New Delhi
32.	Vinay Rojaria (11797)	Ph.D.	Genetic, physiological and molecular characterization of *lpa1*- and *lpa2*-based low phytate maize genotypes	Dr. Vignesh Muthusamy	ICAR-IARI, New Delhi
33.	Aavula Naveen (12083)	Ph.D.	Identification of novel alleles/ genes for grain protein content and essential amino acids through genome wide association mapping in pearl millet [*Pennisetum glaucum* (L.) R. Br.]	Dr. Sumer Pal Singh	ICAR-IARI, New Delhi
34.	Harshitha B S (11798)	Ph.D.	Mapping genomic regions(s) governing uppermost internode length in rice	Dr. Prolay Kumar Bhowmick	ICAR-IARI, New Delhi
35.	Manoranjan Senapati (11525)	Ph.D.	Molecular mapping of QTL(s) governing sheath blight resistance in rice	Dr. Gopala Krishnan S.	ICAR-IARI, New Delhi
36.	Mohit Sharma (11927)	Ph.D.	Genetic analysis and mapping for seed weight in *Brassica juncea* (L.) Czern. & Coss.	Dr. Naveen Singh	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: Genetic Diversity Analysis, Genomics of PGR and Germplasm Conservation.

Theme 1: Genetic Diversity Analysis

Study on morpho-nutritional diversity in wild *Vigna* species

Pulses are a rich and affordable source of vegetable protein, and the genus *Vigna* encompasses several agronomically significant species with substantial economic and environmental importance, including cowpea, urdbean, mungbean, moth bean, adzuki bean, and rice bean. However, challenges such as climate change, new pests and diseases, and changing cultivation practices have impacted the production and productivity of these crops. Consequently, it is essential to screen wild species for agro-morphological and nutritional traits to identify promising accessions for future *Vigna* breeding programs. This study involved the characterization of 71 different accessions of wild *Vigna* for morpho-nutritional traits at two locations: the Centre for Protected Cultivation Technology (CPCT), ICAR-IARI, and the Crop Wild Relative (CWR) Garden, ICAR-NBPGR Pusa farm. Agro-morphological characterization was conducted for 28 qualitative traits and 21 quantitative traits using an Augmented Block Design (ABD). Promising accessions were identified for various traits, ncluding EC1036864, EC1036862, IC553522, and IC553554 for early flowering; EC1170528, EC1170495, IC331623, and IC252904 for highest pod length; EC1036853, EC1036861, EC1036867, and EC1036860 for highest seed weight; and IC550536, IC550531, IC553557, and IC553539 for the highest number of pods per peduncle. Biochemical parameters, including protein, sugar, starch, phenols, moisture, ash, iron, and zinc, were also analysed. The results demonstrated that wild species are nutritionally rich and have the potential to combat malnutrition, hidden hunger, and support nutritional security. The highest protein content was found in EC1170492 (31.13%), IC305193 (30.56%), EC1170508 (30.63%), EC550058 (30.8%), and EC529042 (30.74%). The highest iron content was recorded in IC647555 (110 ppm), EC1170496 (137.6 ppm), IC625714 (99 ppm), and EC1170517 (82.64 ppm). The highest zinc content was observed in EC1170526 (74.25 ppm) and EC1170508 (74.47 ppm). These elite accessions can serve as potential donors to improve cultivated *Vigna* species for various nutritional traits.

Deciphering nutritional and molecular diversity in *Luffa acutangula* L. Roxb.

Vegetable crops are indispensable for a balanced diet due to their rich nutrient profiles, and *Luffa acutangula* (ridge gourd) stands out as a crucial cucurbitaceous vegetable known for itsdiverse uses in culinary and medicinal applications. This study, titled "Deciphering Nutritionaland Molecular Diversity in *Luffa acutangula* (L.) Roxb.," provides an in-depth analysis of 96 accessions to assess their genetic and nutritional variability. Utilizing 16 novel genomic SimpleSequence Repeat (SSR) markers, the molecular characterization uncovered substantial geneticdiversity, with varying Major Allele Frequencies (MAF), gene diversity, and Polymorphism Information Content (PIC) across different loci. Specifically, while some loci showed high MAF indicating reduced genetic variability, others like RGSSR15 displayed high gene diversity, reflecting a rich pool of genetic variation. Population structure analysis identified two primary genetic clusters, with significant genetic diversity found within accessions rather than between different populations. Nutritionally, the accessions exhibited notable variability in key metrics: protein content ranged from 6.31 to 17.61 grams per 100 grams, calcium levels varied from 113.01 to 408.02 mg/100g, iron from 2.09 to 14.32 mg/100g, potassium from 652.45 to 1913.22 mg/100g, and magnesium from 133.86 to 289.18 mg/100g. Additionally, moisture content ranged from 7.85% to 25.12%, influencing post-harvest handling and storage. These findings present identification of some accessions rich in particular nutrients and highlight the potential for breeding programs to select for germplasm with enhanced nutritional profiles and genetic robustness. The study provides a comprehensive foundation for future research, emphasizing that the observed genetic and nutritional diversity within *Luffa acutangula* is crucial for developing improved cultivars with enhanced nutrient profiles.

Molecular diversity and genetic integrity analysis in stored accessions of cotton in the national genebank

Identifying the most divergent genotypes and quantifying the existing genetic diversity in cotton genotypes is a prerequisite for developing heterotic combinations for the breeding of new varieties of cotton.The genetic diversity of 135 cotton genotypes was analysed using 38 microsatellite markers. The study material included 73 released varieties, eight hybrids that included six*Bt* hybrids, 21 parents of hybrids, 20 intra-*hirsutum*, four intra-*arboreum* hybrids, two interspecific hybrids, two breeding lines, four *Gossypium arboretum*varieties and one*G. herbaceum*accession. The 38 microsatellite primers amplified a total of 98 alleles, with the number of alleles ranging from 2 to 4 with an average of 2.47. The average similarity was 68%, which was indicative ofsufficient genetic diversity among the various genotypes. The UPGMA-based analysisclassified the genotypes into three clusters. Generally, genotypes were separated ploidy-wise. It was observed that *Bt* hybrids had a high level of genetic similarity, which is currently being cultivated on a large scale throughout India. Microsatellite primers that have potential use in the genetic purity/integrity analysis in cotton were identified. The genetic integrity of six accessions held in the nationalgenebank throughout the years 2000, 2007 and 2015 were analysed using microsatellite primers. No major change in allele frequencies was observed across the years.

Theme 2: Genomics of PGR

Use of microsatellite markers for diversity analysis and identification of pea (*Pisum sativum* L.) cultivars

Molecular profiling of 66 pea (*Pisum sativum* L.)accessions conserved in the national genebank was carried out using 15 SSR primers. A totalof 43 alleles were detected. The polymorphic Information Content(PIC) of these primers was found to be ranging from 0.09 for AC22 and 0.72 for the primer AD175. On the basis of marker indices such as PIC, Resolving Power and Marker Index, it was found that six SSR primers namely AA122, AD148, AB136, A9, AB140 and AD175 were found to be highly discriminating and useful in diversity analysis, cultivar identification and IPR protection. The cluster analysis based on UPGMA revealed a total of six clusters.

The pairwise similarity among accessions ranged from 12% to 100%. The average genetic similarity of the 66 genotypes revealed was 43.16%. The most diverse accessionsincluded exotic collections - EC598812, IC393731, EC865978, EC598730 and EC865944. ANOVA for agro-morphological diversity revealed that significant variations was present across the 100 accessions for most of the quantitative and qualitative traits. Accessions EC865968 (36.78 g), IC411725 (34.1g), and EC865969 (32.3 g) were found to be promising for the trait seed yield per plant; accessions EC865968 (33.4), EC865978 (32.41), and EC865969 (31.51) were found to be promising for number of pods per plant.

Genome-wide association mapping of stem rust resistance in emmer wheat *(Triticum turgidum* ssp. *dicoccum* Thell) germplasm

Phenotypic screening of 166 emmer wheat germplasm for stem rust resistance against the three pathotypes11, 40A and 40-3 categorized the population into different class of immune, very resistant, moderately resistant, moderately susceptible and highly susceptible for all the pathotypes. The publicly available genotyping data of the 166 lines generated using Affymetrix 35K SNPchip was used to understand the population structure among these lines and for association analysis. Population structure analysis divided entire genotypes into two distinct sub-populationswith 139 genotypes in one sub-population and 27 in the other. The overall LD decay distance for the entire genome (including both A and B sub-genomes) was 18.97 Mb. The GWAS analysis was performed on the phenotypic data for three pathotypes namely 11, 40A and 40-3 collected during the 2023-2024 period under glasshouse conditions. Two models FASTmrMLM and FASTmrEMMA identified significantly associated QTNs for stem rust pathotypes. One QTN (Affx-92278251**)** associated with pathotype11was located on chromosome1B. For pathotypes 40-3, two QTNS (Affx-92278251 and Affx-92715491) were identified on chromosomes 3B and one QTN (Affx-92691383)was located on Chromosome 4A. The candidate gene identification analysis predictedeights expressed transcripts, which were associated with four reliable QTNs/genomic regions identified. These transcripts encoded diverse functional groups of proteins like AP2/B3 transcription factor family protein, Aliphatic sulfonates import ATP-binding protein, O-fucosyl-transferase family protein, ATP-dependent zinc metalloprotease FtsH etc.

Theme 3: Germplasm Conservation

Cryopreservation of *Rubia cordifolia* L. using encapsulation-dehydration

This study examines the cryopreservation of *Rubia cordifolia* L., a botanically significant plant, utilizing the encapsulation-dehydration technique. The depletion of genetic variability in thisspecies due to overexploitation and insufficient cultivation necessitates effective conservation approaches. Cryopreservation offers a viable strategy for the long-term maintenance of plant genetic resources. The research investigates six different combinations of regeneration media and three tissue types as explants for plant cryopreservation. MS + GA3 + 2-iP was identified as the optimal regeneration medium, displaying 50% shoot induction within 3 days and superior mean values for shoot length and number of nodes. Nodal segments (2 mm) emerged as the most effective explant, with a mean shoot length of 3.57±0.20 and a three-day duration for 50% shoot induction. Encapsulation-dehydration involved the utilization of calcium alginate beads and controlled desiccation before storage in liquid nitrogen. The plants exhibited a high survivability of 100.0±0.00 in nearly all scenarios for both control and desiccated explants. Post-liquid nitrogen treatment, the explants predominantly regenerated through callusing, with the highest regeneration rate recorded as 60.00±3.24 in MS + GA3 + 2-iP after 6 h of desiccation under direct air of laminar air flow. However, callus failed to transform in to shoots. These outcomes underscore the efficacy of encapsulation-dehydration in preserving explant viability and fostering regeneration. This investigation represents trailblazing work in the conservation of this plant and can offer valuable guidance for future research endeavors.

Morphological and physiological aspects in seeds of *Artocarpus* spp. for amenability to cryo-storage

This study analyses the morphological and physiological aspects in seeds of *Artocarpus* species, particularly lakoocha and jackfruit, to assess their potential for cryo-storage. The study identified high initial moisture (51-63%), sensitivity to desiccation and structural changes along with viability of these seeds as the key characteristics of their recalcitrant nature. Physiological analysis determined the critical moisture limit of 37% for lakoocha and 33% for jackfruit, below which germination was lost. In storage trials, 15°C was found to be optimum for maintaining viability of seeds. Lakoocha seeds survived for 180 days and jackfruit seeds for 90 days, whereas viability was lost at sub-zero temperatures (-10°C and-20°C). Chemical analysis showed that total soluble sugars, starch and antioxidants decreased during desiccation, which is related to oxidative damage and decline in germination. Histological studies confirmed structural damage such as cell shrinkage and membrane rupture in desiccated seeds, which are consistent with previous research. Cryo-storage attempts, such as vitrification and vacuum infiltration techniques, failed to maintain viability after liquid nitrogen exposure, which are consistent with previous research on similar species. Better results were observed for smaller seed parts containing embryonic axis in lakoocha, which indicate possibilities for future studies.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Rosemary J (21945)	M.Sc.	Use of microsatellite markers for diversity analysis and identification of pea (*Pisum sativum* L.) cultivars	Dr. Mukesh Kumar Rana	*ICAR-NBPGR, New Delhi
2.	Rahul Jahageerdar (21946)	M.Sc.	Study on morpho-nutritional diversity in wild *Vigna* species	Dr. Kuldeep Tripathi	*ICAR-NBPGR, New Delhi
3.	Rehan A Nadaf (21794)	M.Sc.	Cryopreservation of *Rubia cordifolia* L. using encapsulation-dehydration	Dr. Sangeeta Bansal	*ICAR-NBPGR, New Delhi
4.	Suhail Ansari (21928)	M.Sc.	Deciphering nutritional and molecular diversity in *Luffa acutangula* L. Roxb.	Dr. Manjusha Verma	*ICAR-NBPGR, New Delhi
5.	Bhagirath Jha (21947)	M.Sc.	Genome-wide association mapping of stem rust resistance in emmer wheat (*Triticum turgidum* ssp. *dicoccum* Thell) germplasm	Dr Amit Kumar Singh	*ICAR-NBPGR, New Delhi
6.	Anto James (11083)	Ph.D.	Molecular diversity and genetic integrity analysis in stored accessions of cotton in the national genebank	Dr. Mukesh Kumar Rana	*ICAR-NBPGR, New Delhi
7.	Shivam Kumar (10855)	Ph.D.	Morphological and physiological aspects in seeds of *Artocarpus* spp. for amenability to cryo-storage	Dr. Sandhya 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 evaluation and 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 Production Technology

Effect of seed coating with microbial formulations on seed yield and quality in green gram [*Vigna radiata* (L) R. Wilczek]

Green-gram [*Vigna radiata* (L) R. Wilczek], commonly known as Mung bean or Golden gram is an annual plant that belongs to Fabaceae family and widely known for its nutrition value and hardy nature to withstand adverse environmental conditions. This research delves into the evaluation of seed coating using microbial formulations to enhance the seed yield and quality of green gram. The experimental design included varying concentrations of these formulations, such as BF1-4 Cyanobacterial consortium, *Anabaena laxa*, An-Tr biofilm, BF1-4 Cyanobacterial consortium in combination with Thiram + Bavistin (2:1) to standardize the optimal application rates. Alongside these, the experiment was performed with 75% of recommended dose of nitrogen and 100% dose of nitrogen in case of microbial formulation as a control; with objective to assess which microbial formulations are capable to compensate 25% reduction of RDN with an increase in seed yield and quality. The experiments were conducted at ICAR-IARI Research field MB4A, New Delhi during summer and kharif season 2023-24. Preliminary results indicated a notable positive correlation between certain microbial coatings and increased seed germination percentage, field emergence, plant height at different stages, plant stand establishments, leaf chlorophyll content, bulk yield and other yield attributing traits, root parameters as well as storability of the treated seeds. Furthermore, this research also gives an insight about the soil microbial activity and soil nutrient status. The treatment resulted in higher numbers of pods per plant and increased overall yield. However, there was no significant impact on the germination percentage or other quality parameters of harvested seeds. Notably, the application of microbial formulations through seed coating exhibited a positive impact on seed storability. This was evidenced by sustained high level of germination percentage, first count, seed vigour indices and germination speed even after prolonged storage. Intriguingly, certain parameters displayed notable interactions between distinct crop varieties and treatment methods. As modern agriculture seeks more environmentally friendly approaches, the findings of this study present a promising avenue for boosting crop yields and quality. In conclusion, the study underscores the beneficial impact of seed coating with a BF1-4 Cyanobacterial consortium and *Anabaena laxa* on overall plant growth and crop performance with 25 % N savings. Hence, it is recommended that seed coating using this BF1-4

Cyanobacterial and *Anabaena laxa* can be an effective strategy to enhance crop productivity in green gram while reducing the reliance on chemical fertilizers.

Theme 2: Seed Biology Studies

Prediction of seed vigour in rapeseed and mustard using near-infrared spectroscopy (NIRS)

Rapeseed and mustard are crucial oilseed crops, widely cultivated for their significant oil content and diverse applications in food and industry. The ability to accurately assess seed vigour is vital for enhancing crop establishment, yield, and quality. In the quest for improving agricultural productivity and seed quality, this study aimed to develop a non-destructive, rapid, and accurate method for assessing seed vigour in rapeseed and mustard for large-scale screening. Approximately 300 genotypes of rapeseed and mustard, including Brassica juncea, B. rapa subsp. chinensis, B. rapa var. toria, B. rapa var. yellow sarson, B. napus and B. nigra, were analysed for seed germination, seed vigour indices, oil content, and fatty acid composition. Seed germination percentages varied from 2% to 100%, with a mean of 75%, and significant variation was observed in seed vigour indices (I and II). Biochemical analysis revealed oil content ranging from 18.03% to 47.48% and significant variability in fatty acid composition. Correlation studies indicated that seed germination and seed vigour were significantly positively correlated with oil content. Modified Partial Least Squares (MPLS) regression techniques were employed to develop NIRS prediction models for seed germination, seed vigour index-I, and seed vigour index-II. The calibration models showed high internal Rsquared (RSQ) values of 0.902, 0.868, and 0.870, respectively. Validation results confirmed the accuracy of these models, with external RSQ values of 0.731, 0.756, and 0.775, and Ratio Performance Deviation (RPD) values indicating good quantitative prediction. The developed NIRS models offer a non-destructive, cost-effective, and rapid method for large-scale screening of seed viability and vigour, benefiting seed testing laboratories and breeders to speed breed crop variety development for improved vigour thereby improving agricultural productivity. The research thus, bring forth a novel approach for effective and practical seed viability and vigour prediction

Critical moisture levels for anoxia storage in soybean seeds

Seeds are essential for crop production, enabling plants to grow across generations. However, their viability and quality decline over time during storage. Molecular oxygen, the main source of reactive oxygen species (ROS), damages cellular membranes and oxidize key macromolecules such as lipids, proteins, DNA, and RNA. A promising strategy to preserve seeds involves storing in a low-oxygen atmosphere (anoxia or hypoxia). This study evaluated the effects of different storage temperatures and seed moisture levels on the viability and vigor of soybean seeds under varying oxygen levels. Three soybean seed lots with low (~7%) and high (~13%) seed moisture content (SMC) were stored at 20°C and 35°C under hypoxia (<1% O_2), normoxia (~21% O_2), and hyperoxia (>99% O_2) for up to four months. Results showed that total seed germination and seedling vigor (normal seedlings and increased time to reach 50% germination, t_{50} in h) significantly declined at 35°C, especially under normoxia and hyperoxia, when compared to 20°C. Hypoxia storage was beneficial for dry seeds but ineffective for seeds with high moisture content. Further experiments with eight soybean seed lots, varying in seed coat colour and seed moisture content (4%, 7%, 8.5%, 13%, and 17%), revealed that seeds with low moisture (below 8.5%) stored under hypoxia retained better viability and vigor than those exposed to hyperoxia conditions. However, high-moisture seeds did not benefit from low-oxygen storage due to anaerobic respiration, which led to alcohol accumulation and viability loss due to suffocation. Seed lots with black seed coat, such as "EC 396065" and "TGX 722-155 F," exhibited higher longevity irrespective of storage conditions, highlighting their potential for improving seed preservation. Overall, storing dry seeds under hypoxia, particularly conditions normally prevalent in hot climates, is recommended for maintaining better seed quality and ensuring food and nutritional security.

Assessment of the relationship between morphological characteristics, seed germination, and dormancy in *Triticum aestivum* L. and *Triticum durum* Desf. genotypes

The present study investigates the relationship between morphological characteristics, seed germination, and dormancy in two wheat species: *Triticum aestivum* L. and *Triticum durum* Desf. A total of 355 genotypes, with 253 genotypes of *T. aestivum* and 102 genotypes of *T. durum* were taken up for this study. Initially, the existing diversity of different plant, ear, and seed morphological traits among the genotypes and between the species was studied. A reasonable variation in plant, ear and seed characteristics among the wheat genotypes of both *T. aestivum* and *T. durum* were observed. However, no significant strong correlation between plant and ear characteristics and seed germination was observed, which could be attributed to the minimal variation in seed germination as most of the genotypes have > 99% germination. The seed dormancy measured as germination index showed a significant but weak association with some ear and seed characteristics. A significant difference was noticed between the two wheat species regarding plant, ear, and seed characteristics. The principal component analysis could differentiate both species based on these characteristics. Thus, this study paves the way to develop an image-based technique to distinguish these two species. The mean spectral absorbance values significantly differed between the two species. However, due to the overlapping of some of the genotypes, it cannot be generalized to differentiate all the genotypes of these two species. The ABA treatment has successfully induced dormancy in the genotypes of both species and, to a greater extent, in T. durum. The genotypes of both species showed considerable sensitivity to ABA, with 3% and 11% of genotypes showing strong sensitivity and 39% and 11% of genotypes showing low sensitivity in *T. aestivum* and *T. durum*, respectively. These genotypes can be used in breeding programs as well as for studying the dormancy regulation mechanisms in these two species.

Hyperspectral imaging for varietal identification and quality assessment of rice seed lots

The study involved conducting tests to investigate the reflectance values using hyperspectral system and the germination process of 16 Basmati and non-Basmati type rice seed lots under natural storage conditions. Sixteen effective wavelength ranges were identified based on the Savitzky-Golay 2nd derivative at 10 nm gaps, showing significant differences in reflectance among the genotypes. Among the five Machine Learning models used, LDA model achieved the highest prediction accuracy of 82% and 78% with high kappa values of 0.81 and 0.76 for the classification of all the 16 rice genotypes and 11 Basmati rice genotypes, respectively. A relationship between germination parameters and the different ageing duration was established on those same genotypes harvested in 2021, 2022 and 2023. Furthermore, the research aimed to assess the difference in seed viability in naturally stored lots by analysing reflectance values of 2 good and 2 poor storer varieties categorized based on germination values, obtained in hyperspectral range. The dehusked grains of these varieties were used to collect reflectance values using the hyperspectral technique. The studies showed that under ambient storage, aged seed lots in all varieties showed decrease in seed germination and related parameters. PCA based on seed germination parameters of seed lots showed that only first two principal components i.e., contributed to more than 95.5% variation in storability. Aged seeds had higher spectral reflectance values than that of fresh seeds. A significant correlation between spectral reflectance and germination was observed in the red edge and near-infrared regions irrespective of good and poor storers. The information generated using hyperspectral imaging would be useful to determine seed longevity status and rapidly identify closely related basmati rice seed lots without destructing the seed samples. However, improvement in ML model and large input data may be required to achieve a higher identification accuracy.

Theme 3: Seed Longevity Studies

Studies on variability for seed quality traits with respect to seed longevity in onion (*Allium cepa* L.)

Onion (*Allium cepa* L.) is an important vegetable crop of India. The information on seed deterioration associated with the ROS content along with the antioxidant enzymatic activity specifically with respect to storage potential of onion seeds is quite limited. Hence, a study was conducted to assess the storage potential of onion genotypes under natural as well as accelerated ageing conditions. Freshly harvested seeds of 30 onion genotypes were stored under ambient conditions for 12 months as well as subjected to saturated salt accelerated ageing for 3 and 6 days (42^oC and 75% RH). Germination percent ranged from 56-96 percent in unaged seeds, which declined significantly after natural ageing and accelerated ageing. In present study, seed germination and vigour indices decreased significantly, whereas the mean germination time increased after ageing. The study facilitated the categorization of onion genotypes into distinct storage groups (good and poorer storers) by assessing their performance after ageing. A significantly positive correlation was found between 3 days and 6 days of AAT with 6 and 12 months of natural ageing. Further, the biochemical changes in onion genotypes was also studied using good storers (Sukhsagar, Bhima Super) and poor storer (POS 24K, Bhima Shubhra) genotypes. An increase in the activity of NADPH oxidase, ROS as well as malondialdehyde content and decline in antioxidant enzyme activity was observed in onion seeds after 6 and 12 months of ambient storage. In another experiment a total of 7 genes (*AcRBOHD, AcCAT1, AcHB25, AcPSAD1, AcPRX2, AcPOX38* and *AcSOD2*) orthologous to *Arabidopsis thaliana* and *Oryza sativa* were found in onion genome using Gene-based PCR markers. A uniform amplicon size was observed in diverse onion genotypes, due to highly conserved nature of these genes governing seed longevity. This study enhanced our understanding regarding the physiological, biochemical and genetic aspects of seed deterioration via interplay of ROS and antioxidant enzymes, affecting seed storage potential of onion seeds.

Genetic variation for seed longevity trait in diverse soybean genotypes

Soybean seeds are inherently short lived, thus lose vigour and viability faster during open ambient conditions depending on environmental factors, genetic make-up and initial seed quality. Genetic studies on soybean seed longevity use moist ageing assays like accelerated ageing test or controlled deterioration test contrary to dry conditions prevailing in the seed storage warehouses. Hence, the present study aimed at assessing the diversity in their seed morphology and longevity traits under dry storage to identify related marker-trait associations (MTAs). A diverse panel of 273 soybean accessions was used to measure different seed morphological traits, *viz.* seed length, width, area, roundness, eccentricity, and absorbance spectra using image analysis, test weight, and germination parameters in fresh and seeds aged under ambient dry conditions for two years. Significant variation among the accessions for all the measured seed morphological traits and multispectral absorbance (MSA) values at 19 different wavelengths were recorded. Similarly, significant variation was observed among the accessions for total seed germination and critical vigour traits in aged seeds compared to fresh seeds. Aged seeds showed significantly lower germination, uniformity, $AUC_{[80h]}$ values and increased t_{50} and MGT when compared to fresh seeds. GWAS identified several novel MTAs distributed across different chromosomes. Among these, the prominent MTA on chromosome 8 was identified for MSA at 450 nm and 470 nm. The locus 5 on chromosome 16 and locus 2 on chromosome 10 harbour MTAs for seed shape and test weight. Similarly, significant MTAs related to total seed germination and normal seedlings in aged seeds were identified on chromosomes 4,10, 17 and 18. Further, this study identified genotypes with significantly high seed longevity that can be used in breeding programs and contrasting genotypes for developing mapping populations to further decipher genetic and molecular basis of seed longevity trait in soybean.

Physiological and biochemical basis of seed longevity in contrasting maize inbreds

Present study was undertaken to assess storage potential of 89 maize inbreds at ambient conditions for 12 months and to identify the inbreds with good seed vigour and storability and to study biochemical mechanisms involved in seed longevity. The results showed that inbreds *viz.,* MIL 6-105 (19.5%), IC213035(19.9%) and IC213095 (36.2%) had significantly lower germination percent, while many inbreds maintained high germination (>80%), after 12 months of ageing. The inbred MIL 6-105 has highest MGT (96.1hr), t_{50} (96.9 hrs), TMGR (96.9 hr) and lowest AUC (7019.8) and the inbred IC0623163 recorded with least MGT (41.3 hr), t_{50}(39.8 hr), TMGR (38.8 hr)464 and highest AUC (12924.4), after 12 months of ageing. The inbreds *viz.,* MIL 6-105 and IC213035 are considered as poor storers and IC0623163 and IC212929 considered as good storers. These four inbreds were further used for studying the biochemical basis of seed longevity. The selected good storers maintained significantly higher SOD and CAT activity, after 12 months of ageing, in comparison to the poor storers .The activity of APX was almost similar in good and poor storers ,while good storers had slightly higher free radical scavenging activity in comparison to poor storers. Further, poor storers almost lost α-amylase activity after 12 months of ageing whereas the good storers maintained the α-amylase activity without significant reduction. H_2O_2 and Malondialdehyde content increased significantly, after 12 months of ageing, in all the inbreds. However, MDA content increased drastically in poor storers in comparison to good storers. Highly significant and positive correlation was recorded between total seed germination and activities of SOD, CAT, free radical scavenging activity and α amylase. Further, a highly significant negative correlation was observed between total seed germination and MDA, H_2O_2 content. The good and poor storer genotypes identified in this study can be used for crossing and utilized in biparental mapping study to identify the genomic regions governing the seed longevity in maize. In addition, the identified good storers can be used in breeding programmes to develop hybrids with high seed vigour and storability.

Theme 4: Seed Technological Interventions for Biotic/Abiotic Stress Mitigation

Seed technological interventions and phylogenetic studies for lectin genes to mitigate the bruchid infestation in chickpea

In chickpea seed production, seeds stored for eight months after harvest are highly vulnerable to secondary bruchid infestations, which can significantly compromise seed viability within to 2-4 months of storage if not properly managed. Despite the development of various mechanical, physical, chemical, and botanical methods, effective bruchid management during storage remains challenging because of the limitations of each approach. Moreover, the potential for host plant resistance has not yet been thoroughly explored. Therefore, this study was undertaken to evaluate the effectiveness of polymer composite seed coatings in mitigating bruchid infestations during storage. Additionally, as a first step towards leveraging host plant resistance against bruchids in chickpeas, a comprehensive phylogenetic analysis of lectin proteins similar to those reported for bruchid resistance in wild *Phaseolus vulgaris* was conducted. Bruchid bioassay studies showed that seeds coated with polymer composites PC1- PC6, PC11-PC14, PC16, PC20, and PC24 demonstrated complete immunity against bruchid infestation. This was assessed through measures such as oviposition, adult emergence, mean developmental period, growth index, seed damage, and seed weight loss, which were statistically significant compared to the control (non-coated) seeds, without compromising seed quality parameters. PC-24 acts as an oviposition deterrent, whereas the other polymer composites prevent the penetration of bruchid first-instar larvae into the seed. Also PC-coated seeds were as effective as known packaging materials in preventing bruchid infestation and spread during three months of storage. Based on similarities in protein sequences, families, conserved domains, and the sites of known bruchid resistance proteins, 82 proteins were identified across various pulses that may confer host plant resistance in these crops. Phylogenetic analysis of these proteins indicated that gene duplication and expansion led to the divergence of the identified crop-specific putative lectin genes, which are similar to the reported bruchid-resistance lectins in *Phaseolus vulgaris*.

Studies on seed invigoration treatments to mitigate salinity stress in soybean (*Glycine max* L).

Soybean, an important oilseed crop of the *Fabaceae* family, has gained significance due to its nutritional qualities and diverse applications. However, its thin seed coat makes it prone to mechanical and imbibitional damage, leading to high electrolyte leakage upon imbibition. Salinity stress is a major challenge in soybean cultivation, significantly reduces the seed yield. The seed coat characteristics and its composition play a crucial role in seedling development. This study evaluated the role of soybean seed coat color in salinity stress tolerance and explored seed invigoration treatments to mitigate the salinity stress. Seventy-three genotypes with black (25), brown (6), green (5), yellow (11 germplasm and 26 released varieties) seed coats were tested under salinity levels of 0, 3, 6, and 9 dS/m. The effects of salinity stress on all seed quality traits were examined and significant genotypic differences were obtained with black genotypes showing the highest germination % and vigor followed by green and yellow genotypes. Physiological and biochemical analysis revealed that black seed coat genotypes exhibited higher antioxidant activity (CAT, POX, APX, SOD), proline content, and lower lipid peroxidation and ROS-H_2O_2 levels, indicating superior salinity tolerance compared to other seed coat colors. Seed priming with four agents—Jasmonic Acid (JA), Salicylic Acid (SA), Potassium Chloride (KCl), and Paclobutrazol (PAC)—was tested. JA at 20 µM significantly improved seed quality, with 85% germination, higher seedling length, higher vigor indices, and reduced mean germination time. JA-primed seeds further demonstrated enhanced morphological traits, such as root system architecture and leaf area index, under hydroponic conditions. Biochemical improvements included increased K^+ content, reduced Na^+, higher antioxidant enzyme activity, and lower lipid peroxidation and ROS-H_2O_2 levels. These findings underscore the potential of black seed coat genotypes for salinity tolerance and establish JA seed priming as an effective strategy to improve soybean seed quality and stress resilience.

Theme 5: Seed Quality Enhancement

Seed enhancement treatments for improvement of seed quality in onion (*Allium cepa* L.)

Onion (*Allium cepa* L.) is the fourth most important commercial vegetable crop cultivated and consumed widely across the globe. However, its cultivation faces challenges due to poor seed longevity and suboptimal germination rates. The present study focused on priming methods such as osmopriming using PEG-6000 and magnetopriming, along with specific gravity separation for seed quality enhancement. Fresh and carryover seed lots of four genotypes *viz*., Pusa Sobha, Pusa Riddhi, Pusa White Round (PWR) and Pusa Red were selected. The seed quality parameters were assessed and on the basis of difference in various germination parameters, the seed lots of PWR and Pusa Red was selected for further studies. Further, these seeds were subjected to specific gravity separation and divided into five different grades viz., H1 (Heaviest), H2 (Heavy), M (medium), L1 (light) and L2 (lightest). It was observed that specific gravity separation improved the seed quality parameters significantly and the H1 performed significantly better than other fractions. The seeds of fresh lots of PWR and Pusa Red were selected for further studies and were subjected to osmopriming treatments at various concentrations (-0.2 MPa, -0.5 MPa, -1 MPa and -1.5 MPa). It was found that -1 MPa performed the best among all the treatments and significantly enhanced the seedling growth and vigour parameters. Further, the seeds were subjected to magnetopriming and it was validated that magnetopriming was effective in enhancing the seed quality as compared to unprimed seeds. Also, the biochemical and physiological changes viz., alpha amylase, catalase, peroxidase and electrical conductivity were studied in the primed seeds. It was found that priming increased alpha amylase and catalase activity to a significant extent. The findings of this study highlight that specific gravity separation, osmopriming (-1.0 MPa), and magnetopriming with 100mT for 30 minutes are effective strategies for enhancing onion seed quality.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Monika Thakur (21793)	M.Sc.	Seed enhancement treatments for improvement of seed quality in Onion (*Allium cepa* L.).	Dr. Sandeep K. Lal	ICAR-IARI, New Delhi
2.	Ayushi Yadav (21907)	M.Sc.	Prediction of seed vigour in rapeseed and mustard using near-infrared spectroscopy (NIRS)	Dr. Sangita Yadav	ICAR-IARI, New Delhi
3.	Prajapati Dineshbhai Roopshibhai (21908)	M.Sc.	Critical moisture levels for anoxia storage in soybean seeds	Mr. Manjunath Prasad	ICAR-IARI, New Delhi
4.	Nikhita (21909)	M.Sc.	Genetic Variation for Seed Longevity Trait in Diverse Soybean Genotypes	Mr. Manjunath Prasad	ICAR-IARI, New Delhi
5.	Febina A S (21943)	M.Sc.	Seed Technological Interventions and Phylogenetic Studies for Lectin Genes to Mitigate the Bruchid Infestation in Chickpea	Dr. Arun Kumar M.B.	ICAR-IARI, New Delhi
6.	Riya Biswas (21944)	M.Sc.	Physiological and Biochemical Basis of Seed Longevity in Contrasting Maize Inbreds.	Dr. Vijayakumar H.P.	ICAR-IARI, New Delhi
7.	Ashwini (21977)	M.Sc.	Assessment of the relationship between morphological characteristics, seed germination, and dormancy in *Triticum aestivum* L. and *Triticum durum* Desf. Genotypes	Dr. D. Vijay	ICAR-IARI, New Delhi
8.	Samrat Rej (60137)	M.Sc.	Effect of seed coating with microbial formulations on seed yield and quality in green gram [*Vigna radiata* (L.) R. WILCZEK]	Dr. Priya Ranjan Kumar	#ICAR-IARI, Jharkhand
9.	Souvik Chakrabortty (21942)	M.Sc.	Hyperspectral imaging for varietal identification and quality assessment of rice seed lots	Dr. S.K. Chakrabarty	ICAR-IARI, New Delhi
10.	Chaithanya G. (11861)	Ph.D	Studies on Seed Invigoration Treatments to Mitigate Salinity Stress in Soybean (*Glycine max* L).	Dr. Monika A. Joshi	ICAR-IARI, New Delhi
11.	Narender Pal (11866)	Ph.D	Studies on variability for seed quality traits with respect to seed longevity in onion (*Allium cepa* L.)	Dr. Sandeep K. Lal	ICAR-IARI, New Delhi

#IARI off-campus

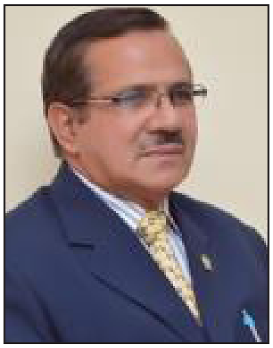
Session II: School of Crop Protection

Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Agricultural Chemicals	08	06
Entomology	13	09
Nematology	05	02
Plant Pathology	11	09
Total	**37**	**26**

SCHOOL OF CROP PROTECTION

Chairperson: Dr. H. C. Sharma, Former Vice Chancellor, YSPUHF, Nauni, Solan, Himachal Pradesh



Dr. H. C. Sharma served as Vice Chancellor of Dr. Y. S. P University of Horticulture & Forestry, Nauni, Solan, Himachal Pradesh; Principal Scientist - International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India, and as a Visiting Scientist - QDPI, Queensland, Australia, and University of Wisconsin, Madison, USA. He has over 40 years of experience in education and research, and has carried out collaborative research with scientists in India, Europe, Asia, Africa, Australia and USA. Under his leadership, YSPUHF was ranked among the top 100 universities in India by NIRF between 2017-2019 and further the University's ranking by ICAR improved from 51st position in 2017 to 11th in 2019. Dr. Sharma has authored over 750 publications [Books - 8, Information bulletins - 13, Research papers - 302, Book chapters - 80. Citations 10,546. Research gate lists his 355 publications with 102,601 reads and 8,584 citations. Based on a study conducted by Stanford University, USA in 2020 and in 2021, Dr Sharma's research contributions figured among the top 2% Scientists in the World (217th position in the world), and top ranked Scientist in Entomology in India. Dr. Sharma's scientific contributions have been recognized by several academic societies including 9 Gold Medals, Millennium Science Award by ICRISAT, Excellence in Science Award by Consultative Group in International Agriculture Research, and Hari Om Trust Award by ICAR. He is a Fellow of 11 academic societies, including National Academy of Agricultural Sciences and Entomological Society of America. Dr. Sharma has also served as Chair/ Member of various International Organizations, namely, as President, Council of International Congresses of Entomology (2008-16) – first Asian elected as President of this 112 years old organization. He also served as President of the 19th International Plant Protection Congress (IPPC 2019), Hyderabad – held for the first time in India in over 100 years. He has also served as Member, Governing Board, International Association of Plant Protection Sciences (2008- 2023).

AGRICULTURAL CHEMICALS

4

Prof. Suman Gupta

Division of Agricultural Chemicals was created in 1966 when Government of India was in the process of formulating pesticide policy and enacting Insecticide Act. Since then, the Division has proved to be 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. Significant research findings of postgraduate students are enlisted under the following themes:

Theme 1: Development and Formulation of Agrochemicals

Synthesis of isoxazole and pyrazole derivatives and their evaluation against plant pathogenic fungi and barnyard grass in rice

A series of forty isoxazole and pyrazole derivatives were synthesized using alkoxy/halo acetophenones and N, N-dimethyl formamide dimethyl acetal, out of which twenty-two (*i.e.* 5b, 5c, 5d, 5e, 5g, 5h, 5i, 5j, 5k, 5l, 5m, 6b, 6c, 6d, 6e, 6g, 6h, 6i, 6j, 6k, 6l and 6m) were reported for the first time. These compounds were characterized by ^{1}H NMR, ^{13}C NMR and LC-HRMS and were evaluated for fungicidal activity against *Rhizoctonia solani* and *Fusarium fujikuroi* and herbicidal activity against *Echinochloa crus-galli.* Among the (5a-5t) series of isoxazole derivatives, 5n (5-(2-chlorophenyl) isoxazole) showed highest fungicidal activity against *R. solani*with ED_{50} of 4.43 μg/mL.In case of *F. fujikuroi,* 5p (5-(2,4-dichloro-2-hydroxylphenyl) isoxazole), having ED_{50} 6.7 μg/mL showed the highest activity. Among the (6a-6t) series pyrazole derivatives, 6r (3-(5-fluoro-2-hydroxylphenyl) pyrazole) showed the highest fungicidal activity against *R. solani*with ED_{50} 2.75 μg/mL. In case of *F. fujikuroi,* 6r (3-(5-fluoro-2-hydroxylphenyl) pyrazole) showed the highest fungicidal activity with ED_{50} 2.75 μg/mL.Pot experiment against *R. solani*revealed that compound 6r (3-(5-fluoro-2-hydroxylphenyl) pyrazole) @ 1000 μg/mL showed higher disease control with % RLH (Relative lesion height %) of 10.74, at par with the hexaconazole (10.78 % RLH). In the case of *F. fujikuroi*, five most effective compounds 5p, 6r, 6s, 6q and 6p were evaluated for pot culture activity. Results revealed compound 6r (3-(5-fluoro-2-hydroxylphenyl) pyrazole) @ 1000 μg/ mL as the most effective with the lowest percent disease incidence, 13.89%. Herbicidal activity of isoxazole and pyrazole derivatives against *E. crus-galli* demonstrated 58.1% and 54.4% inhibition with 5a and 5r, respectively, while 6a and 6s displayed 54.1% and 50.6%inhibition, respectively. Smaller alkoxy derivatives (5a-5e and 6a-6e) demonstrated better weed control than halogen-substituted derivatives. Isoxazole, 5a (2-(isoxazol-5-yl)-5-(methoxy) phenol) had a weed control index (WCI) of 52.86% at 30 DAT, while pyrazole 6a (5-Methoxy-2-(1*H*-pyrazol-3-yl) phenol) showed a WCI of 51.32%, with no rice phytotoxicity.

Triazolyl Schiff's bases and amides based on naturally occurring citronellal as potential plant pathogen and nematode antagonists in rice

A series of eleven novel amides were prepared by condensation of citronellic acid with different alkyl amines in the presence of *Candida antartica*lipase at 60- 90^{o}C in 16-20 h. Reactions were performed without solvents, yielding 72.42-82.32% product. Fifteen citronellic acid based triazolyl Schiff bases were synthesised using a design incorporating the citronellic acid moiety within 4-amino-1,2,4-triazoles, and condensing the key intermediate triazole with various benzaldehydes, in a five-step process, commencing with citronellic acid, then sequentially transforming it to ethyl ester, hydrazide, dithiocarbazinic salt, triazole and ultimately into Schiff bases. The final step of Schiff base synthesis from key intermediate triazole was performed in microwave in 4-5.5 min compared to the conventional 4-6 h giving 86.51% to 92.56% and 76.13% to 85.83% yield, respectively. Synthesized compounds were tested against *Meloidogyne graminicola*, exhibiting promising activity of6e, 6n, 6a, and 3a with LC_{50} 39.87, 57.56, 63.29 and 64.79 mg/L, respectively. In the root dipping and soil drenching methods, activity of the compounds followed 6e >6n >6a >3a with enhanced plant growth parameters. Specifically, 6e at 1000 mg/L showed the lowest number of galls (4.35 inroot dipping and 3.35in soil drenching) proved to be the most effective. *In vitro* activityagainst *Rhizoctonia solani* showed compounds 6b, 6c and 3a as effective with EC_{50} 23.56, 38.49 and 23.61 mg/L, respectively. In case of *Pyricularia oryzae*, compounds 6i, 6b and 3a exhibited effectiveness with EC_{50} 18.53, 23.25 and 24.76 mg/L, respectively. Results of pot study indicated that at 2000 mg/L, compound 6b was the most effective in sheath blight control, exhibiting18.38% RLH whereas,for *P. oryzae*,6i and 6b @ 2000 mg/L exhibited the lowest Percent Disease Incidence of 18.75% and 22.22%, respectively. The highest disease control percentage (60.87%) was seen in plants treated with 6i, followed by 6b and 3a at 2000 mg/L.

Synthesis of prenylated chalcones and their evaluation against plant pathogenic nematodes and fungi in tomato

A series of 32prenylated chalcones was synthesized by microwave assisted green synthesis as well as the conventional method revealing higher yield (86-95%) and lower reaction time(1-4 min) in microwave method compared to conventional method (71-84 %, 12-48 h). Among these, 19 compounds (5M, 5J, 5L, 6A, 6B, 6C, 6D, 6E, 6F, 6G, 6H, 6I, 6J, 6K, 6L, 6M, 6N, 6O, 6P)were novel and were reported for the first time. Compounds were tested against *M. incognita,*revealing 2’-hydroxy-2,6-dichloro-4’-*O*-prenylchalcone (5B) asthe most active with $LC_{50}$of 30.40, 20.11 and 14.47 µg/mL after 24, 48 and 72 h, respectively. Among (6A-6P) series, compound 2’-hydroxy-3-bromo-5’-*O*-prenylchalcone (6F) was found most active with LC_{50} 17.19, 9.22 and 4.69 µg/mL after 24, 48 and 72 h, respectively. Compounds 6B, 6D, 6E and 6F were found to be more potent and were taken for pot study, revealingthe highest activity of compound 6F @1000 µg/mL at 30 DAI and 60 DAI with enhanced plant growth parameters. Among (5A-5P) series, compound 2’-hydroxy-4-bromo-4’-*O*-prenylchalcone (5E) and 2’-hydroxy-2,6-dichloro-4’-*O*-prenylchalcone (5B) having ED_{50} 23.28 and 25.70 µg/mL possessed highest activity against *S. rolfsii* and *F. oxysporum,* respectively. Among (6A-6P) series, 2’-hydroxy-4-benzyloxy-4’-*O*-prenylchalcone (6P), showed the highest antifungal activity against *S. rolfsii*(ED_{50} 25.02 µg/mL)and *F. oxysporum* (ED_{50} 31.87 µg/mL). Compound 5E and 5M were chosen for pot experiments against *S. rolfsii*, revealing significant increase in shoot length for5E followed by 5M @1000 µg/mL at 60 DAI. Minimum percent disease incidence was observed for5E @1000 µg/mL. Recoveryusing modified QuEChERS from fortified soil and tomato samples was in the range 70-120%at 0.05 and 0.1 µg/g fortification levels. The half-lives of the compounds 5E, 5M, 6B, 6D, 6E, 6F, hexaconazole and fluopyramin soil were 1.31, 1.47, 1.60, 1.52, 1.07, 1.51, 18.57 and 26.86 days, respectively.

Synthesis of substituted imines and antifungal evaluation against *Sclerotial* fungi

The world is facing more than 30% agricultural losses due to the number of pests in spite of the use of chemical pesticides and modern crop protection techniques in agriculture. In order to provide sufficient food to the increasing population these crop losses must be prevented. Therefore, the need for efficient, safe, biodegradable protectants has become crucial. Compounds containing imines (>C=N–), have shown promising antifungal properties against a variety of plant pathogens. In the present study 27 imines were prepared from substituted benzaldehydes and several anilines and were characterized using various spectral techniques. *In-vitro* antifungal evaluation was also done for these compounds against *Rhizoctonia solani* and *Macrophominaphaseolina*. The study revealed a number of compounds having antifungal potency with ED_{50} values ranging from 2.57 to 510.14 µg/ml against both the fungi. Structure-activity relationship (SAR) study revealed that chlorine substitution on the phenyl ring resulted in the higher antifungal activity. Similarly, better antifungal activity was observed with bromo substitution at the para position of the phenyl ring originated from the aniline followed by methoxy and ethyl substitutions. Moreover, adding a chloro group into the meta positions of the phenyl ring attached to carbon of the imine group had increased antifungal efficacy against both *R. solani* and *M. phaseolina*. Overall, compounds from the A and B series were more active against both *R. solani* and *M. phaseolina.* The present investigation resulted in the identification of promising antifungal imines which can be taken up as templates for the design and development of new crop protectants for disease management in agriculture.

Synthesis and evaluation of tetrazole derivatives against plant pathogenic fungi

A series of 2-(5-phenyl)-tetrazol-1-yl-chromen-4-one derivatives were synthesized by a four-step synthesis schemeinvolving condensation of substituted 2-hydroxy acetophenone derivatives with N, N-dimethylformamide dimethyl acetal to yield enaminones. The subsequent cyclisation of enaminones with iodine gave 3-idochromones, which on reaction with 5-phenyl tetrazole resulted in the formation of desired 2-(5-phenyl)-tetrazol-1-yl-chromen-4-one derivatives.A total of 20 different 2-(5-phenyl)-tetrazol-1-yl-chromen-4-one derivatives (6a-6t) were synthesised, having yield range of 74.62%-88.21%, and characterized withFT-IR, ^{1}H NMR and ^{13}C NMRtechniques .All synthesised 2-(5-phenyl)-tetrazol-1-yl-chromen-4-one derivatives (6a-6t) showed good antifungal activity against *Sclerotium rolfsii*and *Fusarium oxysporum*. Among the tested compounds, 6r exhibited very good antifungal activity against *S. rolfsii* with ED_{50} 17.75 ppm. In case of *Fusarium oxysporum* compound 6t displayed good activity with ED_{50} 20.50 ppm. Therefore, 6r and 6t were identifiedas the potent molecules for management of *S. rolfsii* and *F. oxysporum*,respectively.

Quantification and insect growth regulatory activity of nimbolide from the leaves of *Azadirachta indica* A. Juss.

Nimbolide, a bitter and one of the major compounds of *Azadirachta indica* leaves was isolated as a white amorphous compound and identified by Co-TLC and spectroscopic techniques (FT-IR, 1D and 2D NMR, MS). The amount of nimbolide in the leaves of *A. indica* was determined by UFLC-PDA together with quercetin-3-O-*β*-glucopyranoside. Study on monthly variation of nimbolide in its leaves were also carried out for five months from December 2023 to April 2024 using UFLC-PDA. The total amount of nimbolide in the leaves was found to be 49.59 ppm, while that of quercetin-3-O-*β*-glucopyranoside was 48.52 ppm. A study on monthly variation of nimbolide content in the leaves, collected from December 2023 to April 2024 showed variable amount of nimbolide, ranging from 13.48-43.98 ppm. The highest amount (43.98 ppm) of nimbolide was found in December and lowest (13.48 ppm) in April. A method for the simultaneous detection and quantification of nimbolide and quercetin-3-O-β-glucopyranoside in its leaves was also developed. It was further evaluated for its insect growth regulatory and antifeedant activities against *Spodoptera frugiperda*(Fall armyworm). The highest reduction of the weight (210.53± 10.34 mg) of the larva was recorded at 5000 ppm due to the growth inhibitory activity of nimbolide as compared to the control (352.26±9.91 mg) treatment. It also showed promising antifeedant activity (72.45±2.99%) at 5000 ppm. This study suggests that the leaves of *A. indica* can be used as a rich source of nimbolidewhich has insect growth regulatory and antifeedant properties against *S. frugiperda*. Its leaves were also identified as a natural source of quercetin-3-O-β-glucopyranoside. This study confirmed that nimbolide has pest control activity and thus need to be explored further.

Bioprospecting of *Datura* sp. for the control of *Bemisia tabaci*

Presence of significant amount and number of alkaloids in*Datura metel*,attracts intervention for pest management purpose. Bioassay guided fractionation was done using five different solvents across polarity. Insecticidal contact toxicity assay of these extracts using no-choice bioassay revealed LC_{50} (%) of 0.61, 0.66, 0.26, 0.22 and 1.48 for hexane, dichloromethane, ethyl acetate, methanol and water extracts after 72 h of exposure, respectively. Methanol extract was found to be the most active fraction and the extraction yield was also maximum (74.4 g kg^{-1}). LC_{50} values ranged between 0.22-1.15% across 24-96h interval. Whitefly adult showed significant deformities especially deformation in wings upon treatment with methanolic extract @ 7500 mg/L. UPLC-ESI-TOF-MS analysis of methanolic extract revealed more than 18 different alkaloids present in the extract. Out of which, three were major compounds viz. apoatropine (m/z 271.1650), scopolamine (m/z 289.1392) and methyl-hyoscyamine (m/z 303.1912). Molecular docking study was done against five different target proteins, out of which ryanodine receptor was found to be the most suitable for docking with Gibbs free energy (ΔG) values of -75.89, -80.96, -135.69 kcal/mol for atropine, scopolamine and hyoscamine, respectively. Soluble concentrate (SL) formulation of the most active methanolic extract was developed by optimizing its constituents. Final SL formulation of methanolic extract was comprised of extract (10 %), surfactant Triton-X 100 (5 %), glycerol (3%) and propylene glycol (1.25 %). Accelerated storage stability test showed significant stability of the formulation, where marker compound (scopolamine) found to be stable (>95% stable) after 14 days storage at 54±2 ºC. The developed formulation showed stable pH before and after the storage study.

Chemical profiling of *Angelica archangelica* L. roots for potential nematicidal action against *Meloidogyne incognita*

Angelica archangelica L. roots have been given immense value due to heavy load of bioactive phytochemicals, therefore could be a potential candidate for the development of botanical pesticides. Bioactive phytochemicals were extracted, characterized and formulated to develop a suitable bionematicide for the management of root-knot nematode, *Meloidogyne incognita*. Essential oil yield was found to be 0.896%, comprising of thirty volatile components particularly, limonene (16.39%), vinylguaiacol (14.10%) and citronellol acetate (13.91%). Cold extraction with various solvents revealed the highest yield of methanolic extract (8.72±0.44%) followed by hexane extract (3.32±0.17%) and DCM extract (2.28±0.11%). These were evaluated against *M. incognita*, revealing hexane extract as the most potent after 24h exposure(LC_{50} 176.4 μg/mL). Comparative assessment of extraction methods among conventional solid liquid extraction (CSLE), ultrasonication assisted extraction (UAE), Microwave assisted extraction (MAE) and high-speed homogenization (HSH) indicated HSH as the best extraction techniques which was further optimized using response surface methodology,achieving impressive extraction yield of 41.69 mg/g sample, employing rotation of 800 rpm, solvent to solute ratio of 50 mL/g sample and 10 min extraction time. Hexane extract was found to containligustilide (43.92%) and butylidenephthalide (12.04%) as predominant components. UPLC-QToF-ESI-MS analysis revealed thirty-five phyto-compounds, among these riligustilide, the dimer of ligustilide was isolated and characterized by FT-IR, ^{1}H-NMR, ^{13}C-NMR and mass. Nanoemulsions, prepared and characterized for emulsion stability and average droplet diameter, showed high effectiveness (LC_{50} 63.80 μg/mL after 24h) against *M. incognita*. Molecular modeling indicated good interaction with odr 1 gene and

AChE, which may be attributed to conventional hydrogen bonding as well as π-π interaction.

Development and evaluation of drone compatible formulation/s for smart pest management in maize

The study aimed to develop multicomponent drone compatible bioinsecticidal sprayable formulations. The active ingredients for OD (SBOD-23) and EC (SBEC-23) formulations were selected through sequential *in silico* and *in vitro* bio assay approaches involving 200 bioactive compounds with pre-reported insecticidal potentials. Chlorantraniliprole (Chl) and emamectin benzoate (EB) outperformed all test compounds. The *in vitro*assay exhibited the order of performance: Chlorantraniliprole alone (LC$_{50}$0.039 ppm); Emamectin benzoate alone (LC$_{50}$0.027 ppm); Chlorantraniprole+Emamectin benzoate in the ratio of 0.75-1:0.9-2.5 (combined LC$_{50}$ 0.01 ppm). Volatile oils EO1, EO2 and their compositions in the ratio of 0.8-1:0.9-1 (EO1+EO2) exhibited LC$_{50}$ of 0.297%, 0.204% and 0.069%, respectively. Auxiliaries for the formulations namely, emulsifiers, dispersant and suspending agent, were standardized w.r.t their stability parameter, dispersion stability, emulsion stability, viscosity and pourability. The SBOD-23 (8-10%) and SBEC-23 (25-30%) formulations passed all the physicochemical tests in accordance to FAO/WHO guidelines and were found stable under accelerated storage conditions at 54+2 °C for 14 days and at 0 °C for 7 days. Under *in-vivo* experiment, the SBOD-23 formulation [Chl+EB (0.75-1:0.9-2.5)] and SBEC-23 formulation (EO1+EO2) showed the least whorl damage and highest weight of the maize plants. The efficacy of these formulations was further evaluated under multilocation field trials (Punjab, IARI-New Delhi, Pune). Both SBOD-23 and SBEC-23 formulations outperformed with superior bio-efficacy over their respective positive checks in terms of reducing FAW infestation and increase in grain yield. Both SBOD-23 (140g/ha) and SBEC-23 (1.36L/ha) formulations showed least leaf damage score (1.39-1.52) using drone application as compared to absolute control (4.44) and positive checks (chemical-2.18; biological-2.25) and highest grain yields of 12.32 t ha^{-1} and 12.26 t ha^{-1} as compared to control and positive checks. The harvest time residues in maize grains for both Chl and EB were below quantifiable limits in case of drone spray. Safety assessment studies revealed no consumer risk for application of SBOD-23 and SBEC-23 through drone at applied dose on maize crop in Indian scenario.

Chemo-profiling of *Gymnema sylvestre* leaves for potential antifungal action against storage pathogens

Bioassay guided extraction of *G.sylvestre* leaves displayed broad spectrum efficacy against storage pathogens, *Penicilliumexpansum* 2995, *Penicilliumdigitatum* 7910, *Aspergillus flavus* 8529, *Aspergillusparasiticus* 6365 and *Fusariumverticilliodes* 8271.Conventional Solid Liquid Extraction (CSLE) of leaves gave highest yield of methanolic extract (7.45±1.21%), followed by EtOAc extract (5.61±1.38%), CHCl$_3$ extract (3.19±0.94%) and hexane extract (2.02±0.34%). The most active EtOAc extract exhibited EC$_{50}$ 102.3 µg/mL against *P. expansum*2995. Ultrasonication assisted extraction showed higher extraction efficiency. It was further optimized using factorial design to reveal 359.51 mg/ 2g sampleextraction yield, employing 38.50 mL solvent, 30.65 W power and 17.45 min time. UPLC-QTOF-MS^{E} analysis gave identification of thirty-seven compounds dominating triterpenoidal saponins, flavonoid, lignan, steroids. Among these, gymnemic acid I, VII and gymnemagenin were isolated, purified and characterized using ^{1}H-NMR, ^{13}C-NMRand QTOF-MS. Gymnemic acid I content was estimated to be 67 mg/g of extract.*In silico* analysis against sterol 1,4-α-demethylasesuggested higher binding efficacy of gymnemic acid I (-33.7 kJ/mol), gymnemagenin (-31.5kJ/mol) andgymnemanol (-29.0 kJ/mol) through low-distance conventional hydrogen bonds and hydrophobic pi-alkyl interactions.Ergosterol inhibition (87.50±4.96%) was recorded with the treatment of 1000 µg/mL concentration to *P. expansum* 2995 with significant increase in membrane ionic concentration 3–34 µg/mL.Gymnemic acid I rich extractwas encapsulated with chitosan to develop edible coatings for apples to provide protection from *P. expansum*2995 decay.After 30 days of storage, the coating was found to be highly effective, exhibiting only 21.42±1.51%decay, retaining fruit quality such as weight loss (8.48±0.94%), firmness (6.83±0.01 N), skin elasticity (1.64±0.02 mm), stiffness (3.86±0.11 mm), and flesh penetration (3.96±0.07NSec^{-1}), TPC (13.27±1.01 mg GAE/g), TFC (6.79±0.96 mg QE/g) and antioxidant potential (29.36 µg/mL in DPPH assay and 41.34 µg/mL in ABTS assay).Release of gymnemic acid I followed First-order kinetics with the release pattern of Fickian diffusion.

Theme 2: Assessment and Management of Contaminants

Status of glyphosate residues in waters of NCR region and it's sorption behavior in soil

Glyphosate, a widely used herbicide, has become a significant environmental concerndue to its presence in water, alongside its toxic metabolite AMPA. The International Agency for Research on Cancer (IARC) classified glyphosate as a probable carcinogen linked to liver cancer, diabetes, and cardiovascular diseases. Detecting low levels of glyphosate and AMPA in water is challenging due to their high polarity, lack of chromophore groups, and low volatility. In India, there was no prior research on glyphosate and AMPA residues in water. A new method for their trace-level quantification was developed using an Agilent 6470 LC-TQ/MS. The method involved extracting glyphosate from water by derivatizing with 9-FMOC-Cl, partitioning with dichloromethane and analysis by LC-MS/MS. Single laboratory validation confirmed the method's specificity, linearity, sensitivity, accuracy, precision, and matrix effect. A good linear relationship was found for glyphosate (0.01–0.25 µg/L) and AMPA (0.1–2.5 µg/L), with limits of quantification (LOQ) of 0.05 µg/L for glyphosate-FMOC and 0.5 µg/L for AMPA-FMOC. Recovery rates were 77.33-81.33% for glyphosate-FMOC and 74.0-80.4% for AMPA-FMOC, with repeatability confirmed through SANTE/11312/2021 guidelines. Real water samples from the NCR region and other parts of India were analyzed, revealing glyphosate residues up to 0.346 µg/mL. Glyphosate sorption was highest in soils with higher organic carbon content. In sandy soils like those in Haryana, leaching was significant, while in clay-rich soils like IARI soil, no residues in leachate were observed.

Dissipation of oxytetracycline antibiotic in honey

An instrumental method was standardized for the trace-level detection and quantification oftetracyclines (TCs) and chloramphenicol (CMP) in honey with good sensitivity, precision, repeatability andreproducibility. Na_2EDTA –McIlvaine buffer assisted extraction and clean up with solid phaseextraction (SPE) using HLB 60 mg cartridge was optimized to extract tetracyclines from honeysamples. Liquid – Liquid extraction using ethyl acetate as an extraction solvent was optimized as thebest method for extracting chloramphenicol from honey. To find out the effect of different types ofhoney, storage temperature, spiking levels, and effect of processing on the dissipation ofoxytetracycline and chloramphenicol antibiotics, studies were conducted in five different honey typesbelonging to honeydew honey, monofloral honey (acacia honey, wild thyme honey, mustard honey)and multiflora honey. The order of Half-life (DT_{50}) of oxytetracycline (OTC) in different honeysamples followed the order: Acacia (4 days); Wild thyme (4 days);Honeydew (6 days);Multiflora(10 days); Mustard (28 days). Acacia and wild thyme honey were degrading oxytetracycline fastercompared with all other honey samples. Half-life (DT_{50}) of chloramphenicol (CMP) in differenthoney samples followed the order: Multiflora (5 days); Honeydew (8 days); Acacia (9 days); Wildthyme (14 days);Mustard (17 days). Processed samples of honeydew (DT_{50}: ~10 days) and acacia(DT_{50}: ~9 days) showed slower degradation compared to unprocessed samples of honeydew (DT_{50}:~6 days) and acacia (DT_{50}: ~4 days). Among the two antibiotics tested, oxytetracycline residues wereconsiderably reduced in the processed honey samples as compared to chloramphenicol. Degradation was slightlyfaster when the incubation temperature increased from 25ºC to 35ºC. The dissipation of antibioticsvaries with the type and physicochemical properties of honey as well as the chemical nature of theantibiotic molecules. Minimum waiting period of 3-4 monthsis required for the complete degradation of antibiotic residues in honey.

Synthesis of molecularly imprinted polymers for selective removal of triclosan from water

The extensive use of xenobiotics has inadvertently introduced emerging contaminants (ECs) into both terrestrial and aquatic environments, posing substantial health risks to humans and animals. Among these, endocrine-disrupting compounds (EDCs) are particularly concerning due to their ability to disrupt hormonal systems, leading to detrimental developmental, reproductive and metabolic effects in mammals. The complexity of environmental matrices and the trace levels at which these contaminants are present make their detection and analysis particularly challenging. In this context, molecularly imprinting technology emerges as an innovative tool for the selective recognition and extraction of contaminants from complex matrices. In this research, sixteen triclosan specific MIPs and NIPs, including magnetic and surface modified, were synthesized and characterized using FTIR, SEM, TEM, VSM, and BET techniques. High-performance liquid chromatography (HPLC) method with calibration range from 0.01 to 10 μg/mL was developed for triclosan analysis (R^2 0.998). Based on preliminary screening and imprinting factors, four polymers were selected for detailed studies. Adsorption experiments showed that MIPs had higher binding capacity due to triclosan-specific imprints on their surfaces. The adsorption data fitted well to pseudo-second-order kinetic model (R^2 0.967 to 0.990), indicating a chemically driven process. Adsorption data were satisfactorily modelled by the Freundlich isotherm (R^2 0.974-0.994, $1/n < 1$), indicating adsorption on a heterogeneous surface is favourable. Negative values of ΔG, ΔH, and ΔS confirm that the process is spontaneous and exothermic. The Scatchard plot analysis showed two distinct binding sites on the MIPs for triclosan, with one site having a much higher affinity (C_{max}: 264525.25 to 965931.03 μg/g) than the other (C_{max}: 18.87 to 89.28 μg/g). The separation factor values demonstrate the high selectivity of MIPs for triclosan over structural analogue bisphenol-A. Prepared MIPs retained their high sorption capacity even after multiple washing and regeneration cycles. The selected MIPs achieved removal rates of 92.43% to 97.25% from field water samples. These MIPs, with high selectivity for triclosan and the added benefit of easy separation using an external magnet, are ideal for removing triclosan from industrial effluents, municipal wastewater, and for trace-level detection in complex matrices.

Bio-augmentation for managing degradation of persistent pesticides in biomixtures

Present study evaluated adsorption-desorption and degradation of glyphosate and tricyclazole. Sorption was studied in rice straw-compost (BM1) and 1% wheat straw biochar (WBC) [WBCBM1(1%)] and 5% WBC [WBCBM1(5%)] biomixtures. Tricyclazole was more sorbed than glyphosate in all biomixtureswhich can be attributed to its lower water solubility. The WBC increased the sorption of both the pesticides and the sorption was best explained by Freundlich isotherm.Degradation of glyphosate in unexposed soil biomixture (BM1) and glyphosate pre-exposed soil (BM2-soil, 11-12y history of glyphosate, last treated 6m before; BM3-soil 4-5y history of glyphosate, last treated 45 days before) was studied. Glyphosate pre-exposure and timing of last application significantly affected the degradation of glyphosate and metabolite aminomethylphosphonic acid (AMPA). Glyphosate degradation was 240% faster in BM3 biomixture than BM2 biomixture. No effect of tricyclazole pre-exposed soil was observed on fungicide's degradation. The WBC significantly affected degradation of pesticides and effect varied with nature of pesticide and WBC level. Bioaugmentation of biomixtures with glyphosate degrading *Bacillus piscis* significantly enhanced glyphosate and AMPA degradation in BM1, WBCBM1(1%) and WBCBM1(5%) biomixtures which varied from 110 % (BM1) to 137% [WBCBM1(1%)] for glyphosate and 101% (BM1) to 133% [WBCBM1(1%)] for glyphosate+AMPA. However, *Phanerochaetechrysosporium* showed marginal increase in degradation of glyphosate and tricyclazole. Degradation of glyphosate (5000 μg) and tricyclazole (5000 μg) was evaluated in *B. piscis* inoculated BM3, WBCBM3(1%) and WBCBM3(5%) biobeds.

After 150 days, no detectable levels of glyphosate and AMPA were detected in BM3 and WBCBM3(1%) biobeds. However, 159.80 µg glyphosate and 24.34 µgAMPA were recovered from WBCBM3(5%) biobed. Similarly, complete tricyclazole degradation was observed in WBCBM3(5%) biobed after 90 days, while 736.84µg and 105.23 µg tricyclazole were recovered from BM3 and WBCBM3(1%) biobeds, respectively. The study suggested that bioaugmented biomixtures prepared using pre-exposed soil and biochar can be exploited for detoxification of these pesticides in bio-purification systems.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Subhajit Rakshit (21805)	M.Sc.	Status of glyphosate residues in waters of NCR region and it's sorption behavior in soil	Dr. Tirthankar Banerjee	ICAR-IARI, New Delhi
2.	Anirban Barik (21806)	M.Sc.	Chemical profiling of *Angelica archangelica* L. roots for potential nematicidal action against *Meloidogyne incognita*	Dr. Aditi Kundu	ICAR-IARI, New Delhi
3.	Neeraj Dhakar (21807)	M.Sc.	Quantification and insect growth regulatory activity of nimbolide from the leaves of *Azadirachta indica* A. Juss	Dr. V.S. Rana	ICAR-IARI, New Delhi
4.	Amandeep (21808)	M.Sc.	Synthesis of molecularly imprinted polymers for selective removal of triclosan from water	Dr. Suman Gupta	ICAR-IARI, New Delhi
5.	Arunima MU (21809)	M.Sc.	Dissipation of oxytetracycline antibiotic in honey	Dr. Neethu Narayanan	ICAR-IARI, New Delhi
6.	Koyel Mondal (21810)	M.Sc.	Synthesis of substituted imines and antifungal evaluation against Sclerotial fungi	Dr. Rajesh Kumar	ICAR-IARI, New Delhi
7.	Geetanjali (21811)	M.Sc.	Synthesis and evaluation of tetrazole derivatives against plant pathogenic fungi	Dr. Parshant Kaushik	ICAR-IARI, New Delhi
8.	Astha Priya (21911)	M.Sc	Bioprospecting of *Datura* sp. for the control of *Bemisia tabaci*	Dr. Supradip Saha	ICAR-IARI, New Delhi
9.	Kailash Pati Tripathi (11156)	Ph.D.	Synthesis of isoxazole and pyrazole derivatives and their evaluation against plant pathogenic fungi and barnyard grass in rice	Dr. N.A. Shakil	ICAR-IARI, New Delhi
10.	Rajni Godara (11665)	Ph.D.	Synthesis of prenylated chalcones and their evaluation against plant pathogenic nematodes and fungi in tomato	Dr. N.A. Shakil	ICAR-IARI, New Delhi
11.	Sameer Ranjan Misra (10932)	Ph.D.	Triazolyl Schiff's bases and amides based on naturally occurring citronellal as potential plant pathogen and nematode antagonists in rice	Dr. N.A. Shakil	ICAR-IARI, New Delhi
12.	Shreosi Biswas (11663)	Ph.D.	Development and evaluation of drone compatible formulation/s for smart pest management in maize	Dr. Anupama Singh	ICAR-IARI, New Delhi
13.	Garima Sethi (11667)	Ph.D.	Bio-augmentation for managing degradation of persistent pesticides in biomixtures	Dr. Neera Singh	ICAR-IARI, New Delhi
14.	Shila Neel (11666)	Ph.D.	Chemo-profiling of *Gymnema sylvestre* leaves for potential antifungal action against storage pathogens	Dr. Aditi Kundu	ICAR-IARI, New Delhi

ENTOMOLOGY

5

Prof. S. Subramanian

The Division of Entomology, one of the five oldest Divisions of this institute that has been making significant contributions to basic and applied research in plant protection. The teaching and research activities of the division align well with the requirements of the farmers. The major focus of the Division includes Insect Taxonomy and Biosystematics, Insect Physiology and host plant resistance, insect toxicology and Insect pest management. The diversified research activities deploy both conventional and modern technological tools for advancement of Entomological research in the country. Significant research findings of postgraduate students are enlisted under the following themes:

Theme1: Insect Taxonomy and Biosystematics

Biosystematic studies on bees (Hymenoptera: Apoidea) of Meghalaya

Bee diversity comprises of 20,925 species globally, including 755 species from India. They vary in structure, size, habits and food preferences and are crucial for pollination, which is vital for many ecosystems and agriculture. Information on Indian bee diversity is scanty, especially from Northeast India. The bee fauna of Meghalaya has not been studied comprehensively. Therefore, the present studies were undertaken to evaluate the bee fauna status of Meghalaya. Taxonomically, bees are distinguished from wasps by characteristics like branched plumose hairs, broader hind basitarsi, longer proboscis and presence of scopa. Explorations of various agro-ecosystems in seven districts of Meghalaya were conducted for bee collection. The specimens were brought to the laboratory, processed, pinned and mounted for detailed study, and finally deposited in National Pusa Collection, Division of Entomology, ICAR-IARI, New Delhi. An up to date checklist of bee species of Meghalaya complied, indicated a total of 108 species under 30 genera viz. Colletes, Andrena, Apis, Tetralonioidella, Amegilla, Ceratina, Xylocopa, Bombus, Elaphropoda, Habropoda, Thyreus, Tetragonula, Lepidotrigona, Nomada, Patellapis, Lasioglossum, Halictus, Thrincostoma, Sphecodes, Hoplonomia, Maynenomia, Curvinomia, Austronomia, Lipotriches, Megachile, Coelioxys, Anthidiellum, Euaspis, Trachusa and Aglaoapis. Valid names, synonyms and distribution records were included in the checklist. Description of the two new species, few redescriptions and diagnoses of 42 species under 19 genera and 5 families are included. Several new characters including male genitalia, 44 coloured plates with approximately 370 photographs have been included in the study. Diagnostic keys were compiled for identification of taxa at different levels of hierarchy. Furthermore, the study established 9 country records for India with 24 records for Meghalaya state. Host association of 76 plant species with bees were recorded. These findings contribute significantly to the understanding of bee diversity in Meghalaya and provide a foundation for future conservation efforts in the region.

Taxonomic studies on subfamily Agrypninae (Coleoptera: Elateridae) from India

The Elateridae Leach, 1815, is the ninth largest family and contains approximately 11,000 identified species, which are distributed in 18 subfamilies and 37 tribes recorded worldwide. In India, more than 835 species of Elateridae are classified across 113 genera and eight subfamilies. Agrypninae is the second largest subfamily next to Elaterinae. The members of Agrypninae are emerging as important pests in several crops, and most of them are known from the genus level only. The identification of elaterid beetles is quite difficult; even the common species are not known to the researchers. There is a huge gap in the existing knowledge of the taxonomy of these beetles, as most of them are known from original descriptions that dates back to a century. So, it is very important to identify and document the Agrypninae fauna of India. In the current study, for the first time, we present a catalogue on the subfamily Agrypninae in Indian context. Currently, 257 species of Agrypninae belonging to 26 genera classified into 6 tribes are documented from India. Thirteen new combinations were proposed: Notably this study proposed one new species to science, *Adelocera kyrdemkulaiensi s*sp. nov.; along with two new country records and 15 state records from India. The current taxonomical studies on Agrypninae revealed that India is rich in the biodiversity of Agrypninae yet future explorations and studies may result in more additions to the Indian fauna.

Identification of agriculturally important insects associated with cruciferous crops (*Brassicaceae*) using artificial intelligence

Insects are an integral part of an agroecosystem. Some of them are pestiferous, while some are beneficial like-natural enemies and pollinators. Therefore, it is very important to identify and manage them timely. In present study we identified 20 species associated with crucifer crops. We have provided brief morphological description for 14 insect species with illustrations, and comparative diagnostic characters with the related species. We prepared a comprehensive checklist of agriculturally important insects associated with crucifers, comprising 289 species, with special reference to their functional roles and analyzed species diversity and functional diversity. Further, for identification of insects and their damage symptoms in crucifer crops, we developed YOLOv5l-based single-stage object detection model. A total of 2,730 images are captured from different fields and polyhouses using different smartphones and an SLR camera. The images are curated, annotated, resized, augmented, split, and, trained, validated, and tested through five variants of YOLOv5 viz. nano (n), small (s), medium (m), large (l), and extra-large (x). After all the experiments, YOLOv5l is found to be the best-performing model, acquiring an average accuracy, precision, recall, and F1-score of 99.5%, 92.0%, 83.0%, and 0.873, respectively in the test images. The inference time and computational complexity of YOLOv5l are also significantly lower than those of YOLOv5x. Therefore, to achieve an optimal balance between complexity and performance, YOLOv5l has emerged as the most viable option for integration with AI-DISC mobile application. In conclusion, this study is a novel approach wherein taxonomic identification of insects on crucifers is linked with developing artificial intelligence based detection model.

Development of isothermal nucleic acid amplification assays for detection of *Phthorimaea absoluta* (Meyrick) (Lepidoptera: Gelechiidae)

South American tomato pinworm, *Phthorimaea absoluta* (Lepidoptera: Gelechiidae), causes severe yield loss of 80–100%. For efficient management of this pest, detection at the point of entry is important. To accurately diagnose *P. absoluta*, Loop Mediated Isothermal Amplification (LAMP) and Recombinase Polymerase Amplification (RPA) assays were developed. The LAMP assay can identify *P. absoluta* within 60 minutes at 65 °C after sample extraction. The RPA The assay could successfully detect the *P. absoluta* within 45 minutes at 37 °C. Validation against three closely related non-target species, *Phthorimaea operculella* (Zeller, 1873), *Pectinophora gossypiella* (Saunders, 1844), and *Aproaerema modicella* (Deventer, 1904) confirmed species specificity of these assays. The LAMP assay showed high sensitivity to *P. absoluta* DNA up to 1×10^{-8} ng/µL and for plasmid DNA up to 1×10^{-14} ng/µL. The RPA assay showed sensitivity up to 1×10^{-8} ng/µL for genomic DNA and 1×10^{-10} ng/µL for plasmid DNA. In addition, LAMP and RPA assays were successful in the laboratory for detecting larvae, pupa, and adult stages of *P. absoluta*. We tested the LAMP assay and RPA assay for field application with quick and simple crude DNA extraction procedures and found double distilled water (ddH_2O) for LAMP and 0.02 M EDTA for RPA as an effective extraction solution. These assays were validated in the field using moths collected from pheromone traps followed by crude extraction and incubation. These assays had shown a hundred percent accuracy under field conditions. LAMP and RPA assays developed in this study are efficient molecular tools to detect the target organism, *P absoluta* at sensitive points.

Theme 2: Insect Physiology

Functional characterization of core gut bacteria in honeybees *Apis mellifera* / *Apis cerana* (Apidae, Hymenoptera)

The gut micro-organisms are indispensable in the health and ecology of disparate animal species, yet the connection between social behaviors and microbial communities is underexplored. Honey bees, known for their highly social nature, offer a valuable model to study intra-species microbial diversity, as their behavioral tasks expose them to distinct environmental conditions.This study used both culture-dependent and culture-independent methods to investigate the gut microbiome of two closely related honey bee species, *Apis mellifera* and *Apis cerana*. Additionally, enzyme assays were conducted to assess the ability of these gut bacteria to break down complex molecules. Culture-dependent techniques yielded 42 isolates, including 10 core isolates meanwhile, 16S rRNA sequencing and metagenomics revealed core bacterial species like *Gilliamella apicola*, *Bartonella apis*, *Commensali bacterintestini*, *Snodgra sellaalvi*, and *Frischella perrara*, with both species hosting bacteria predominantly from the phyla *Proteobacteria, Firmicutes, Bacteroidetes*, and *Actinobacteria*. The diversity analysis revealed a greater bacterial diversity and functional capacity in *A. mellifera* compared to *A. cerana*. Our results also emphasized the significant contribution of these core bacteria towards major metabolic pathways and enzyme analysis of core bacteria revealed their capacities in breaking down complex molecules like cellulose, hemicellulose, lipids, pectin and sucrose. These gut microbes boost the nutrition and health of honey bees by facilitating the breakdown of complex carbohydrates and lipids.Understanding the bee microbiome's functional roles is crucial for digesting complex carbohydrates, lipids, and sucrose, supporting honeybee health. Furthermore, identifying isolates with enzymatic potential such as potent pectinolytic or invertase activity holds promise for industrial uses including food processing and biofuel production.

Comparative symbiotic bacterial communities associated with litchi leaf roller, *Statherotis leucaspis* (Meyrick, 1902) (Lepidoptera: Tortricidae) reared on different litchi varieties

Leaf roller, *Statherotis leucaspis* Meyrick has recently been recorded as the most dominant species and causes substantial yield loss to litchi in India. The present studies were carried out during 2023-2024 at ICAR RCER, Farming System Research Centre for Hill and Plateau Region, Plandu, Ranchi with the main objective of leaf biochemical mediated effect on *S. leucaspis* reared on three different litchi varieties. The present study focussed on the assessment of the diversity of gut-associated bacteria in the larvae of *S. leucaspis* reared on three different litchi varieties viz., Shahi, Swarna Roopa, China using 16S rRNA gene sequences obtained by the Illumina MiSeq technology. The substantial variations in the level of infestation of *S. leucaspis*, the biochemical composition of leaves, and host-fed mediated bacteria were observed. A total of 853 amplicon sequence variants (ASVs) were found to be common across all the samples of *S. leucaspis*, with a 97 % similarity threshold. Alpha diversity indices showed maximum species richness in the larvae of *S. leucaspis* reared on the litchi variety Swarna Roopa. The phyla Proteobacteria followed by Firmicutes, Bacteriodetes, and Actinobacteria, exhibited the highest levels of abundance across all the samples. The major bacterial phyla like Proteobacteria and Firmicutes were identified in greater proportion in *S. leucaspis* feeding on varieties with less amounts of phenols, flavonoids, free amino acids, carbohydrates, and more soluble proteins. The variations in the biochemical composition variation lead gut microbiota can lead to novel approaches for the control of insect pests by modifying the symbiotic relationship between symbionts and their hosts.

Genome-wide analysis and identification, characterization, expression and functional analysis of odorant-binding proteins and chemosensory proteins in the whitefly, *Bemisia tabaci*

This study presents a comprehensive genomic and functional analysis of odorant-binding proteins (OBPs), chemosensory proteins (CSPs), and ejaculatory bulb proteins (EBPs) in *Bemisia tabaci* Asia II-1, a key agricultural pest. Fourteen OBPs, including six novel proteins, and 14 CSPs were identified, with phylogenetic analysis revealing their evolutionary relationships among Hemipteran insects and cryptic *B. tabaci* species, such as Asia I, II-1, MEAM1, and MED. RT-qPCR demonstrated high expression of OBP3, OBP8, CSP4, and CSP8 across developmental stages and tissues, with OBP10 predominantly expressed in the abdomen. Molecular docking and competitive fluorescence assays showed that OBP3 and OBP10 had high affinities for ligands like β-caryophyllene and limonene. Behavioral assays indicated that β-caryophyllene and carvacrol acted as attractants, while β-ocimene and limonene were repellents, and γ-terpinene and β-ocimene were oviposition deterrents. RNAi-mediated silencing of OBP3 and OBP10 confirmed their critical roles in host recognition.Furthermore, CSP1 and CSP5 were shown to bind insecticides imidacloprid and fipronil, with binding energies of -5.7 to -9.3 kcal/mol, implicating these proteins in insecticide resistance mechanisms. Additionally, 10 ejaculatory bulb proteins (EBPs) were identified in *B. tabaci* Asia I and II-1, with structural similarities to chemosensory proteins, including conserved cysteine residues. Transcriptomic analysis revealed differential expression between these genetic groups, with EBPs transferred from males to females during mating. RNAi silencing of EBP genes (EBP-3, 7, and 8 in Asia I; EBP-8, 9, and 10 in Asia II-1) disrupted this transfer, reducing female reproductive success.This study provides novel insights into the genomic landscape of OBPs, CSPs, and EBPs in *B. tabaci*, highlighting their roles in chemosensory signaling, insecticide resistance, and reproduction. These findings offer potential avenues for developing innovative pest management strategies targeting host recognition and reproductive processes.

Elucidation and characterization of gut bacteria associated with nitrogen cycling in white grubs (Scarabaeidae: Coleoptera)

The insect gut microbiome supports host nutrition, immunity, and nitrogen cycling, vital for scarab beetles due to their nitrogen-poor diets. Nitrogen-fixing and denitrifying bacteria in their gut aid in nitrogen cycling. The study identified 34 and 22 aerobic bacteria in *Maladera insanabilis* and *Lepidiota mansueta*, respectively. In *M. insanabilis*, Firmicutes (43.75%), Bacillota (43.75%), and Pseudomonadota (31.25%) dominated, with *Bacillus* (44%) and *Brucella* (25%) as major genera. Barot, H.P., isolates showed Bacillota (61.12%) and Pseudomonadota (38.88%), with *Bacillus* (56%) and *Enterobacter* (17%). Anaerobic isolates totalled 16 (*M. insanabilis*) and 10 (*L. mansueta*). Metagenomics revealed 134 shared ASVs, with *Burkholderia* in the foregut, *Paenibacillus* in the midgut, and *Desulfovibrio* in the hindgut. The study analyzed nitrate reductase activity in anaerobic gut bacterial isolates from *Maladera insanabilis* (Ghaziabad, UP; Barot, HP) and *Lepidiota mansueta* (Majuli, Assam), revealing significant variability ($p<0.0001$). *Burkholderia contaminans* (47.967±0.852 nmol min^{-1} ml^{-1}), *Staphylococcus hominis* (46.367±1.245 nmol min^{-1} ml^{-1}), and *Paenibacillus dendritiformis* (49.900±1.504 nmol min^{-1} ml^{-1}) showed the highest nitrate reductase activities. Michaelis-Menten kinetics demonstrated high nitrate and nitrite reduction efficiency. These activities, linked to nitrification and denitrification, underscore the bacteria's significant role in gut nitrogen cycling.This study examined the expression of five nitrogen cycling genes (*HZO, nifH, Amx, nirS, nirK*) in the gut compartments of *Maladera insanabilis* and *Lepidiota mansueta* larvae under treatments of naturally infested soil, farmyard manure, and vermicompost. Vermicompost consistently induced the highest gene expression. These findings highlight the gut's pivotal role in nitrogen cycling, driven by processes like anammox, nitrogen fixation, and denitrification. This research underscores the potential role of gut bacteria in pest management, and biofuel production.

Investigations on heat stress *vis-a-vis* reproductive pathways of common cutworm, *Spodoptera litura* (Fabricius) (Lepidoptera: Noctuidae)

The common cutworm, *Spodoptera litura*, is a major agricultural pest affecting over 100 crops across tropical and subtropical Asia. This study investigates the molecular mechanisms of heat stress in *S. litura* by analyzing transcriptional changes under varying temperatures. When 4thinstar larvae were exposed to 44°C, 11,390 transcripts were differentially expressed, with 262 upregulated and 61 downregulated genes. Key differentially expressed genes (DEGs) included heat shock proteins (*hsp60, hsp67, hsp70, hsp68, hsp27, hsp26*), developmental genes (*Tret1, mora, stv, stipe-1, sgt, foxO, trap1, mlf, DNAJ/DROJ*), cuticular protein genes, ribosomal genes, antioxidative genes (Pxd, Sod), mitochondrial genes, CYP450, cell cycle regulators, and chromatin proteins (*cdc, cdk, barr, nesd, mr, feo, caf-1, cap-D2*), and immune-related genes. Exposure to sub-lethal temperatures (LT_{25}: 43.8°C, LT_{50}: 44.93°C, LT_{75}: 46.7°C) led to reduced reproductive traits, including adult weight, pupal weight, sperm bundle count, GSI, and mating success, alongside increased female calling and copulation durations. Antioxidant enzymes (SOD, POD, CAT, GST) were elevated, indicating an oxidative stress response. Male accessory glands (mAGs) from heat-stressed (44°C) and control (27°C) moths were dissected for RNA sequencing. Of 15,783 differentially expressed unigenes, 345 were downregulated and 229 upregulated. Downregulated genes included carboxypeptidase, JHEPH, JHAMT, serine proteases, circadian-controlled clock, lipase, glucose dehydrogenase, chymotrypsin, and odorant receptors, while upregulated genes included odorant binding proteins, acyl co-A desaturase, insulin-like growth factor, double-sex- and mab-3-related transcription factor, Nose resistant to fluoxetine protein 6, Elongation of very long chain fatty acids protein, and juvenile hormone-suppressible protein 2. These gene networks collectively mitigated heat stress effects, supporting oxidative stress management, hormonal balance, sperm viability, and reproductive efficiency. This study provides insights into molecular responses to heat stress, offering potential targets for sustainable pest management strategies against *S. litura* in the face of climate change.

Investigations on plant resistance to fall armyworm, *Spodoptera frugiperda* (J.E. Smith) in maize

The fall armyworm, *Spodoptera frugiperda*, has emerged as a significant global pest, posing challenges to maize production in India. Developing insect-resistant maize hybrids is essential for sustainable cultivation and requires a thorough understanding of resistance traits and mechanisms in parental lines.Therefore, present study was carried out to determine the establishment behaviour, biological fitness of *S. frugiperda*, and the role of plant phenological traits and biochemical constituents in imparting defense against the pest.The study revealed that the A-lines AI 178, DMS 4B and AI 544, and R-lines AI 541 and CML 442 were less preferred and damaged by *S. frugiperda*, and had lower leaf chlorophyll content, higher anthocyanin pigmentation, moderate leaf glossiness, and a moderate number of leaf trichomes as compared to other A- and R-lines.The *S. frugiperda* larvae fed on A-lines CML 565, AI 544, AI 196, PDIM 639, PDM 77-A, DMS 4B, AI 518, AI 501 and AI 178, and R-lines AI 125, AI 155, AI 1100, AI 542, PML 105 andCML 442 resulted in extended developmental duration, lower survival rate, and reduced pupal weight and fecundity than those fed on other test maize lines.Due to *S. frugiperda* damage, the photosynthetic pigments significantly decreased, while rest other test biochemicals increased across the test maize lines. The aforesaid maize lines were found to impart greater detrimental effect on various biological parameters of *S. frugiperda*, and harbored greater amount of constitutive and insect-induced secondary metabolites (total phenols, tannins, antioxidants and FRAP), and plant defense enzymes (PAL, TAL, AO, APX and CAT) as compared to other test maize lines. Furthermore, among the test biochemical constituents *viz.*,phenols, FRAP, tannins, CAT, PAL, TAL and APX significantly contributed to defense against *S. frugiperda*, and can be used in hybrid breeding program to develop *S. frugiperda*-resistant maize hybrids.

Deciphering mechanisms of plant resistance to *Chilo partellus* (Swinhoe) in maize

This study characterized thirty maize inbred lines for antibiosis and antixenosis mechanisms, and elucidated pheno-morphological, and constitutive and induced biochemical defense against *C. partellus*. The plant pheno-morphological traits, preference of *C. partellus* neonates and extent of damage, significantly varied among the test maize lines. The maize A-lines DDM 2309-O, AI 546, AI 1116, AI 501, CML 565 and AI 540, and R-lines AI 542 and AI 125including resistant check CML 442 were less preferred and damaged by *C. partellus* relative to other lines. Biological parameters and life table parameters of *C. partellus* also varied significantly among the test maize lines. The A-lines AI 501, CML 565, PDIM 639, C 70, AI 196, AI 544 and DDM 2309-O, and R-lines AI 542, AI 125, AI 525, AI 117 and AI 1100 including the resistant check CML 442, exhibited extended developmental duration, lower survival, reduced pupal weight, and decreased fecundity of *C. partellus* as compared to that on other test maize lines. Constitutive and *C. partellus* induced levels of all the test biochemicals significantly varied among the test maize lines. The damage by C. *partellus* further increased the levels of all the test biochemicals, except the photosynthetic pigments. The levels of total sugars, proteins and photosynthetic pigments in these lines were significantly lower than susceptible check UMI 1210. Both under constitutive and insect-induced conditions, the aforesaid maize lines were found with greater levels of total phenols, tannins, antioxidants, FRAP and antioxidant enzymes (PAL, TAL, AO, APX and CAT), and imparted deleterious effect on biological attributes of *C. partellus*. The aforesaid maize lines were found with greater constitutive and induced phytochemicals like total proteins, phenols, tannins, AO, PAL and CAT, and significantly contributed to antibiosis against *C. partellus*, thus can be used in hybrid breeding program to develop stem borer-resistant maize hybrids.

Theme 3: Insect Toxicology

Identification and evaluation of behaviour modulating plant volatiles for leafhopper, *Amrasca* (*Sundapteryx*) *biguttula* (Ishida)

Leafhopper, *Amrasca (Sundapteryx) biguttula* is a destructive sucking insect pest that causes severe yield losses every year in several crops like okra, brinjal, cotton etc. The monitoring of this pest is usually done with the help of sticky traps but many times it is not successful because of inadequate attraction of leafhoppers. The present study aimed to identify leaf hopper semiochemicals, particularly attractant and repellent plant volatiles/volatile organic compounds (VOCs). GC-MS profiling identified 22 VOCs from a tolerant okra variety (DOV-92) and 25 VOCs in a susceptible variety (Pusa Bhendi-5). PCA biplot analysis distinguished compounds like D-Limonene and Benzene, 1-ethyl-2-methyl- as associated with the tolerant variety. Additionally, VOCs such as 3-Carene, γ-Terpinene, and

Benzene, 1-methyl-3-(1-methylethyl)- were detected exclusively in the tolerant variety. Based on VOCs identified from okra plants and a literature search, a total of 19 VOCs were evaluated for their effect on behaviour modulation of male and female leafhopper, *A. biguttula*. The Y-tube olfactometer bioassay revealed that nine VOCs elicited attraction with OPI values of 1.41 to 1.69 and ten VOCs caused repellence with OPI (Olfactrometric Preference Index) values of 0.28 to 0.80. Further field evaluation of promising attractant compounds by using a yellow sticky trap in combination with compound lures identified the three most promising attractants with an increase in trap catches in the range of 168.63% to 386.27% compared to the control (only yellow sticky trap). The semi-field bioassays of potential repellent compounds could identify the two most promising repellents which showed settling response in the range of 5.75% to 11.25%. The studies conclude that these semiochemicals (repellents and attractants) can be further upscaled and evaluated for the development of a novel management strategy for the leafhopper, *A. biguttula.*

Comparative toxicity evaluation of conventional and alternate contact insecticides against red rust flour beetle, *Tribolium castaneum* (Herbst.)

Red flour beetle, *T. castaneum* is a very destructive pest of several commodities in storage. In the present study, the toxicities of five newer insecticides were evaluated using different surfaces and also joint toxicity of the best alternate insecticide with deltamethrin was determined. Among insecticides, spinetoram was found to be the most effective alternate insecticide with lethal doses (LC50) of 250.07, 240.23 and 232.63 mg/m^2 on glass surface, 233.17, 221.48 and 215.58 mg/m^2 on tile surface and 323.55, 314.72 and 309.77 mg/m^2 jute surface for 24, 48 and 72h exposure period, respectively, followed by chlorfenapyr with 167.55, 160.52 and 158.23 mg/m^2 on glass surface, 252.50, 243.22 and 236.55 mg/m^2 on tile surface and 254.08, 243.12 and 240.90 mg/m^2 on jute surface for 24, 48 and 72h respectively. Spinetoram was 1.68- 2.60 fold and chlorfenapyr was 1.42-1.89 fold more toxic than deltamethrin. Relative susceptibility of seven geographically different populations of *T. castaneum* revealed that the Delhi state population was most resistant to deltamethrin with resistance ratios varying from 2.23-2.27, followed by the Orissa population with resistance ratio varying from 2.14-2.17 and the Punjab population was most resistant to spinetoram with resistance ratio values from 2.65-2.75 followed by Orissa population with 2.39-2.49 resistance ratios. Estimation of cross-resistance revealed that the populations resistant to deltamethrin are also more likely to exhibit resistance to spinetoram in these areas. The joint toxicities of deltamethrin and spinetoram at different proportions revealed that combinations 9:1 and 4:1 were synergistic. The study concluded that spinetoram and chlorfenapyr can be explored as alternatives to deltamethrin against red flour beetle *T. castaneum* and spinetoram can be used in combination with deltamethrin to enhance the efficacy.

Termite scenario in maize residue based conservation agriculture system in north India

This study investigates the effect of tillage and nitrogen fertilizer on the abundance and damage by major insect pests (termites, and pink stem borer (PSB) and their natural enemies (ants, coccinellids) in wheat, chickpea managed under three tillage practices and three nitrogen doses. Test tillage practices are, permanent bed (PB), zero-till (ZT), and conventional tillage (CT) in unprotected (without insecticide) condition; and three nitrogen treatments *viz*.; 100: 60: 40 kg/ha (T_1), 125: 60: 40 kg/ha (T_2), & 150: 60: 40 kg/ha (T_3) in wheat; and 0: 40: 40 kg/ha (T_1), 15: 40: 40 kg/ha (T_2), & 30: 40: 40 kg/ha (T_3) in chickpea; allocated in two-factorial split-plot design. Type of tillage practices had significant effect ($P<0.05$) on termite infestation in wheat but various nitrogen treatment and their interaction had no significant effect on termite damage in wheat. Active termite infestation was recorded during heading stage of wheat. Significant effect ($P<0.05$) of tillage type and nitrogen treatment on PSB infestation in wheat was investigated but their interaction had no significant effect. Tillage practices had no significant effect on coccinellids. Cumulative damage data of termites and pink stem borers make the result more pronounced and distinct as compared to the fresh damage profiles. Type of tillage practices, nitrogen treatment and their interaction had significant effect ($P<0.05$) on termite infestation in chickpea. Active termite infestation in chickpea was recorded during maturity stage. *Spodoptera* infestation in mung bean was more in PB-practice and comparatively low in CT-system. In conclusion, this short-term study is a step forward in this direction, which needs to be strengthened further with long-term evaluations of course.

Theme 4: Integrated Pest Management (IPM)

Effect of rice crop phenology on brown planthopper (BPH), *Nilaparvata lugens* (Stal) incidence and role of BPH induced plant volatiles on wolf spider, *Pardosa pseudoannulata* (Bosenberg and Strand)

Brown planthopper (BPH), *Nilaparvata lugens* is a destructive insect pest causing severe yield loss every year in rice crop. The present study was conducted to understand the effect of transplanting time and crop phenology on BPH incidence, and BPH induced rice plant volatiles on wolf spider behaviour. A significant interaction between crop phenology and transplanting time was observed in all three years. Biological parameters such as fecundity, nymphal emergence, nymphal developmental period, nymphal survival and growth index were highest during early crop growth stages such as tillering and booting and decreased towards maturity. Honeydew excretion peaked at tillering and booting and decreased towards maturity stage indicating potential mechanical barriers or less appealing plant sap in later growth stages. Biochemical parameters in rice plants across phenological stages, showed significant differences in constitutive and induced biochemical contents. Differences in constitutive and induced defensive enzyme activity were observed at various stages, with the highest constitutive catalase at dough and induced catalase during milking. Constitutive peroxidase peaked at milking, induced peroxidase at anthesis. Constitutive PPO peaked at dough, induced PPO at dough and milking. Y-olfactometer studies found that wolf spiders prefer rice plants damaged by BPH nymphs, males, and females over undamaged and mechanically damaged plants. The highest spider response observed with 48-hour female and 72-hour nymph damage. These findings suggest that herbivore-induced rice volatiles can attract wolf spiders, potentially enhancing their predatory abilities for better brown planthopper control. The headspace volatile profile at ambient and elevated CO_2 showed significant variations in total compound production, with the highest in female-damaged plants at elevated CO_2 and the lowest in undamaged plants at ambient CO_2. Y-olfactometer studies revealed wolf spiders exhibiting distinct preferences for volatiles from brown planthopper (BPH)-damaged plants, with a significant preference for BPH-damaged plant volatiles over undamaged plants at both CO_2 levels.

Pollinator diversity studies in integrated farming systems

This study assessed the impact two Integrated Farming System models (IFS 1 and IFS 2) with a Conventional Farm (CF) on pollinator diversity and pollination services. Pollinator diversity was comparatively higher in IFS I and IFS II models with 29 and 33 species/ morphotypes as compared to only 17 species/ morphotypes recorded in CF. Further, total pollinator counts were markedly higher in IFS 1 (17,583) and IFS 2 (17,122) as compared to CF (6,783). Higher abundance of pollinators such as *Apis mellifera*, *Apis cerana*, and *Apis dorsata* were observed in IFS models. Simpson index, Shannon-Wiener index, Brillouin index, Fisher's alpha and Chao-I indicated that IFS models had more diversity and species richness than CF. While, the higher Dominance index and Eveness index values reflecting the dominance of few species in CF. Network analysis indicated enhanced connectance and interaction complexity in IFS models with IFS 2demonstrating the highest ecological resilience.

Group-level indices revealed broader foraging and greater interaction redundancy in IFS 1. Bee bowl traps also showed highest pollinator abundance (798individuals), including notable increases in *Lasioglossum albescens* and *Hermetia illucens*, compared to IFS 1 (636 individuals) and CF (386 individuals).Fruit set and yield parameters were significantly reduced in pollinator exclusion treatment showing important role of insect pollination. In IFS 1, mustard experienced a 46.14% increase in fruit set and a33.33% increase in pod weight under open pollination, while brinjal showed a 43.39% higher fruit set and a 96.95% increase in fruit weight. IFS 2 reported similar benefits, with a 47.24% increase in mustard fruit set and a 142.65% increase in brinjal fruit weight under open pollination. Economic value of insect pollination services was estimated to be Rs. 53,259.52 in IFS 1 and Rs. 51,854.23 in IFS 2, emphasizing the ecological and economic significance of pollinators.

Foraging behaviour and pollination efficiency of stingless bee, *Tetragonula ruficornis* on bitter gourd grown under protected conditions

In Pusa Rasdar variety of bitter gourd, staminate and pistillate flowers were produced at 33.5 ± 2.02 and 42 ±1.23 DAT with a sex ratio and pollen-to-ovule ratio of 1:4.65 and 625.94 ±208.30, respectively during summer season. Blooming period of staminate and pistillate lasted for 52.5 ±1.44 and 43 ±1.73 days. Anther dehiscence occurred between 0500-0615 hrs. Anthesis of pistillate and staminate flowers occurred between 0530-0700 hrs and 0600-0800 hrs. Only staminate flowers provided nectar and pollen with the maximum nectar production 3.1 mm column in capillary tube at 1000-1200 hrs. Six native floral visitors *viz*., *Apis dorsata*, *A. cerana*, *A, florea*, *Tetragonula ruficornis*, *Halictus* sp. and *Zizeeria karsandra* were observed foraging on bitter gourd in open field conditions. *Apis florea* had maximum abundance of 1.96 bees/sq. m/5mand maximum pollinator abundance during 0800-1000hrs (2.14 bees/sq. m/5 m). *Z. karsandra* shown maximum foraging rate among the native pollinators (9.50 flowers /m). *A. dorsata* carried more loose pollen grains (83,800.00 ±3061.59 /bee). In net house, maximum foraging speed of *Tetragonula ruficornis* was observed at 1200- 1400 hrs (31.23± 8.47 sec/male flower). Time spent per male flower for nectar collection was more than pollen collection. The maximum foraging intensity was observed during 1000-1200 hrs with 6.75±0.48 bees/sq. m/5 min. Foraging rate of *T. ruficornis*was maximum during 1200-1400 hrs in net house condition with 2.90± 0.21 flowers visited/min. Maximum number of outgoing bees was observed at 1000-1200 hrs (23.8± 1.93 bees/5 m) and maximum numbers of incoming bees was during 1200-1400 hrs (24.2± 0.92bees/5m). Yield parameters and number of seeds per fruit in bitter gourd pollinated by stingless bees under net house condition were superior compared to hand and open pollination. However percent fruit set was minimum in stingless bee pollination (55.94± 0.79 %) and maximum in hand pollination (89.55± 2.96).

Biocontrol potential of *Cheilomenes sexmaculata* (Fabricius) against cotton whitefly, *Bemisia tabaci* (Gennadius)

Cheilomenes sexmaculata (Coccinellidae: Coleoptera), is one of the important native coccinellid species with high biocontrol potential. It's active all year on a variety of hosts. Thecotton whitefly, *Bemisia tabaci* (Aleurodidae: Hemiptera), is one of the notorious and destructive insect pests of cotton, damage about 600 plant species and transmit numerous plant viruses. Each instars grub of *C. sexmaculata* showed a significant difference in predation rate, nymphs (*F*: 476.728; *P*: <0.0001), pupae (*F*: 477.686; *P*: <0.0001) and adults (*F*: 568.890; *P*: <0.0001) of *B. tabaci* by displaying an increase in consumption with the advancement of the stage. However, the adult beetles exhibited a high consumption rate over grubs because of its long duration, with significantly higher consumption by females than males. The polynomial logistic regression confirmed the type-II functional response for all the stages of predator against the *B. tabaci* nymphs, pupae and adults. The fourth instar grub showed the highest (41.7) daily consumption while adults exhibited maximum total predation. Fourth instar grub showed the highest attack rate (2.72) while by the female beetle showed the lowest handling time (0.04).IGP of *C. sexmaculata* in absence of EG-prey (*B. tabaci*) preyed on *C. septempunctata* it was unidirectional and decreasing pattern. However, in presence of EG-prey (*B. tabaci*) it had reduced in a unidirectional manner. When, *C. sexmaculata* preyed on *B. suturalis* in the absence of EG-prey (*B. tabaci*) it was in the same way in decreasing pattern. Whereas, in presence of EG-prey (*B. tabaci*) it had reduced in a unidirectional manner. In absence of EG-prey (*B. tabaci*) when *C. septempunctata* preyed on IG-prey, *C. sexmaculata* it was in the same direction and shown in decreasing pattern. However, in presence of EG-prey it was reduced in unidirectional manner.

Investigations on optimal foraging in six spotted ladybird beetle, *Cheilomenes sexmaculata* (F.)

The six-spotted ladybird beetle, *Cheilomenes sexmaculata* Fabricius is a key predator of major sucking pests of cotton. This study examined the predator's foraging strategies, functional responses, and prey selection based on nutritional composition. Experiments were conducted with densities of 10, 20, 30, 40, and 50 of each prey species to work out the handling times for the predatory stages, and five prey patch compositions: balanced (40:40:40:40) and skewed (80:20:20:40, 20:80:40:20, 20:40:80:20, 40:20:20:80) to know the optimal foraging strategies, and mixed prey densities of 8, 16, 32, 64, 128 and 256 to understand the functional response of the *C. sexmaculata* against mixed prey densities. Results indicated *P. marginatus* had the lowest handling time (0.0050 days), while *B. tabaci* had the highest (0.1102 days). Across all compositions, *A. gossypii* was the most preferred prey. The average food intake was the highest from the *A. gossypii* for the fourth instar grub, female and male as 12.43, 13.95, and 16.14, respectively. The fourth instar grub (11.38) and male (9.45) achieved the highest gain rate from the *A. gossypii*-dominated patch, while the female (11.38) excelled in the balanced patch. Nutritional analyses revealed that the prey biomass and nutrient composition significantly influenced the predator preferences; with lipid, protein, and carbohydrate-rich prey (*A. gossypii*) influenced the optimal prey selection. Functional response experiments revealed the type-II response across all predator stages, with high attack rates recorded for the first and fourth instar grubs. Predation efficiency and lowest handling times were observed in the third and fourth instar grubs and adults. Therefore, it is suggested that the third-instar grub, fourth-instar grub, and adults of *C. sexmaculata* are ideal for augmentative control programs in cotton.

Screening and characterisation of okra germplasm against okra yellow vein mosaic disease transmitted by whitefly (*Bemicia tabaci* Gennadius)

The study assessed the resistance of 16 okra germplasm entries, including wild accessions, cultivated lines, and advanced breeding lines, against okra yellow vein mosaic disease (OYVMD) and its vector, whitefly (*Bemisia tabaci*), under artificial condition at ICAR-NIBSM during Summer 2024. Disease incidence and whitefly population showed significant positive correlations with total sugars, reducing sugars, and protein content and significant negative correlations with traits such as trichome density, trichome angle, phenolic compounds, and defensive enzyme activity. Wild germplasm *A. moschatus sub. sp. moschatus* (IC 629859) and *A. tuberosus* (IC 470750) exhibited high resistance (0% disease incidence), low whitefly population (intrinsic rate: 0.026–0.027; finite rate: 3.60–3.85), and high population doubling time (25.71–27.08 days). Resistance was linked to high trichome density (891.88–12228.10/cm²), long trichomes (605.07–1370.93 µm), high phenolic content (2.27–3.04 mg/g), tannins (5.23–5.73 mg/g), and high enzyme activity for peroxidase (53.85–57.87 µmol/min/mg protein), catalase (181.99–199.52 nmol/min/mg protein), and SOD (95.78–97.42 units/mg). One germplasm of *A. esculentus* (IC 117262-1) showed moderate resistance to whitefly population and disease incidence with high tannin content. Cultivated entries IC 117288 and IC 117299 were highly susceptible (>75% disease incidence) with low trichome density

(33.80–141.89/cm²), reduced enzyme activity (peroxidase: 11.28–20.67 µmol/min/mg protein), and high sugar (3.36–4.61%) and protein (14.87–15.15 mg/g) levels. The study highlighted resistance as a multifactorial trait governed by morphological, biochemical, and enzymatic factors, offering valuable insights for breeding programs targeting OYVMD resistance.

Studies on the effect of silicon amendment on pink stem borer *Sesamia inferens* Walker in wheat under climate change scenario

This study investigates the impact of silicon amendment on wheat plants infested with the pink stem borer (*Sesamia inferens*) under climate change conditions using an open-top chamber (OTC) setup. The experiment included four scenarios: elevated CO2 (600 ± 25 PPM), elevated temperature (+3°C), their combination, and ambient conditions. Silicon significantly reduced stem borer damage, with the lowest percentage of dead hearts (1.56% at 3 DAR) observed in silicon-treated plants under ambient conditions (T4). In contrast, the highest damage occurred under elevated CO2 without silicon (T5). The highest mean damage (28.68%) was recorded in T5, compared to the lowest (12.93%) in T4. While, T5 recorded the highest larval number (7.67), weight (111.53 mg), and length (19.09 mm). T2 had the shortest larvae (15.64 mm). Plant growth was optimal in T1, with the longest shoots (56.97 cm), roots (15.00 cm), and the highest fresh (48.27 g) and dry weights (9.21 g). The shortest shoots (38.23 cm) and roots (10.60 cm), along with the lowest fresh weight (38.84 g), were observed in T6, while the lowest dry weight was in T2 (6.54 g). Biochemical analyses revealed that silicon influenced total soluble sugars (highest: 2.10% in T13; lowest: 1.03% in T7), phenol (highest: 6.12 in T5; lowest: 1.95 in T3), and protein concentrations (highest: 18.45 mg/g in T8; lowest: 6.55 mg/g in T1). Defensive enzyme activities showed peak peroxidase (22.16 µmol/min/mg) and polyphenol oxidase (3.62 change in absorbance/min/g) in T1, highest superoxide dismutase activity in T5 (93.75 units/mg), and catalase activity in T9 (12.78 nmol/min/mg). Silicon also reduced larval mandible dimensions, with the smallest incisor length (247.21 µm) and width (283.21 µm) in T2. This study underscores silicon's pivotal role in reducing pest damage, enhancing plant growth, and boosting biochemical and defensive responses, providing vital strategies for sustainable agriculture under changing climatic conditions.

Studies on genetic diversity and population dynamics of *Amrasca biguttula* (Ishida) in okra in Chhattisgarh

Okra (*Abelmoschus esculentus* (L.)), is an important vegetable crop in Chhattisgarh, India, which faces various biotic and abiotic stresses, including infestation by the okra leafhopper (*Amrasca biguttula*). Genetic analysis identified seven haplotypes and two clades of *A. biguttula* in Chhattisgarh. The most widespread and dominant haplotype was CLHH 7, found throughout the state, suggesting its greater adaptability. Other haplotypes were localized: CLHH 1 (Balod district), CLHH 2 (Kondagaon district), CLHH 3 (Dhamtari district), CLHH 4 (Kanker district), CLHH 5 (Surguja district), and CLHH 6 (Durg district). The divergence between the north and central populations of Chhattisgarh was 0.00191, between the north and south populations was 0.00186, and between the central and south populations was 0.00215. The late-sown okra had the lowest leafhopper population compared to mid-sown and early-sown. The peak leafhopper population occurred during the 9th and 10th standard weeks (9.411 and 9.944 leafhoppers/3 leaves, respectively). Weather parameters revealed that the leafhopper populations were positively correlated with both maximum temperature (0.775, 0.774, and 0.689 for T1, T2, and T3) and minimum temperature (0.737, 0.736, and 0.564 for T1, T2, and T3), while relative humidity had a negative correlation (-0.684, -0.696, and -0.606). Damage scores were lowest in late-sown okra (T3): 1.23, 2.03, 2.53, and 3.5 at 30, 45, 55, and 60 days after sowing (DAS), respectively. Damage in mid-sown okra (T2) was 1.37, 2.17, 2.97, and

3.4, while the highest damage occurred in early-sown okra (T1) with 1.8, 2.7, 3.27, and 4.1. The study indicates that later sowing, particularly in early December, helps reduce leafhopper infestation and damage. Additionally, leafhoppers preferentially congregated on the middle leaves of okra, with an average of 31 nymphs per leaf during the 10th standard week.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1	Sourav Chakrabarty (21816)	M.Sc.	Identification of agriculturally important insects associated with cruciferous crops (Brassicaceae) using artificial intelligence	Dr. Shashank P. R.	ICAR-IARI, New Delhi
2	Arindam Kumar (21817)	M.Sc.	Development of isothermal nucleic acid amplification assays for detection of *Phthorimaea absoluta* (Meyrick) (Lepidoptera: Gelechiidae)	Dr. Shashank P. R.	ICAR-IARI, New Delhi
3	Pradeep (21819)	M.Sc.	Identification and evaluation of behaviour modulating plant volatiles for leafhopper, *Amrasca* (*Sundapteryx*) *biguttula* (Ishida)	Dr. Suresh M. Nebapure	ICAR-IARI, New Delhi
4	Sharath R (21820)	M.Sc.	Comparative toxicity evaluation of conventional and alternate contact insecticides against red rust flour beetle, *Tribolium castaneum* (herbst.)	Dr. Suresh M. Nebapure	ICAR-IARI, New Delhi
5	Raiza Nazrin M R (21821)	M.Sc.	Functional characterization of core gut bacteria in Honeybees *Apis mellifera* /*Apis cerana* (Apidae, Hymenoptera)	Dr. S. Subramanian	ICAR-IARI, New Delhi
6	Debkumar Mandal (21822)	M.Sc.	Termite scenario in maize residue based conservation agriculture system in north India	Dr. G. K. Mahapatro	ICAR-IARI, New Delhi
7	Kanchan RangraoDhurve (21823)	M.Sc.	Foraging behaviour and pollination efficiency of stingless bee, *Tetragonularu ficornis* on bitter gourd grown under protected conditions	Dr. Kumaranag K. M.	ICAR-IARI, New Delhi
8	Vinotha, S (21914)	M.Sc.	Pollinator diversity studies in integrated farming systems	Dr. Kumaranag K. M.	ICAR-IARI, New Delhi
9	Akash Kotru (21972)	M.Sc.	Taxonomic studies on subfamily Agrypninae (Coleoptera: Elateridae) from India	Dr. Nithya Chandran	ICAR-IARI, New Delhi
10	Mitte Komal Priya (60132)	M.Sc.	Comparative symbiotic bacterial communities associated with litchi leaf roller, *Statherotis leucaspis* (Meyrick, 1902) (Lepidoptera: Tortricidae) reared on different litchi varieties	Dr. Jaipal Singh Choudhary	*ICAR-NIBSM Raipur
11	Debanjan Basu Roy (80028)	M.Sc.	Screening and characterisation of okra germplasm against okra yellow vein mosaic disease transmitted by whitefly (*Bemisia tabaci* Gennadius)	Dr. Mallikarjuna Jeer	*ICAR-NIBSM Raipur
12	Chethankumar M (80031)	M.Sc.	Studies on the effect of silicon amendment on pink stem borer *Sesamia inferens* Walker in wheat under climate change scenario	Dr. K. C. Sharma	*ICAR-NIBSM Raipur

13	Sneha Sharma (80032)	M.Sc	Studies on genetic diversity and population dynamics of *Amrasca biguttula* (Ishida) in okra in Chhattisgarh	Dr. J. Sridhar	*ICAR-NIBSM Raipur
14	Padala Vinod Kumar (10787)	Ph.D	Effect of rice crop phenology on brown planthopper (BPH), *Nilaparvata lugens* (Stal) incidence and role of BPH induced plant volatiles on wolf spider, *Pardosa pseudoannulata* (Bosenberg and Strand)	Dr. Subhash Chander	ICAR-IARI, New Delhi
15	Anil (11241)	Ph.D	Elucidation and characterization of gut bacteria associated with nitrogen cycling in white grubs (Scarabaeidae: Coleoptera)	Dr. S. Subramanian	ICAR-IARI, New Delhi
16	Rakesh Kumar (11245)	Ph.D	Biocontrol potential of *Cheilomenes sexmaculata* (Fabricius) against cotton whitefly, *Bemisia tabaci* (Gennadius)	Dr. Sachin Suroshe	ICAR-IARI, New Delhi
17	Pynhunlin Dohling (11489)	Ph.D	Biosystematic studies on bees (Hymenoptera: Apoidea) of Meghalaya	Dr. Debjani Dey	ICAR-IARI, New Delhi
18	Hemant Kumar (11757)	Ph.D	Investigations on heat stress vis-a-vis reproductive pathways of common cutworm, *Spodoptera litura* (Fabricius) (Lepidoptera: Noctuidae)	Dr. Sagar D.	ICAR-IARI, New Delhi
19	Chaitanya (12032)	Ph.D	Investigations on optimal foraging in six spotted ladybird beetle, *Cheilomenes sexmaculata* (F.)	Dr. Sachin Suroshe	ICAR-IARI, New Delhi
20	Rudra Gouda M N (12033)	Ph.D	Genome-wide analysis and identification, characterization, expression and functional analysis of odorant-binding proteins and chemosensory proteins in the whitefly, *Bemisia tabaci*	Dr. S. Subramanian	ICAR-IARI, New Delhi
21	Kalyanam Sai Iswarya (12035)	Ph.D	Investigations on plant resistance to fall armyworm, *Spodoptera frugiperda* (J.E. Smith) in maize	Dr. M. K. Dhillon	ICAR-IARI, New Delhi
22	Mahendra K R (12036)	Ph.D	Deciphering mechanisms of plant resistance to *Chilo partellus* (Swinhoe) in maize	Dr. M. K. Dhillon	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 all kind of habitats. Plant parasitic nematodes are microscopic, worm-like organisms that feed on plants, either inside their tissues (endoparasites) or outside (ectoparasites). These nematodes are obligate parasites, meaning they must draw their nutrition from plant hosts, which debilitates the plants in the process. The plant parasitic nematodes inflict indirect damage to crop plants by pre-disposing them to other co-inhabiting pathogenic bacteria, fungi, pathogens etc. They cause significant damage to crops, leading to substantial economic losses. The extent of damage depends on factors such as nematode population density, host susceptibility, and environmental conditions. It is not that all nematodes are parasitic on plants, some are also beneficial to crops, such as entomopathogenic nematodes. Entomopathogenic nematodes have been successfully utilized as potential biocontrol agents, for the management of insect pests of crops. The research achievements of the post graduate students are presented below under the following themes:

Theme 1: Nematode Diversity and Biosystematics

Diversity and community profile of plant and soil nematodes associated with various crops under protected cultivation

Protected cultivation systems enhance crop productivity and resource efficiency but also provide a favourable environment for plant parasitic nematodes, which threaten crop health.A random survey has been made to explores the diversity and community analysis of plant and soil nematodes associated with various crops cultivated under protected cultivation from different regions Karnataka, Delhi NCR, Haryana and Uttar Pradesh. Total 19 soil and plant nematode genera have been encountered during present study. Among them, eight belong to plant parasitic nematodes (PPN), *Meloidogyne* sp., *Pratylenchus* sp., *Hoplolaimus* sp., *Rotylenchulus* sp., *Tylenchorhynchus* sp., *Helicotylenchus* sp., *Hemicriconemoides* sp. and *Paratylenchus* sp.; six were predatory nematodes (PRN) viz., *Discolaimus* sp., *Aporcelaimellus* sp., *Mesodorylaimus* sp., *Discolaimium* sp., *Iotonchus* sp., and *Mylonchulus* sp., and five belong to microbivorus nematodes (MBN) viz., *Eucephalobus* sp., *Acrobeloides* sp., *Panagrolaimus* sp., *Chiloplachus* sp., and *Acrobeles* sp. Data revealed that, *Helicotylenchus* sp. and *Tylenchorhynchus* sp.were the most frequent and dominant species in the plant parasitic nematode community, while *Aporcelaimellus* sp. dominated predatory nematode communities. In case of microbivorous nematodes like *Eucephalobus* sp. and *Acrobeles* sp. were prominent in the community. Key nematode *Meloidogyne* sp., *Rotylenchulus* sp., *Pratylenchus* sp., *Hoplolaimus* sp.,and *Helicotylenchus* sp. were abundant throughout the region. Soil pH showed strong negative correlations with plant parasitic nematodes indicating that higher pH reduce their populations.The study provides valuable insights into nematode dynamics under protected cultivation, emphasizing the need for tailored integrated nematode management (INM) strategies to enhance crop productivity and mitigate crop losses in these specialized environments.

Morphological and molecular identification of cyst nematodes (*Heterodera* spp.) from IARI farm, New Delhi

Soil samples were collected from the wheat-maize sequence and pigeon pea fields at the Indian Agricultural Research Institute (IARI) farm in New Delhi to look for the presence of the cyst nematode (*Heterodera* spp.). No cyst nematodes were found in the sorghum and finger millet fields. The occurrence of *Heterodera avenae* Wollenweber, 1924 and *Heterodera cajani* Koshy, 1967 was confirmed by using morphological and molecular methods. Morphology and morphometrics of cyst, vulval cone, second stage juvenile (J2) and eggs of *H. avenae* and *H.cajani* were studied for species identification. Further, the genomic DNA of typical cysts were extracted, amplified and sequenced for the species identification. Sequences of *CO1* mitochondrial DNA of *H. avenae* (PQ069711) and the D2-D3 expansion segment of the 28S rRNA gene of *H. cajani* (PQ044634) were submitted to the NCBI Database. Bayesian phylogenetic trees were constructed for *H. avenae* and *H. cajani* using *CO1* and D2-D3 to establish their relationship with sequences in the database. The cysts of various types obtained from the crop sequences were further confirmed using species-specific primers of *H. avenae*, *H. filipjevi*, *H. zeae* and *H. cajani*. The amplicon of the 109 bp fragment using the species-specific primer set AVEN-*CO1* (F/R) confirmed the presence of *H. avenae*. Similarly, *H.cajani* was confirmed using species-specific primers HcajF1 and HcajR1, which yielded an amplicon of 157bp. Thus, this study adopted an integrative approach of morphological and molecular methods and confirmed the presence of both *H. avenae* and *H.cajani* in the IARI fields. No cysts of *H. zeae* and *H. filipjevi* were found in the wheat-maize crop sequence, and other crops were grown at the IARI farm.

Detection and molecular characterization of rice white tip nematode, *Aphelenchoides besseyi*

Plant parasitic nematodes are significant pests causing substantial losses in rice crop. Among them, rice white tip nematode, *Aphelenchoides besseyi*, is a seed-borne nematode that poses a major threat to rice cultivation by surviving desiccation and spreading through infected seeds. Due to its seed dissemination potential, it is classified as a quarantine pest in several countries. This study aimed to investigate the seed dissemination of *A. besseyi* and perform molecular characterization and phylogenetic analysis of nematode populations collected from different areas. Total of 150 rice samples were observed for the presence of *A. besseyi*, out of which 44 samples (29.33%) were found infected with *A. besseyi*. The infection rate was 28.88% and 29.59% for exotic and indigenous samples, respectively. Samples from 23 Indian states and Union Territories and eight other countries were observed for presence of nematodes. It was detected in samples from 13 states of India and all eight countries indicating the widespread distribution of *A. besseyi* across rice-growing areas. Highest number of infected samples was found from Telangana followed by Odisha and West Bengal. Among exotic samples, the Philippines and USA had the highest infection rates. A detailed infection analysis, revealed significant variation in the number of infected seeds per sample. The number of nematodes per ten seeds varied from none to 328. In some instances, upto 64 nematodes per seed were recorded, highlighting its high infection. Molecular characterization was performed using the D2-D3 expansion segments of the 28S rDNA gene. PCR amplification produced bands ranging from 700 to 900 base pairs in all twelve samples. Sequencing results, analyzed using BLASTn, showed high sequence similarity with *A. besseyi* populations from Spain, USA, Brazil, and Costa Rica. Phylogenetic analysis using the Maximum Likelihood (ML) method revealed that the studied populations of *A. besseyi* were closely related, with some proximity to *A. pseudobesseyi*. However, the *A. besseyi* populations were distinct from other genera within the Aphelenchidae family. The study highlights the widespread presence of *A. besseyi* in rice-growing regions and its significant dissemination potential through seeds and warrants the seed treatment to prevent its further spread. The sequence information generated can be used for development of diagnostics and management of *A. besseyi* by regulatory agencies.

Theme 2: Nematode Management

Effect of nano-emulsions of essential oils on *Meloidogyne graminicola* infecting rice

The essential oils extracted from garlic, citronella and annona were analyzed using Gas Chromatography-Mass Spectrometry (GC-MS), which revealed an oil yield of 0.24%, 0.97% and 22.2% respectively. GC-MS analysis identified different compounds in these oils which have nematicidal properties. Garlic oil contains Diallyl trisulfide (59.02%), Diallyl disulfide (17.21%), Methyl allyl trisulfide (13.19%), Diallyl tetrasulfide (7.43%) as major compounds. The citronella oil was mostly composed of citronellal (35.53%), citronellol (16.97%), geraniol (23.6%), and geranial (3.92%). The primary fatty acids found in the annona oil were oleic acid (50.1%), linoleic acid (23.85%), palmitic acid (14.24%), and stearic acid (11.81%). Both the macroemulsions and nanoemulsions were evaluated for their nematicidal activity against J2s and eggs of the rice root-knot nematode, Meloidogyne graminicola, under in-vitro and in-vivo conditions. The invitro tests were conducted at varying concentrations (1000, 500, 250, 125 and 62.5 ppm), and results indicated that higher concentrations all the oil nanoemulsions significantly increased nematode mortality and inhibited egg hatching compared to the control and also showed that garlic nanoemulsions was most effective as nematicide than other nanoemulsions and macroemulsions also. Additionally, nematode mortality and hatching inhibition increased with both the concentration and duration of exposure. In terms of toxicity (LC50), the garlic nanoemulsion was found to be more toxic to J2s of M. graminicola than the others at lower doses after 96 hours of exposure, following the toxicity order: garlic nanoemulsion>garlic oil macroemulsion>citronella oil nanoemulsion>citronella oil macroemulsion>annona oil nanoemulsion>annona oil macroemulsion. In-vivo experiments conducted through seedling root dip and soil drenching methods in 15 cm earthen pots demonstrated that plant growth parameters significantly improved with higher concentrations of both garlic and citronella nanoemulsions after 30 days post-inoculation (DPI) but garlic nanoemulsion showed better plant growth than citronella nanoemulsion. Conversely, the formation of galls decreased at 1000 and 500 ppm concentrations of garlic nanoemulsion. Based on these findings and the LC50 analysis, it can be concluded that garlic nanoemulsion is more toxic to nematodes compared to the citronella, annonananoemulsions and its macroemulsions. Therefore, garlic nanoemulsion holds promise as an effective management strategy for M. graminicola infestations in rice.

Theme 3: Molecular Nematology

Determination of G-protein coupled receptors involved in odor- and chemo- reception in *Heterorhabditis bacteriophora*

Chemoreception plays a major role in host finding for the infective juveniles (IJs) of entomopathogenic nematode (EPN) *Heterorhabditis bacteriophora*. The IJs locate their insect hosts by sensing universal host cues(CO2) or insect/plant-derive dodorants, which bind mainly to G-protein-coupled receptors (GPCRs). Nematode chemosensory GPCRs (NemChRs) bind to a diverse set of ligands, including odor molecules. 21GPCRs were identified from the *H. bacteriophora* genome using a stringent bioinformatic pipeline. Among these, four (Hba_18427,Hba_18743,Hba_17528,Hba_07805) were identified as NemChRs by Google's DeepMind. The predicted Local Distance Difference Test (plDDT) scores for all these models were >90, signifying high accuracy. Moreover, structural analysis of models refined by the Galaxy Refine2 server exhibited high-quality scores, minimum z-scores and the majority of residues in the favoured regions of the Ramachandran plot, indicating good stability. The quality parameters, pertaining to Molecular dynamics simulation analyses, done at 100ns in GROMACS, documented stable RMSD, RMSF, potential energy and partial density curves. Molecular docking analyses of these NemChRs with selected volatile compounds released by different insects, conducted using AutoDock Vina showed very low binding affinity scores, indicating very strong interactions. Hba_07805 (-5.3 kCal/mol) and Hba_18743 (-6.2 kCal/mol) formed the best docking complexes with p-cymene.On the other hand,Hba_18427(-4.8kCal/mol) and Hba_17528 (-6.6 kCal/mol) formed the strongest configuration with methyl salicylate. Six insect-emitted odors were tested against *H. bacteriophora* IJs in attraction assays and two odors (2-butanone and Propionic Acid) were found to be repellent,while four molecules(Aceticacid,1- propanol, p-cymene, and Methyl Salicylate) behaved as attractants. Among the biological homogenates,root exudates of PB1121 had no effect on the behaviour of IJs,whereas *E.coli* OP50 culture exhibited a repellent response. Rest of the biological treatments, *Galleria mellonella* heamolymph, termite and mealybug homogenates and *P. Luminescens* TTO1 cultures behaved as attractants.Varied expression of NemChRs were observed against different insect-emcompounds and biological homogenates over time through qRT-PCR analysis. Hba_18427 showed slight down regulation upon dsRNA soaking through *in-vitro* RNAi, however, Hba_18743 exhibited upregulation. Hba_18427silenced IJs showed altered responses towards insect-emitted compounds and biological homogenates, however, Hba_18743 exhibited aberrant responses in phenotyping bioassay. The *Caenorhabditis elegans* strains knocked down for the homologous NemChRs showed an opposite reaction for the highly attractive acetic acid and the major repellent 2-butanone, suggesting that the identified GPCRs work in concert or alone for determining the nematode chemosensory behavior. This knowledge might help in developing novel insect-pest management strategies by tweaking EPN IJ behaviour, and in discovering novel drug targets for parasitic nematode management.

Genes and pathways for parasitism and development of *Anguina tritici* on wheat

Anguina tritici, the wheat seed gall nematode, causes the 'ear-cockle' or seed gall disease of wheat (*Triticum* spp.), leading to an extensive decline of yield in the range of 30 to 70%. Nematode's unique characteristics like, feeding in wheat stem and floral primordia along with survival in a dormant stage for decades attracted us to study its biorhythm. This study was conducted to understand bionomics and molecular pathways behind nematode parasitism and survival. It was observed that the duration of nematode's life cycle was affectedby wheat crop sowing time and external environment especially temperature. After calculating Growing degree days or heat units it was found that life cycle of nematode varies from 90-140 days synchronizing with wheat plants. To escape off-season, nematodes survive in anhydrobiotic J2 stage in seed galls. For understanding the anhydrobiotic survival and above ground parasitism at gene/molecular level, this study presents the first transcriptome assembly of *A. tritici*. The final 133.2 Mb assembly consists of 1,05,606 transcripts (including isoforms) with the following BUSCO scores against Nematoda database: 80.3% complete (16.4% single copy and 63.9% duplicated) 2.1% fragmented, and 17.6% missing. Functional annotation of assembly and differential expression analysis underscored the dynamic nature of gene regulation, with significant upregulation and downregulation of transcripts associated with anhydrobiosis and revival. Presence of large number of glycolases, lyases, hydrolases and 14-3-3, SNARE like effector support the above ground parasitism. The expression of gene homologues of *CBR-DAF-2* and CBR-*DAF-21* in *A. tritici* suggests the significant role of dauer formation and longevity pathways in the nematode's survival mechanisms. Heat shock proteins and protein kinases are integral components of the *MAPK*, ErBb, *FoxO*, and *mTOR*signaling pathways in nematodewhich are associated with stress resistance and help inescaping adverse conditions. This study lays a foundation for future investigations into the genetic and biochemical pathways that enable *A. tritici* to survive extreme conditions and thrive as a plant parasite.

Theme 4. Entomopathogenic Nematodes

Exploration and evaluation of entomopathogenic nematodes associated with arecanut (*Areca catechu* L.) rhizosphere from Dakshina Kannada district of Karnataka

In a pursuit of exploring entomopathogenic nematodes, a surveyhas been conductedand 65 soil samples were collected from different locations of Belthangadi, Puttur, Buntwal, Kadaba and Sullia taluks of Dakshina Kannada district of Karnataka. Out of them, 5 samples showed positive for the presence of EPNs.Among these five EPNs, one each was obtained from Buntwal and Puttur taluk, whereas three from Belthangady taluk. These EPNs were identified as *Heterorhabditis indica* (IARI-EPN-KA-22 and IARI-EPN-KA-24), *Oschieusmyrio philus* (IARI-EPN-KA-16), *Oschieus* sp.*(*IARI-EPN-KA-15) and *Metarhabditis rainai* (IARI-EPN-KA-10)on the basis of morphological and molecular characterization. Initially their pathogenicity of five isolated EPNs was tested against greater wax moth larvae, *Galleria mellonella.* Results showed that three isolates *viz*., *H. indica* (IARI-EPN-KA-22), *H. indica* (IARI-EPN-KA-24) and *O.myriophilus* (IARI-EPN-KA-16) caused 100% mortality, followed by *Oscheius* sp. (IARI-EPN-KA-15) showed 87%. Whereas *M.rainai* (IARI-EPN-KA-10) caused less mortality (80%). In further experiments their efficacy was tested against arecanut root grub *Leucopholis* sp. and *Spodoptera frugiperda.* The probit analysis was done to find the Median lethal concentration (LC_{50}) value. The median lethal concentration (LC_{50}) of the EPNs was tested at five different concentrations viz., 10, 20, 30, 40 and, 50 IJs of *H. indica* (IARI-EPN-KA-22 and IARI-EPN-KA-24). For other three remaining EPNs viz. *O. myriophilus* (IARI-EPN-KA-16), *Oscheius*sp. (IARI-EPN-KA-15) and *M. rainai* (IARI-EPN-KA-10) concentrations of 25, 50, 75, 100 and 125 IJs were used. Probit analysis indicated that, required less number of *H. indica* (IARI-EPN-KA-24) 19.88 IJs/larva to provoke 50% mortality, whereas *Oscheius* sp. (IARI-EPN-KA-15) took more IJs (108.54 IJs/larva) to provoke 50 % mortality of S. *frugiperda.* In case of *Leucopholis* sp., probit analysis indicated that, required less number of *H. indica* (IARI-EPN-KA-24)40.07 IJs/grub to provoke 50% mortality, whereas *Oscheius* sp. (IARI-EPN-KA-15) took more IJs (185.5 IJs/grub) to provoke 50 % mortality.Considering the data, we elucidate that *H. indica* (IARI-EPN-KA-24) were most virulent against GWML, *S. frugiperda* larvae as well as native arecanut root grub *Leucopholis* sp. The results and insights generated from present study have thrown light on the EPN diversity in the region and also opened new dimension of exploring their efficacy against other local pest population. Utilization of these native strains could result in better pest control as they are naturally adopted and co-evolved to the region.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Suman Panja (21824)	M.Sc.	Effect of nanoemulsions of essential oils on *Meloidogyne graminicola* infecting rice	Dr. Pankaj	ICAR-IARI, New Delhi
2.	Preetham V (21930)	M.Sc.	Exploration and evaluation of entomopathogenic nematodes associated with arecanut (*Areca catechu* L.) rhizosphere from Dakshina Kannada district of Karnataka	Dr. Rashid Pervez	ICAR-IARI, New Delhi
3.	Sharad (21932)	M.Sc.	Detection and molecular characterization of rice white tip nematode, *Aphelenchoides besseyi*	Dr. Bharat H Gawade	ICAR-IARI, New Delhi
4.	Srinivasa G (21951)	M.Sc.	Diversity and community profile of plant and soil nematodes associated with various crops under protected cultivation	Dr. Rashid Pervez	ICAR-IARI, New Delhi
5.	Bijaylokhimi Saikia (21952)	M.Sc.	Morphological and molecular identification of cyst nematodes (*Heterodera* spp.) from IARI farm, New Delhi	Dr. M.R. Khan	ICAR-IARI, New Delhi
6.	Artha Kundu (11553)	Ph.D.	Determination of G-protein coupled receptors involved in odor- and chemo- reception in *Heterorhabditis bacteriophora*	Dr. Vishal Singh Somvanshi	ICAR-IARI, New Delhi
7.	Manish Kumar (11555)	Ph.D.	Genes and pathways for parasitism and development of *Anguina tritici* on wheat	Dr. Anil Sirohi	ICAR-IARI, New Delhi

PLANT PATHOLOGY

7

Prof. Aundy Kumar

The Division of Plant Pathology, encompasses Mycology, Fungal Pathology, Bacteriology, and Virology, advanced disease diagnosis, pathogenomics, host-pathogen interactions, and microbiome-based biocontrol. Research spans nanotechnology, dsRNA-based management, genome editing, and RNAi for disease-resistant crops. The division also leads in plant disease modeling and human resource development. The achievements of the students are presented in following themes, as below:

Theme 1: Mycology

Diversity of *Fusarium* species associated with fruits in Delhi mandis

Fruits are essential for global nutrition and economic stability, yet postharvest losses due to fungal diseases pose significant challenges to food security. Among these, *Fusarium* species are major pathogens, affecting a wide range of fruits and producing mycotoxins that impact quality and market value. This study investigated the morphological and molecular characterization of *Fusarium* species associated with postharvest fruit diseases in major markets of Delhi. A survey across five mandis revealed a high prevalence of *Fusarium*, accounting for 43% of the fungal isolates. The study examined banana, papaya, dragon fruit, kiwi, mandarin, tomato, and apple—fruits commonly available during the sampling period. Besides *Fusarium*, other postharvest pathogens identified included *Penicillium, Colletotrichum, Alternaria, Sclerotinia, Cladosporium, Geotrichum, Botrytis, Curvularia, Venturia, Mucor, Arthobotrytis, Rhizopus,* and *Phoma.* Morphological and molecular characterization using *tef-1α* and *rpb2* gene sequencing identified ten distinct *Fusarium* species classified into five species complexes: *F. pernambucanum* (syn. *F. incarnatum*), *F. irregulare, F. tanahbumbuense, F. brevicaudatum* (syn. *F. equiseti*), *F. chlamydosporum, F. oxysporum, F. sacchari, F. proliferatum, F. verticillioides,* and *F. solani*, with *F. pernambucanum* being the most frequently isolated and infecting a broad range of fruits, highlighting its significance as a postharvest pathogen. Pathogenicity tests confirmed that all *Fusarium* species were capable of infecting their respective host fruits, with 23% of isolates being weakly pathogenic, 20% mildly pathogenic, and 13% highly pathogenic. ISSR marker analysis revealed considerable genetic variability, clustering the isolates into four distinct clades. These findings emphasize the critical role of *Fusarium* in postharvest fruit decay, highlighting the urgent need for effective management strategies to reduce losses and enhance food security.

Antimicrobial activity and optimization of production of bioactive secondary metabolite produced by antagonist yeast *Hanseniaspora uvarum* strain

Postharvest losses in fruits are primarily caused by fungal diseases. Biocontrol-based pathogen inhibition offers a safe alternative for managing these losses. This study optimized parameters such as temperature, salt concentration, radiation, and pH to enhance biomass production and antibacterial metabolite yield of *Hanseniaspora uvarum*.

The antagonistic potential of *H. uvarum* crude extracts was tested against *Colletotrichum* species, including *C. gloeosporioides, C. capsici,* and *C. musae*. Dextrose and glucose were identified as the best carbon sources, while yeast extract was the most effective nitrogen source. A 0.1% salt concentration promoted optimal growth. Yeast Extract Peptone Dextrose (YEPD) broth supported maximum biomass and antimicrobial metabolite production at 25–30°C and pH 6–7, effectively inhibiting *Colletotrichum* spp. mycelial growth. Ethyl acetate crude extract exhibited mycelial growth inhibition ranging from 59.61% to 100% for *C. gloeosporioides*, 57.27% to 100% for *C. capsici*, and 55.69% to 100% for *C. musae* under in vitro conditions. In vivo experiments confirmed its effectiveness in reducing disease severity in mango, chilli, and banana. UPLC-QToF-MS/MS analysis identified ten major non-volatile organic compounds, with *β-damascenone, 2-hexylfuran,* and *6-methyl-3,5-heptadiene-2-one* showing the highest peaks. These compounds likely contribute to *H. uvarum*-antifungal activity. The findings support its potential as a biocontrol agent for postharvest disease management.

Theme 2: Fungal Pathology

Characterization of some Indian wheat collection for stripe (yellow) rust resistance

Rusts are among the most serious biotic threats to wheat, causing significant economic losses worldwide, including in India. Host resistance remains the most effective and economical means of managing the disease. This study characterized seedling and adult plant resistance in different wheat genotypes, evaluating the effectiveness of race-specific and non-race-specific resistance in reducing yield losses under high stripe and leaf rust pressure. Using the gene-matching technique with multi-pathotype data, four stripe rust resistance genes—*YrA, Yr2, Yr9,* and *Yr18*—were identified, either singly or in combination. Adult plant slow-rusting resistance was assessed through host response and epidemiological parameters (FDS, CI, AUDPC, and r). Promising slow-rusting resistance was observed at both seedling and adult stages. The Indian wheat collection exhibited significant diversity in resistance, ranging from complete resistance to susceptibility, with most genotypes showing MR/MS or MSS reactions under high disease pressure. Various levels of adult plant resistance to stripe rust were identified. Some genotypes susceptible at the seedling stage showed MR-MS reactions at the adult stage, suggesting the presence of major genes or a combination of major and minor genes conferring resistance against all virulence tested. These genotypes could be valuable for wheat improvement programs after confirmatory studies to develop durable rust-resistant varieties. Given the frequent breakdown of race-specific resistance due to the rapid evolution of new pathogen races, breeding efforts should prioritize non-race-specific resistance or a combination of race-specific and non-race-specific resistance rather than relying solely on race-specific genes.

Genomics led population diversity studies of leaf blight isolates infecting wheat

Wheat, a staple crop for 35% of the world's population, is increasingly threatened by Helminthosporium leaf blight (HLB) in warm and humid conditions. While *Bipolaris sorokiniana* is the predominant pathogen in India, the diversity of pathogenic populations associated with the HLB complex remains underexplored. An analysis of 32 leaf blight isolates collected from six wheat-growing zones between 2020 and 2022 identified a complex of pathogens: *B. sorokiniana* (75%), *Bipolaris spicifera* (12.5%), *Exserohilum rostratum* (9.3%), and *Bipolaris oryzae* (3.1%). These were characterized through morphological traits, ITS-rDNA and *GAPDH* sequence analysis, diagnostic SCAR markers, and pathogenicity studies on wheat varieties Sonalika and HD2733. Whole-genome sequencing of eight representative isolates revealed an average of 11,500 protein-coding genes per isolate, including genes linked to secondary metabolite biosynthesis, carbohydrate-active enzymes (CAZymes), and effector proteins. Comparative genomics of three pathogenic species showed that 60.48% of the total proteome and 65.39% of CAZymes were conserved, while only 26.77% of secretory proteins exhibited conservation, indicating a more rapid evolution of pathogenicity factors compared to the core genome. Secretory proteins were notably enriched in effector-like genes, small cysteine-rich proteins, and CAZymes, emphasizing their role in host-pathogen interactions. Gene expression analysis, based on *in silico* selection of key pathogenicity genes from the PHI database, revealed the highest upregulation in virulent isolates LB-18 and LB-28 at 48 hours post-inoculation, with Sonalika consistently showing higher expression levels than HD2733. These findings provide crucial insights into pathogen diversity, genomic adaptations, and host-pathogen interactions, contributing to the development of targeted disease management strategies and resistance breeding programs in wheat.

Characterization of *Tilletia indica,* assessment of bioagents and identification of resistant sources for Karnal bunt of wheat

Karnal bunt of wheat, caused by *Tilletia indica*, is a significant quarantine disease with a zero-tolerance limit. The genetic diversity and population structure of *T. indica* isolates were analyzed using 15 genome-based SSR markers. Among 22 *T. indica* isolates, 41 alleles were amplified, with 2–6 alleles per marker. The highest number of alleles (six) was observed in TiSSR12. The polymorphic information content (PIC) value ranged from 0.05 to 0.60, with TiSSR11 showing the highest PIC value and being the only highly informative SSR marker, while the others were moderate to less informative. Dendrogram analysis showed that *T. indica* isolates did not cluster according to their geographic locations. Population structure analysis indicated a maximum K value of 3, revealing the presence of three genetic sub-populations among the 22 *T. indica* isolates. Most isolates contained genetic mixing from multiple sub-populations, demonstrating genetic diversity. In pathogenicity tests, *T. indica* isolates from Bandikui, Rajasthan, were the most virulent. Screening of 238 bread wheat genotypes identified 17 genotypes (IC111822, CHK1, IC296437, IC311079, IC35076, IC416046, IC416111, IC47797, IC531275, IC531820, IC529681, IC532086, IC566636, IC582705, IC398298, IC273946, and EC362041) with stable resistance to Karnal bunt in both 2022–23 and 2023–24. Disease incidence was lower in durum wheat than in bread wheat genotypes. In vitro analysis of biocontrol agents showed that *Trichoderma asperellum* 6413 (T17) exhibited the highest inhibition, with 42.07% and 63.97% suppression of *T. indica* isolates Ti12 and Ti18, respectively. *T. harzianum* isolates were not effective. GC-MS analysis identified antifungal volatile organic compounds, including heptanes, 2,3-butanediol, and 1-hexanol, in both *T. asperellum* 6413 and *T. asperellum* 8619, while 2H-pyran-2-one, acetic acid, and toluene were exclusive to *T. asperellum* 8619. Plant studies with selected biocontrol agents showed that both pre- and post-inoculation applications of *T. asperellum* 6413 significantly reduced disease incidence.

Characterization of wheat genotypes for *Fusarium* head blight resistance through phenotyping and molecular markers

Fusarium head blight (FHB) is a major threat to wheat cultivation worldwide. Among the identified resistance loci, *Fhb1* has the most significant effect in reducing FHB severity, while *Fhb2* and *Fhb4* contribute moderately to overall resistance. A molecular marker analysis using TaHRC-GSM, GWM644, and Xgwm513, linked to *Fhb1*, *Fhb2*, and *Fhb4*, respectively, was conducted across FHBSN, MDSN, and AVT genotypes. The *Fhb1* locus was detected only in Sumai3 from FHBSN, whereas *Fhb2* and *Fhb4* were present across all tested genotypes. A controlled glasshouse evaluation of FHB resistance revealed that Sumai3 was the only genotype to show a resistant response, scoring 1 at 14 days post-inoculation (DAI). Sumai3, carrying *Fhb1*, *Fhb2*, and *Fhb4*, recorded the lowest area under the disease progress curve (AUDPC) at 120.00, indicating strong resistance. Among the tested genotypes, 198 were moderately susceptible (score 3), while 31 were susceptible (score 4). AUDPC analysis showed that 86 genotypes had values below 500, suggesting slower disease progression in these lines.

Patho-genetical studies of *Fusarium* wilt resistance in tomato

This study aimed to characterize field isolates of *Fusarium* species and screen tomato germplasm lines from the Division of Vegetable Science, IARI, for pathogen inoculum. All isolates were pathogenic under artificial inoculation on the susceptible tomato cultivar Pusa Rohini, exhibiting varying pathogenicity levels. Four isolates with the highest PDI were identified as the most virulent. Molecular analysis confirmed multiple *Fusarium* species associated with tomato vascular wilt, including the highly virulent *F. pernambucanum* isolate TOFU-CPCT-5, belonging to the FIESC complex and also pathogenic in eggplant. Field evaluation of 19 genotypes across rabi and summer seasons showed that all 13 rabi and 5 summer lines were highly resistant, with yields ranging from 0.1 to 2.3 kg/plant. Pot culture studies revealed that the 13 resistant rabi genotypes became susceptible, while among the six summer-resistant lines, K-69-2-4 big fruit (HR) and K-70-1-1 orange (R) exhibited the highest resistance, with vascular wilt incidence between 0 and 21%. These findings suggest that field resistance observed in rabi could be due to "disease escape," likely influenced by unfavourable environmental conditions for the pathogen. In contrast, resistance identified in summer appears to be "true resistance," as disease incidence remained low even under inoculated conditions. Compared to the susceptible Pusa Rohini, K-69-2-4 big fruit showed significantly higher expression of three candidate genes, suggesting the activation of defense genes by unknown R genes as a potential resistance mechanism, warranting further investigation.

Deciphering histo-pathological and molecular interaction of *Fusarium fujikuroi* – rice in Bakanae disease development

Bakanae disease of rice, caused by *Fusarium fujikuroi*, threatens Basmati rice production in northwestern India. The pathogen, transmitted through seeds, seedlings, and florets, leads to elongated, pale yellow plants with reduced tillering, often resulting in empty or seed-sparse panicles.This study examined tissue-specific pathogen colonization and transcriptomic variations in infected rice seedlings and florets. In the susceptible variety PB1121, inoculated plants showed reduced seed germination, plant height, and root length, while the resistant genotype C101A51 remained unaffected. Photosynthesis, transpiration, and stomatal conductance initially increased in infected plants but later declined. Xylem sap volume was inversely related to disease severity, with the highest (28.3 µL) in healthy plants and lowest (19.8 µL) in rotted ones. Pathogen isolation revealed higher fungal DNA in lower plant parts, with maximum accumulation in PB1121 roots (107.04 ng/200 mg) and minimal in leaves. In resistant genotypes, *F. fujikuroi* was found only in roots.RNA sequencing identified 38,676 differentially expressed genes (DEGs), with significant tissue-specific variations. GO analysis linked DEGs to catalytic activity, stimulus response, and stress response. Genes related to stress response, immune processes, and secondary metabolite biosynthesis were upregulated, with jasmonic acid, salicylic acid, and abscisic acid playing key regulatory roles. ABA biosynthesis and isoprenoid biosynthesis genes were upregulated in florets. qRT-PCR validated transcriptomic data.GC-MS metabolome profiling detected 73 compounds, with gluconolactone and deoxyglucose accumulating in panicles of susceptible genotypes.This study highlights tissue-specific colonization patterns of the pathogen and molecular responses in rice, providing insights for resistance breeding and disease management strategies against Bakanae disease.

Exploring the potential of mycogenic nanoparticles for management of *Alternaria brassicae* in *Brassica juncea*

Growing concerns over chemical fungicides necessitate alternative disease management strategies. This study explores the eco-friendly mycosynthesis of zinc oxide nanoparticles (ZnO NPs) using *Trichoderma harzianum* culture filtrate and evaluates their antifungal efficacy against *Alternaria brassicae*. Nanoparticle synthesis was optimized based on culture filtrate concentration, substrate concentration, pH, and temperature. UV-Vis spectroscopy detected a peak between 200–400 nm, while XRD confirmed a hexagonal crystal structure with an average size of 29 nm. DLS and zeta potential analysis showed a hydrodynamic size of 50.79 nm and a surface charge of -17.49 mV. FTIR identified functional groups (C=O, N-O, O-H) responsible for nanoparticle stabilization. SEM and HR-TEM revealed spherical, rod-shaped, and hexagonal nanoparticles ranging from 12 to 41 nm. M-ZnO NPs inhibited *A. brassicae* mycelial growth by 91.48% at 200 µg/mL, outperforming C-ZnO NPs (79.62%) and mancozeb (82.96%). SEM-EDX showed hyphal deformation and nanoparticle absorption, while CLSM confirmed increased ROS generation and membrane disruption. Defense enzyme analysis recorded the highest expression of SOD (44.2 U/mol) and CAT (39.6 U/mol) at 200 µg/mL M-ZnO NPs. At 200 mg L^{-1}, M-ZnO NPs significantly reduced PDI (14.66%), AUDPC (264.46), and infection rate (0.084 units day^{-1}) in *Brassica juncea*. Screening of 262 genotypes identified 97 as moderately resistant, with NB-115 exhibiting the lowest PDI (3.42), infection rate (0.0619), and AUDPC (68.36). M-ZnO NPs enhanced chlorophyll content and zinc bioaccumulation (239 ± 2.44 mg kg^{-1} DW). Antioxidant enzyme (POX, CAT, SOD) and polyphenol levels increased significantly in M-ZnO NPs + pathogen-treated plants at 72–96 h post-inoculation. Gene expression analysis showed upregulation of antioxidant (CAT, POX, CET, SOD) and pathogenesis-related (PR1, PR3, PR4, PR12) genes at 72 h. Metabolic profiling identified 44 key metabolites influencing glyoxylate, dicarboxylate metabolism, and the TCA cycle. Hormone analysis revealed enhanced JA-mediated defenses with reduced SA and ABA levels.

Metabarcoding and functional analysis of maize endophytic microbiome for suppression of *Bipolaris maydis*

The phyllosphere hosts diverse microbial communities, collectively termed the phyllomicrobiome. This study analyzed endophytic bacterial communities in MLB-resistant (SC-7) and susceptible (CM-119) maize cultivars. Microbiological and metagenomic analyses identified key phyla, including Proteobacteria and Actinobacteria, with notable genera such as *Caproiciproducens, Prevotella, Lactobacillus,* and *Acetobacter.Lactobacillus* was more abundant in resistant maize, while *Acetobacter* dominated in the susceptible cultivar. 16S rRNA sequencing identified ten bacterial species, including *Alcaligenes, Brevundimonas, Pseudomonas, Microbacterium, Proteus,* and *Stenotrophomonas.* Core genera (*Pseudomonas, Brevundimonas,* and *Stenotrophomonas*) showed strong antagonism against *Bipolaris maydis* through volatile and secretory metabolites. Over 50% of isolates exhibited antifungal activity, with *P. aeruginosa, B. olei,* and *S. maltophilia* achieving >60% MLB suppression in pathogen-challenge trials. These strains also demonstrated plant growth-promoting traits, including phosphate, potassium, zinc, and silica solubilization. Transcriptional analysis revealed dual roles in pathogen inhibition and host immune priming. These findings highlight microbiome-based strategies as a sustainable approach for MLB management and crop resilience.

Deciphering endophytic mycobiome of maize for management of banded leaf and sheath blight caused by *Rhizoctonia solani* f. sp. *sasakii*

Banded leaf and sheath blight (BLSB) of maize, caused by *Rhizoctonia solani* f. sp. *sasakii*, poses a significant threat worldwide. Harnessing endophytic fungal communities, which share the maize mycobiome's ecological niche, offers a promising but underexplored approach for disease management. Maize samples were collected from Patna, Bihar, and New Delhi across contrasting seasons (Kharif and Rabi) under conventional tillage (CT) and reduced tillage (RT). mNGS analysis from Bihar revealed over 80% unknown fungal populations, with identified genera including *Thermomyces, Leptosphaeria, Phoma, Rhizopus, Alternaria, Penicillium,* and *Aspergillus.* Delhi samples also had >80% unknown fungi, along with *Calcarisporiella, Cryptococcus, Rhizopus,* *Ustilago, Mortierella,* and *Agrocybe.* Classical microbiology confirmed maize-associated fungi like *Alternaria, Aspergillus, Fusarium, Cladosporium,* and *Penicillium.Aspergillus niger* (Bihar) and *Penicillium oxalicum* (Delhi) significantly reduced BLSB in *in planta* and *in vitro* assays and field trials, inducing defense genes (*SOD, PPO, POA, CAT,* and *β-1,3-glucanase*). These findings highlight mycobiome reengineering as a sustainable strategy for maize disease management.

Enumeration of seed mycoflora and their management with *Beauveria bassiana* and *Trichoderma asperellum* in IARI newly released chickpea varieties

The mycoflora associated with chickpea seeds was analyzed in three varieties: Pusa 3022, Pusa Chickpea 10216, and Pusa Chickpea Manav. Enumeration methods included blotter paper, agar plate, and rolling paper towel techniques to assess their impact on seed germination and seedling vigor. The efficacy of *Beauveria bassiana* and *Trichoderma asperellum* as biocontrol agents against major seed-borne fungi was also evaluated. Fourteen fungal species were identified, with *Aspergillus niger, A. flavus,* and *Rhizopus stolonifer* being the most prevalent. The blotter and agar plate methods proved more effective than the rolling paper towel method. *A. niger, A. flavus, R. stolonifer, Curvularia lunata,* and *Rhizoctonia bataticola* significantly reduced seed germination, with infection rates in Pusa 3022 leading to a 70-80% decline in germination and adversely affecting seedling vigor across varieties. The antagonistic potential of *B. bassiana* isolates (BbR1, BbR2, BbR3, BbR4) and *T. asperellum* isolates (ITCC 8687, ITCC 8619, ITCC 8541) was assessed using dual culture assays. *T. asperellum* (ITCC 8687) showed the highest inhibition against *A. niger* (68.50%), *A. flavus* (75.33%), and *C. lunata* (80.25%). *T. asperellum* (ITCC 8619) also suppressed *A. niger* (63.67%) and *C. lunata* (82.60%). Among *B. bassiana* isolates, BbR2 and BbR3 inhibited *A. niger* (52.33% and 50.76%) and *C. lunata* (56.25% and 55.50%). Application of *T. asperellum* and *B. bassiana* improved seed germination and plant growth in all chickpea cultivars. *T. asperellum* (ITCC 8687) was the most effective, increasing germination to 98% in Pusa 3022 and achieving a seedling vigor index (SVI) of 3969.34. *B. bassiana* (BbR2) enhanced germination to 95-97%, with an SVI of 3429.89 in Pusa Chickpea. This study highlights seed-borne fungal pathogens in new chickpea varieties and demonstrates the effectiveness of *B. bassiana* (BbR2) and *T. asperellum* (ITCC 8687) in improving seed health and plant growth. The findings support biological control as a viable alternative to chemical treatments for managing these pathogens.

Comparative efficacy of selected microbial bioagents and identification of resistance sources against stem rot of chickpea caused by *Sclerotinia sclerotiorum*

The efficacy of *Beauveria bassiana* and *Trichoderma asperellum* as biocontrol agents against stem rot disease of chickpea caused by *Sclerotinia sclerotiorum* was evaluated through in vitro and in planta experiments. Among the tested isolates, *T. asperellum* ITCC 8687 exhibited the highest mycelial inhibition (63.92%), followed by *T. asperellum* ITCC 8619 (57.25%), *B. bassiana* BbR2 (31.92%), and *B. bassiana* BbR3 (28.72%). In planta studies confirmed significant disease suppression, with *T. asperellum* ITCC 8687 and *B. bassiana* BbR2 reducing disease incidence by 44.60% and 36.31%, respectively, and enhancing chlorophyll content, though benefits declined post-pathogen challenge. Biochemical assays indicated increased systemic resistance, with *T. asperellum* ITCC 8687 showing a 2.05-fold rise in peroxidase activity, 1.41-fold in polyphenol oxidase, and 2.86-fold in total phenol content. Growth parameters improved significantly, with *T. asperellum* ITCC 8687-treated plants achieving a seedling vigor index I of 1.76 and index II of 1.94. Screening of 99 chickpea germplasm lines identified IGK 2021-54 and GJG 2206 as highly resistant, with six lines showing moderate resistance. These findings underscore the potential of *B. bassiana* and *T. asperellum* in managing *S. sclerotiorum* and highlight the importance of integrating biocontrol strategies with genetic resistance for sustainable chickpea production.

Deciphering bio-compatibility between *Trichoderma* spp. and *Pseudomonas* spp. and its bio-efficacy against *Sclerotinia sclerotiorum*

Indian mustard (*Brassica juncea* L. Czern & Coss.) is an important edible oilseed crop, with *Sclerotinia sclerotiorum* being a major constraint in its cultivation. Reducing sclerotia production is crucial for managing this pathogen. Indigenous biocontrol agents, suited to local environments, can compete effectively with native microorganisms and suppress local pathogen strains. While combining biocontrol agents has been shown to enhance disease control, little is known about their molecular interactions. This study evaluated *Trichoderma* spp. and *Pseudomonas fluorescens*, isolated from different soil regions, for their potential as biological control agents against *S. sclerotiorum*. In vitro assays showed significant inhibition of mycelial growth, with reductions of 82.27% and 66.67% by *Trichoderma* spp. and *P. fluorescens*, respectively, both individually and in dual cultures. *Trichoderma* spp. exhibited mycoparasitism, while *P. fluorescens* displayed antibiosis. Compatibility tests showed no inhibition zones between *Trichoderma* spp. and *P. fluorescens*, suggesting their potential for integrated disease management. Volatile metabolites from both organisms, individually and in combination, effectively reduced pathogen growth. Plants treated with the microbial consortia showed improved seed germination, plant growth, and yield parameters in both pathogen-challenged and pathogen-free conditions. Increased plant length, fresh weight, number of leaves, and seedling vigor index were recorded, highlighting the potential of these biocontrol agents in sustainable mustard cultivation.

Theme 3: Plant Bacteriology

Elucidating major TAL effectors of *Xanthomonas oryzae* pv. *oryzae* (Race 4) for their role in bacterial blight development in rice

Bacterial leaf blight of rice, caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo), poses a serious threat as it affects rice from the seedling stage (kresek) to active tillering (leaf blight). Indian Xoo Race 4, predominant in North-Western India, was analyzed for its TAL effector profile to identify key TAL effectors and their target genes in rice that contribute to disease development. Southern hybridization revealed sixteen TAL effectors of varying sizes in the genome of Indian Xoo Race 4, with variations observed in the TAL-ome profiles of six different Indian Xoo races. These TAL effectors were cloned into pCAMBIA1300, and their presence was confirmed through dot blot analysis and restriction digestion with *BamHI* and *MscI*. Whole-genome analysis using Anno-TALE confirmed sixteen TAL effectors, with complete sequences retrieved for nine. TALE 4 was identified as a type B truncated TALE, possessing a single nuclear localization signal and lacking an activation domain. PrediTAL analysis predicted targets for eight TAL effectors, with three *SWEET* genes identified as direct targets: *OsSWEET13* (Os12t0476200-010) and *OsSWEET12* (Os03t0347500-01) by TALE 2, and *OsSWEET7e* (Os09t0256650-00) by TALE 12. Agro-inoculation of *Agrobacterium tumefaciens* EHA105 carrying RTBV-MIVG+PDS, RTBV-MIVG+OsSWEET7e, and RTBV-MIVGS+OsSWEET13 into 21-day-old PB 1 rice seedlings revealed that silencing *OsSWEET13* significantly reduced blight lesion length, bacterial count, and bacterial copy number. In contrast, *OsSWEET7e* silencing showed no significant effect compared to non-silenced plants challenged with Indian Xoo Race 4. These findings confirm that *OsSWEET13*, induced by TALE 2 of Indian Xoo Race 4, plays a crucial role in blight development.

Elucidation of structural features and functional role of Hpa1 like type three translocators of *Xanthomonas axonopodis* pv. *punicae* in the induction of bacterial blight on pomegranate

Xanthomonas axonopodis pv. *punicae* (Xap) causes bacterial blight in pomegranate, severely impacting export quality. While previous studies have explored Xap's virulence factors, including TTSS, TALEs, and *Xanthomonas* outer protein effectors, the role of Hpa1, a key virulence protein in other *Xanthomonas* species, remained unexplored in Xap. This study investigated functional relevance of Hpa1 in bacterial virulence and its impact on pomegranate immune responses. Structural analysis using bioinformatics tools like I-TASSER revealed distinct features of Hpa1, including its extracellular localization and involvement in ion binding, thiamine biosynthesis, and phosphate metabolism. To understand its role, a null mutant for Hpa1 was generated, and experimental analyses highlighted its crucial role in bacterial growth and virulence. The Hpa1 mutant exhibited reduced colonization and symptom expression compared to the wild-type Xap. Hpa1 was found to suppress callose deposition, inhibit reactive oxygen species (ROS) production, and modulate immune-responsive genes in pomegranate leaves, indicating its role in subverting plant defenses. These findings underscore Hpa1's critical function in promoting bacterial virulence and symptom severity. This study establishes Hpa1 as a pivotal virulence factor in Xap, emphasizing its potential as a target for resistance strategies. Targeted approaches, such as silencing Hpa1 or its interacting proteins, may enhance resistance against bacterial blight. In summary, this investigation sheds light on role of Hpa1 in pathogenicity in pomegranate and highlights its significance as a potential target for developing resistance strategies against this destructive disease

Targeting bacterial blight resistance through CRISPR/Cas9 mediated editing of rice *SWEET* genes

Rice, a staple for over half the world's population, is vital in Asia, where millions depend on it for sustenance and livelihoods. India, the second-largest producer after China, faces significant yield losses (20–50%) due to bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo), particularly in tropical and subtropical regions. SWEET transporters, essential for sugar transport, play key roles in rice growth, development, and stress responses, with *OsSWEET11* and *OsSWEET14* crucial for sucrose movement from leaves to grains. This study analyzed variations in *OsSWEET* gene promoters, revealing that Indian *Xoo* race 4 predominantly induces *OsSWEET11*, followed by *OsSWEET14, OsSWEET13,* and *OsSWEET15*, suggesting *OsSWEET15* as a potential new target. CRISPR/Cas9 editing of *OsSWEET11* and *OsSWEET14* resulted in edited rice lines (M2, M3, M24 for *OsSWEET11*; M3, M5, M12, M16, M20 for *OsSWEET14*) that significantly reduced disease severity. These lines are promising for breeding programs and host-pathogen interaction studies, highlighting the potential of targeting additional *OsSWEET* genes for broad-spectrum resistance to bacterial blight.

Genome and metabolome characterization of phyllosphere adapted *Pantoea* species for antimicrobial metabolites against blast and bacterial blight in rice

Three *Pantoea* isolates (*Os-Ep-PPA-1b, Os-Ep-PPA-3b,* and *Os-Ep-VPA-9a*), obtained from the rice phyllosphere, exhibited antimicrobial activity against key rice foliar diseases—blast and bacterial leaf blight. Morphological, phenotypic, and genotypic analyses identified them as *Pantoea agglomerans, Pantoea vagans,* and *Pantoea deleyi,* respectively. Draft genome sequencing revealed genome sizes of 4,442,272 bp, 4,350,313 bp, and 4,578,694 bp, with an average G+C content of 57%. *P. agglomerans* and *P. vagans* showed 87–88% similarity to related strains in public databases, while *P. deleyi* exhibited 99% similarity to the LMG24200 isolate. Comparative pan-genome analysis between these non-pathogenic rice phyllosphere-adapted *Pantoea* isolates and pathogenic *Pantoea ananatis* revealed 423 gene clusters absent in the pathogen. Biosynthetic gene cluster (BGC) analysis identified 502, 579, and 518 BGCs encoding secondary metabolites in *P. agglomerans, P. vagans,* and *P. deleyi,* respectively. These isolates suppressed *Magnaporthe oryzae* and *Xanthomonas oryzae* pv. *oryzae* through secondary metabolites and volatile compounds, demonstrating fungistatic and bactericidal activity. Cell-free extracts inhibited rice pathogens by 55.13%–78.34%, affecting *M. oryzae* conidial morphology and showing enhanced antibacterial activity against *X. oryzae* pv. *oryzae.* Hydroxamate-type siderophores were identified as key secondary metabolites. Metabolome and volatilome analyses using LC-MS and GC-MS revealed diverse antimicrobial compounds. In planta assays demonstrated up to 100% blast suppression in detached leaf assays, while bacterial blight suppression ranged from 23.67% to 54.35%. Field trials highlighted the effectiveness of these *Pantoea* isolates in promoting plant growth, improving flag leaf length, panicle number, grains per panicle, and reducing chaffy grains. These findings establish *Pantoea* isolates as promising bioagents for rice cultivation.

Theme 4: Plant Virology

Characterization of virus associated with shoe-string disease affected tomato plant and management through exogenous application of dsRNA

A newly emerging disease, marked by a distinctive shoestring-like pattern on leaves and the formation of unripe, small, and hard fruit, is posing a serious threat to tomato cultivation in India. An initial survey in the experimental field showed that over 50% of the plants exhibited symptoms of shoestring disease, leading to significant reductions in both fruit yield and quality. Transmission electron microscopy (TEM) and molecular analyses confirmed the presence of a new strain of tomato mottle mosaic virus (ToMMV) in the affected plants. Mechanical inoculation of partially purified ToMMV into tomato cv. Pusa Ruby successfully reproduced the characteristic symptoms. The present shoestring isolate of ToMMV was found to infect most major commercial tomato varieties under experimental conditions, highlighting its aggressive nature. Host range studies showed that this ToMMV isolate could infect several solanaceous species, while cucurbitaceous hosts remained unaffected. The virus was also found to be seed-transmissible, with a small percentage of seedlings from infected plants displaying symptoms. In this study, a dsRNA expression construct was prepared in the L4440 vector, targeting the coat protein (CP) gene and a segment of the movement protein (MP) gene of ToMMV. dsRNA purified from *E. coli* HT115 cells was topically applied to tomato cv. Pusa Ruby plants, significantly reducing the development of shoestring symptoms upon virus challenge inoculation. Quantitative reverse transcription polymerase chain reaction (qRT-PCR) analysis showed a more than 90% reduction in virus accumulation in all dsRNA-treated plants. Prophylactic application of dsRNA before virus inoculation provided the highest level of protection, effectively suppressing both symptom development and virus accumulation.

Determination of genetic diversity of *Citrus tristeza virus* causing decline of Assam lemon (Citrus lemon) in Northeast India and development of disease-free planting material

Citrus tristeza virus (CTV), transmitted by *Toxoptera citricidus*, has devastated millions of citrus trees worldwide, including in India. The virus has flexuous filamentous particles (2000 × 11 nm) and a +ssRNA genome (~19.3 kb) encoding 19 proteins. CTV causes decline, yellowing, stunting, and stem pitting, severely affecting fruit yield and quality. In India, it has persisted for over a century, killing more than one million citrus trees and infecting all commercial citrus varieties. Assam lemon (*Citrus limon*), or Kaji Nemu, is a key citrus crop in Northeast India, but its production is threatened by tristeza-induced decline. A survey across 13 farms in Assam and Meghalaya revealed symptoms such as decline, chlorosis, poor canopy, and stunting. CTV incidence was estimated at 76.3% in 114 samples based on DAC-ELISA and PCR, indicating its widespread occurrence. Fourteen CTV isolates were characterized through CP gene (672nt) sequencing, showing 88–100% nucleotide identity. Phylogenetic analysis grouped them into three genogroups: one with Indian isolates TK1/K5, another with isolate Kpg3, and a third with the decline-inducing Israeli isolate VT. Five isolates (JAL-5, JAL-6, JAL-28, JAL-30, JAL-46) were identified as recombinants, with Kpg3 as the major donor and TP6 as the minor donor. CTV-free Assam lemon mother stocks were identified for producing and distributing disease-free planting materials. Since the virus primarily spreads through infected planting material, ensuring CTV-free stock is essential for sustaining citrus cultivation in Northeast India.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1	Ankita (21785)	M.Sc.	Diversity of *Fusarium* species associated with fruits in Delhi mandis.	Dr. Amrita Das	ICAR-IARI, New Delhi
2	H S Hemanth Gowda (21786)	M.Sc.	Characterization of some Indian wheat collection for stripe (yellow) rust resistance	Dr. Vaibhav K. Singh	ICAR-IARI, New Delhi
3	Pallavi Bisht (21787)	M.Sc.	Antimicrobial activity and optimization of production of bioactive secondary metabolite produced by antagonist yeast *Hanseniaspora uvarum* strain	Dr. Amrita Das	ICAR-IARI, New Delhi
4	Prantik Mazumder (21789)	M. Sc	Characterization of virus associated with shoe-string disease affected tomato plant and management through exogenous application of dsRNA	Dr. Anirban Roy	ICAR-IARI, New Delhi
5	Sangale Smita Bhausaheb (21902)	M.Sc.	Characterization of *Tilletia indica*, assessment of bioagents and identification of resistant sources for Karnal bunt of wheat	Dr. Malkhan S. Gurjar	ICAR-IARI, New Delhi
6	Shivaraj (21903)	M.Sc.	Characterization of wheat genotypes for *Fusarium* head blight resistance through phenotyping and molecular markers	Dr. M.S. Saharan	ICAR-IARI, New Delhi
7	Shreya Shreeshail Maigur (21924)	M.Sc.	Comparative efficacy of selected microbial bioagents and identification of resistance sources against stem rot of chickpea caused by *Sclerotinia sclerotiorum*	Dr. T. K. Bag	ICAR-IARI, New Delhi
8	Chandrakesh Gautam (21926)	M.Sc.	Determination of genetic diversity of *Citrus tristeza* virus causing decline of Assam lemon (Citrus lemon) in northeast India and development of disease-free planting material	Dr. K.K. Biswas	ICAR-IARI, New Delhi
9	Chaitra Channappa Sarawad (21976)	M.Sc.	Enumeration of seed mycoflora and their management with *Beauveria bassiana* and *Trichoderma asperellum* in IARI newly released chickpea varieties	Dr. T. K. Bag	ICAR-IARI, New Delhi
10	Jyoti Kumari Agrwal (60130)	M.Sc.	Patho-genetical studies of *Fusarium* wilt resistance in tomato	Dr. V. Shanmugam	#ICAR-IARI, Jharkhand
11	Tanisha Metia (60135)	M.Sc.	Deciphering bio-compatibility between *Trichoderma* spp. and *Pseudomonas* spp. and its bio-efficacy against Sclerotinia sclerotiorum	Dr. Lakshman Prasad	#ICAR-IARI, Jharkhand

12	Kalaivanan (10861)	Ph. D	Elucidating major TAL effectors of *Xanthomonas oryzae* pv. *oryzae* (Race 4) for their role in bacterial blight development in rice	Dr. K.K. Mondal	ICAR-IARI, New Delhi
13	Jagdish Yadav (11086)	Ph. D	Deciphering histo-pathological and molecular interaction of *Fusarium fujikuroi* – rice in Bakanae disease development	Dr. Bishnumaya Bashyal	ICAR-IARI, New Delhi
14	Vineeth Vijayan (11313)	Ph. D	Deciphering endophytic mycobiome of maize for management of banded leaf and sheath blight caused by *Rhizoctonia solani* f. sp. sasa*kii*	Dr. Robin Gogoi	ICAR-IARI, New Delhi
15	Mrutyunjaya S (11315)	Ph. D	Elucidation of structural features and functional role of Hpa1 like type three translocators of *Xanthomonas axonopodis* pv. punicae in the induction of bacterial blight on pomegranate	Dr. K.K. Mondal	ICAR-IARI, New Delhi
16	Charisma, K (11568)	Ph. D	Genome and metabolome characterization of phyllosphere adapted *Pantoea* species for antimicrobial metabolites against blast and bacterial blight in rice	Dr. A. Kumar	ICAR-IARI, New Delhi
17	Rashmi E R (11569)	Ph. D	Targeting bacterial blight resistance through CRISPR/Cas9 mediated editing of rice *SWEET* genes	Dr. K.K. Mondal	ICAR-IARI, New Delhi
18	Sanghmitra Aditya (11577)	Ph.D.	Genomics led population diversity studies of leaf blight isolates infecting wheat	Dr. M. S. Saharan	ICAR-IARI, New Delhi
19	Sudeepta Pattanayak (11846)	Ph. D	Metabarcoding and functional analysis of maize endophytic microbiome for suppression of *Bipolaris maydis*	Dr. Robin Gogoi	ICAR-IARI, New Delhi
20	Deep Narayan Mishra (12137)	Ph. D	Exploring the potential of mycogenic nanoparticles for management of *Alternaria brassicae* in *Brassica juncea*	Dr. Lakshman Prasad	ICAR-IARI, New Delhi

#IARI off-campus

Session III: School of Natural Resource Management

Thesis Summary

Discipline	Number of Thesis Submitted	
	M. Sc./M. Tech	Ph.D.
Agricultural Engineering	10	13
Agricultural Physics	06	02
Agronomy	09	09
Environmental Sciences	11	04
Microbiology	07	07
Soil Science and Agricultural Chemistry	12	15
Water Science and Technology	02	01
Total	**57**	**51**

SCHOOL OF NATURAL RESOURCE MANAGEMENT

Chairperson: Dr. B. Venkateswarlu, Former Vice Chancellor VNMKV, Parbhani and Former Director, ICAR-CRIDA, Hyderabad

Dr. B. Venkateswarlu is the former Vice Chancellor, Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani and former Director, ICAR-Central Research Institute for Dryland Agriculture (CRIDA), Hyderabad. He is an agricultural microbiologist by training and has served in ICAR for over 35 years under different capacities in research and research administration, and for a brief period in ICRISAT. His main areas of research are biological nitrogen fixation, role of microorganisms in abiotic stress tolerance, dryland agriculture and climate change. As Director, CRIDA he conceptualized and implemented the NICRA project in ICAR. He has published over 250 research papers with total citations of 13,500 with a h-index of 55 and has two patents to his credit. Dr. Venkateswarlu is a fellow of National Academy of Agriculture Sciences (NAAS) and Telangana Academy of Sciences. He received several awards and recognitions from ICAR, the important ones being Fakruddin Ali Ahmed Award, Vasantrao Naik Award and Hari Om Ashram Trust award. He delivered J. N. Mukherjee memorial lecture of Indian Society of Soil Science, and is a recipient of 7th International Crop Science Congress Award and the FAI Golden Jubilee Award. He has been recognized as Honorary Fellow for his lifetime contributions to Dryland Agriculture research by Indian Society of Dryland Agriculture (ISDA), and Arid Zone Research Association of India. He has served in different committees and Task forces in DBT, DST, ICAR, and NITI Ayog related to agriculture research and policy. He was also a former member of GEAC. He chaired QRT and RACs of CAZRI, Jodhpur, CICR, Nagpur, NIASM, Baramati and as member in few other ICAR institutes. Currently he is the Chair of the Expert Committee of NICRA project, Member, Empowered Committee of National Agricultural Science Fund (NASF) of ICAR and President, Agribiotech Foundation, Hyderabad.

AGRICULTURAL ENGINEERING

8

Prof. A.K. Mishra

The Division of Agricultural Engineering was established in 1945 to develop and introduce appropriate machinery, implements and soil water conservation systems in Indian agriculture. Subsequently, postgraduate teaching and research on these aspects were added to the mandate of the Division. With the establishment of Water Technology Centre in 1972, the soil and water conservation research component was transferred to the Water Technology Centre, although teaching in this sub-discipline continued to form an integral part of the P.G. teaching of the Agricultural Engineering Division. The Division has the mandate for conducting strategic research on design and development of technologies/equipment in the area of Farm Machinery & Power, Agricultural Processing and Structures, Protected Cultivation, Soil and Water Engineering and Renewable Energy Sources with extension of technologies to farmers and entrepreneurs. The Division also provides Post Graduate teaching.The research work carried out by the students of the Division during 2023-24 can broadly be classified into following seven themes, for which the significant findings are presented below:

Theme 1: Resource Conservation Technologies

Development of non-destructive adulteration detention protocol for saffron using advanced imaging techniques

Saffron, the world's most expensive spice, faces a significant challenge of adulteration, which traditional detection methods struggle to address due to their high costs and time requirements. This study explored advanced non-destructive techniques, specifically RGB and hyperspectral imaging, to detect saffron adulteration efficiently and reliably. The study evaluated five adulterants: Chrysanthemum (S1), Pot sunflower + Kumkum (S2), Maize threads + Turmeric + Surf (S3), Pot sunflower + Maroon color + Original Pot sunflower (S4), and Maize threads + Maroon color (S5). Physico-chemical analyses revealed ash content values above 8 or below 5, except for S1, and distinct L*, a*, b* color values for adulterants. RGB imaging datasets (7,786 images) were acquired under controlled conditions and categorized into seven classes, including pure saffron (with and without yellow styles). Data were split into training (64%), validation (25%), and testing (11%), and machine learning models such as MobileNet, MobileNetV2, VGG19, DenseNet121, and InceptionV3 were evaluated. MobileNetV2 emerged as the best model, achieving perfect accuracy, the fastest prediction time (37 ms), and high real-time detection efficiency, outperforming others by 58–80% in speed. Hyperspectral imaging (400–1000 nm) was also employed, with data pre-processed using spatial and spectral techniques and reduced to three principal components preserving 99.87% of information. Classification models (PLS-DA and KNN) achieved perfect accuracy rates, with PLS-DA performing more consistently. The study demonstrated that hyperspectral imaging's unique spectral fingerprints and efficient preprocessing significantly improved adulteration detection. The combined RGB and hyperspectral imaging protocols proved to be fast, reliable, and non-destructive, offering a cost-effective and practical solution for saffron authentication, significantly enhancing efficiency compared to traditional methods.

AI-based crop growth modelling in vertical hydroponic systems

The growing global population and rapid urbanization necessitate innovative agricultural solutions like vertical hydroponic farming to ensure food security and sustainability. Traditional methods struggle to meet rising demands, highlighting the need for predictive models that optimize crop growth in controlled environments. This study addresses the gap by developing an AI-based crop growth model for green leafy vegetables in vertical hydroponic systems. Conducted in a greenhouse at the Centre for Protected Cultivation Technology (CPCT), ICAR-IARI, New Delhi, the experiment included two nutrient solutions, two supporting media and two structural setups, resulting in eight treatments. Growth parameters such as plant height, shoot length, root length, leaf area, chlorophyll content, and biomass were collected across three cropping seasons and used to train machine learning models, including Random Forest, Support Vector Regression (SVR), k-Nearest Neighbours (k-NN), and Classification and Regression Trees (CART). Random Forest emerged as the most accurate algorithm, achieving an R^2 value of 0.92 and an RMSE of 2.5 for predicting plant height. Among treatments, T3 (N2 M1 S1), which combined Nutrient Solution 2, Supporting Media 1, and Structure 1, showed superior performance with a plant height of 18.75 cm, shoot length of 9.5 cm, and chlorophyll content of 32.12 at 42 days. In contrast, T8 (N2 M2 S2) performed the worst, confirming the significant influence of media and structure on crop outcomes. The AI models provided reliable predictions and actionable insights into plant growth patterns across setups. This study demonstrates the potential of AI-based models to optimize vertical hydroponic farming, offering data-driven tools for improving crop management, minimizing resource waste, and enhancing yield efficiency. The findings highlight the transformative potential of integrating AI into urban agriculture, paving the way for scalable and sustainable solutions in controlled-environment farming.

AI-based nutrition modelling for vertical hydroponics farming

The rise in global food demand and shrinking agricultural land, vertical hydroponic systems combined with AI-based nutrient management provide a promising solution for optimizing crop production in controlled environments. Limited research exists on AI models tailored to nutrient management in vertical farming, which this study sought to address. The research, conducted at the Centre for Protected Cultivation Technology (CPCT), ICAR-IARI, New Delhi, focused on cultivating Bok Choy (*Brassica rapa*) using the Nutrient Film Technique (NFT) on A-frame vertical structures. Eight treatments were tested, involving two nutrient solutions, four nutrient concentrations (varying electrical conductivity and pH), and two supporting media (clay balls and rock wool). Growth parameters like plant height, shoot length, root length, chlorophyll content, leaf count and biomass were measured across three growing seasons. Several machine learning models were developed, including Random Forest, Support Vector Machine (SVM), k-Nearest Neighbours (k-NN), Linear Model (LM), Bayesian model, Multivariate Adaptive Regression Splines (MARS), and Classification and Regression Trees (CART). The k-Nearest Neighbours (k-NN) model emerged as the most accurate, achieving an R^2 value of 0.9648 and an RMSE of 0.2147 for predicting total dry weight. It consistently delivered high accuracy for other parameters like shoot length and fresh weight. The best-performing treatment was T7 (N2 D3), which utilized Hasan et al.'s nutrient solution with medium nutrient concentration (EC 1.5-2.2, pH 5.5-6.0). This treatment resulted in the highest fresh weight (99.2 g) and total dry weight (14.06 g), demonstrating optimal growth and nutrient uptake. The study concluded that the k-NN model is a reliable tool for predicting crop performance, while T7 (N2 D3) offers the most effective nutrient management strategy. Integrating AI models with vertical hydroponics can enhance nutrient efficiency, improve crop yields, and support sustainable urban agriculture.

Theme 2: Precision Farm Equipment

Design and development of embedded system-controlled site-specific seed cum fertilizer applicator

Maize (*Zea mays* L.), a key crop for food security, faces yield stagnation, necessitating improved nutrient management strategies for sustainable cultivation. A field study at ICAR-IARI, New Delhi, investigated reduced-rate nutrient applications combined with precision placement using the maize variety Pusa HPQM-1 in a Randomized Block Design (RBD) with seven treatments. The results revealed that 100% RDF (Recommended Dose of Fertilizer) point placement significantly improved growth parameters such as plant height, leaf area index, and root metrics, outperforming traditional band and broadcast methods. Even with a 25% reduction in fertilizer through point placement, yields were maintained, peaking at 6.97 t/ha (2022) and 6.81 t/ha (2023). Soil nitrogen showed significant depletion post-30 DAS, while phosphorus and potassium levels varied minimally. To enhance efficiency and address traditional farming inefficiencies like uneven seed distribution and excessive fertilizer use, a site-specific seed-cum-fertilizer applicator controlled by an embedded system was developed. The applicator integrates seed and fertilizer delivery, reducing wastage and labor. For maize cultivation, it achieved optimal performance at 2 km/h with a mean seed spacing of 21.5 cm, 88.28% feed quality, and 93.07% precision. Field trials reported 0.32 ha/h capacity, 76.82% efficiency, and 12.1 L/ha fuel consumption, with a 1.1-year payback period. This technology, particularly advantageous for smallholders, ensures precise fertilizer application, conserves up to 25% fertilizer without yield loss, and improves planting accuracy. By combining economic viability with environmental sustainability, it marks a significant advancement in precision agriculture, supporting higher productivity while addressing ecological and financial challenges.

Design and development of robotic pesticide applicator for greenhouse

Greenhouses are space-efficient structures for quality produce, but operators face occupational health risks, such as chemical exposure and ergonomic challenges during pesticide application. This study evaluated operator exposure and designed a robotic pesticide applicator to mitigate risks and improve efficiency. Chemical exposure during spraying was assessed for battery-powered and stationary sprayers under continuous and alternate row spraying. Potential Dermal Exposure (PDE) was higher in continuous row spraying (54–70 mL h^{-1}), while alternate row spraying reduced PDE by 16–25%. Ergonomic assessments revealed that the battery sprayer required a lower energy expenditure rate (210 ± 35 W) and had lower discomfort scores compared to the stationary sprayer.To address these issues, a robotic pesticide applicator was developed, utilizing sensors to target crop foliage and optimize pesticide use. Field evaluations tested three parameters (robot forward speed, nozzle distance, and nozzle type) using a Central Composite Design and Response Surface Methodology. The best spray coverage (44.56%), volume median diameter (197.33 µm), and droplet density (82.72/cm^2) were achieved with a flat fan nozzle at 1 km/h forward speed and a 20.10 cm nozzle-to-target distance. The robot reduced pesticide use by 24.95% compared to manual methods, minimizing chemical waste and environmental degradation. Although the robotic system cost Rs. 1,20,000/- (20 times more than a battery sprayer), it significantly improved efficiency. It sprayed a 1500 m^2 greenhouse in 0.75 hours compared to four hours with a traditional knapsack sprayer, saving 5.3 times the time. While the robot's operating cost was 1.74 times higher, it offered precise pesticide application, reduced operator exposure, and enhanced sustainability, making it a valuable innovation for greenhouse farming.

Design and development of crop canopy reflectance based real-time variable rate fertilizer application system

Rice is a staple crop for over 60% of India's population, requiring production to meet a projected demand of 140 million tonnes by 2050. However, low nitrogen use efficiency (NUE) in rice leads to overuse of nitrogen fertilizers, causing environmental and economic challenges. This study developed a nitrogen assessment and prescription (NAP) device using vegetation indices (NDVI, NDRE, and RVI) for real-time, site-specific nitrogen management. The device analysed rice canopy spectral characteristics, optimized nitrogen levels, and integrated a soil slit-cutting mechanism with an aqueous urea metering system. It was compared to commercial devices like Green Seeker and Spectroradio meter, showing strong correlations in assessing vegetation indices. A paired t-test revealed no significant difference ($p < 0.05$) between the developed device and commercial counterparts, with optimal performance at a sensing height of 30 cm and a field of view of 36.86 degrees. The device demonstrated precision and accuracy exceeding 98% and 94%, respectively. NDVI and NDRE were reliable indicators of nitrogen status, while RVI was effective during later growth stages. The device, costing ₹5218, was economically viable and paired with a high-clearance vehicle for variable-rate subsurface application of aqueous urea across three rows simultaneously. Operating at 1.83 km/h with a sensing height of 31.44 cm, the system achieved a precision rate of 90.62%. It reduced nitrogen fertilizer use by 22.38% and 28.35% during the first and second top-dressing stages, respectively, while increasing yield by 12.28%. NUE improved by 53.69%, and fertilizer costs decreased by 25.44%. This study highlights the potential of the NAP device to enhance nitrogen management in rice cultivation, improving yields, reducing environmental impact, and providing significant economic benefits, contributing to sustainable rice production.

Development of computer vision-based disease management system for tomato crop

This study presents a novel hybrid Vision Transformer (ViT) model optimized for real-time disease classification in tomato crops and a computer vision (CV)-based precision sprayer for targeted pesticide application. The ViT model achieved 91.53% classification accuracy by optimizing hyper-parameters - epochs, batch size, and learning rate, using response surface methodology (RSM) on a dataset of 1,690 images of healthy and diseased tomato leaves. To address pesticide application challenges, spray characterization was performed using three nozzle types (flat fan, hollow cone, and flower (8-hole)) at varying pressures (196, 294, and 392 kPa). Droplets properties, including size distribution, specific surface area (SSA), and spray deposition, were analyzed. Results showed smaller droplet sizes and increased SSA with higher pressures, improving pesticide coverage. A CV-based precision sprayer was developed and evaluated in a polyhouse environment. It demonstrated high detection efficiency for diseased plants, achieving 95.83% at 0.34 km/h, with optimized sensor-to-nozzle distances ensuring precise spray alignment. The precision system reduced pesticide application rates for late blight and powdery mildew to 355.66 L/ha and 257.72 L/ha, respectively, compared to 902.04 L/ha with conventional methods. Controlled experiments highlighted significant influences of spraying height and pesticide type on droplet characteristics, coverage, and deposition. Metalaxyl 8% + Mancozeb 64% WP achieved maximum droplet density (30.93 droplets/cm^2) and coverage (26.54%) at lower spraying heights. Economic analysis confirmed feasibility with an operational cost of ₹82.60 per hour and a break-even point of 25.5 hectares per year. The system's high detection accuracy, reduced agrochemical usage, and environmental benefits establish it as a viable solution for sustainable agriculture.

Development of canopy volume based variable rate spraying system for pomegranate orchard

Pomegranate crops are highly prone to pests and diseases, leading growers to rely on intensive spraying, often exceeding 45 sprays per season. Traditional air-blast sprayers waste 30–50% of chemicals through drift, runoff, and residue, applying chemicals uniformly without considering canopy variations, resulting in inefficient pest control. A variable rate spraying system was developed to optimize spray volume based on canopy volume. Laboratory tests was conducted with experimental variable rate spraying system at sensor spacing (0.30, 0.48 and

0.66 m), object depth (0.75, 1, 1.25 m), and forward speed (0.57, 0.7 and 0.83 m s^{-1}) with two types of objects (i.e. flat surface object and plant).MAPE in spray volume delivery was observed from 5.99 to 6.87% for flat surface object and 11.03 to 12.44% for plant, demonstrating the acceptable accuracy for field application. The developed system was further tested in field-controlled conditions across three pomegranate orchards (2, 4 and 8year-old) to optimize specific spray volume based on the canopy size, varying nozzle flow rate (1.6, 2.1, and 2.6 L min^{-1}) and forward speed (0.43, 0.71, and 0.95 m s^{-1}).Spray deposit analysis showed a negative correlation with forward speed and a positive correlation with nozzle flow rate, while droplet size (VMD) remained consistent. Forward speed significantly influenced all responses than the nozzle flow rate, with inner canopies receiving lower deposits than outer zones. Using Response Surface Methodology, optimal specific spray volumes of 0.093, 0.084, and 0.077 L m^{-3}were identified for selected orchards, meeting the criteria for effective pesticide application. Field tests at 0.085 L m^{-3}achieved VMD of 261.21 - 320.78 µm, spray coverage of 20.17 - 41.0%, droplet density of 44.39 - 85.40 droplets cm^{-2}, and deposits of 1.42 - 2.40 µl cm^{-2}, with 46.81% chemical savings compared to conventional sprayers.

Theme 3: Ergonomics and Operator's Safety in Agriculture

Ergonomic assessment of powered cylindrical lawn mower for enhanced operator's comfort

Landscaping equipment like lawn mowers is widely used for maintaining lawns and gardens but poses ergonomic and occupational health risks due to excessive noise and vibration. This study assessed the noise, hand-arm vibration (HAV), and ergonomic impacts of a 5-hp diesel-powered cylindrical lawn mower with a 524 mm width of cut, commonly used at ICAR-IARI, New Delhi. Noise levels (87.40–95.47 dB(A)) exceeded OSHA, ACGIH, ISO, and NIOSH standards, with frequency peaks in the 1000–6000 Hz range, increasing the risk of Noise-Induced Hearing Loss (NIHL). HAV ranged from 10.81 to 23.03 ms^{-2}, with frequencies matching the hand-arm system's resonance (25–50 Hz), posing a higher risk of Vibration-Induced White Finger (VIWF). Human factors like heart rate, BPDS (48), and ODS (4) indicated moderate discomfort, while RULA (4) and REBA (7) scores required corrective measures. Safe exposure durations for noise were limited to 3.75 hours (OSHA) and 0.71 hours (ACGIH), and finger blanching prevalence was estimated at 1.7 years for 10% of exposed operators. To address these hazards, a polycarbonate, glass wool, and plywood acoustic enclosure reduced noise by up to 10.13%, extending safe exposure durations to 14.32 hours (OSHA). Polyurethane sheets and bushes reduced HAV by 56.74%, increasing finger blanching prevalence to 4.02 years. While the interventions slightly increased heart rate and machine weight, they significantly improved operator safety. The cost of modifications was ₹5350/-, making these simple retrofits cost-effective solutions to enhance safety. Additional recommendations include ear protection aids and anti-vibration gloves to further mitigate risks.

Ergonomic studies on hand cranking operation of women workers

Human energy remains a key power source in India's agricultural sector, with women increasingly participating due to the migration of male workers to other sectors. This study optimized cranking parameters for female agricultural workers based on physiological workload, postural interaction, and muscle fatigue studies. Key parameters included cranking height (800–1100 mm), cranking length (180–300 mm), and power (30–70 W). Physiological workload was evaluated through heart rate, cardiovascular stress index, oxygen consumption, energy expenditure rate, overall discomfort rate, and cranking efficiency. Using response surface methodology, optimal values were determined as a cranking height of 910.8 mm, cranking length of 249.3 mm, and 38.10 W power. At these levels, muscle fatigue for the flexor digitorum superficialis, biceps, deltoid, and overall muscles were 7.51%, 17.34%, 14.95%, and 11.92%, respectively. Biomechanical analysis showed consistent compressive forces of 379.70 N across all cranking parameter levels. Shear forces averaged 24.13 N, 33.79 N, and 22.12 N for lower, higher, and optimized parameter levels, respectively, demonstrating reduced force requirements at the optimized settings. A reach envelope in the sagittal plane for hand cranking in a standing posture was developed, indicating that the cranking shaft should be positioned 437–571 mm forward of the worker's body centreline for optimal reach and comfort. This study provides critical insights for designing ergonomic cranking systems that reduce physical strain and improve efficiency for female agricultural workers, supporting their growing role in India's agricultural workforce.

Theme 4: Climate Change Impacts and Integrated Water Resources Management

Enhancing water productivity in Jargo medium irrigation project, U.P., under changing climatic conditions

the research conducted in the Jargo River Watershed (JRW) in Mirzapur district, Uttar Pradesh, aimed to assess surface runoff, sediment yield, and crop water productivity. Using the NRCS-CN method and RS/GIS techniques, the study found that surface runoff depth over a 32-year period ranged from 169 mm to 228.10 mm, with an average of 199 mm. The runoff volume for the JRW was estimated at 121,266,112 m³. The RUSLE model integrated with ArcGIS estimated the average annual soil loss at 0.28 t.ha-1.yr-1, with most areas experiencing slight erosion. Sediment yield (SY) varied based on five area-based methods, with Parmar's method yielding the highest sediment delivery ratio (SDR). Significant fluctuations in the Jargo Reservoir's water area were observed from 2001 to 2022, with a notable reduction in size by 2021.The study also estimated crop water requirements (CWR) for major crops in the Mirzapur district using the CROPWAT 8.0 model. Sugarcane showed the highest CWR, while Pea had the lowest. Water productivity (CWP) and irrigation water use efficiency (IWUE) were also calculated, with Sugarcane demonstrating the highest CWP and IWUE. The study suggested various water retention structures, improved water scheduling, soil moisture management, and the adoption of technologies like drip irrigation and micro-sprinklers for enhancing water productivity. The research highlighted the utility of the NRCS-CN method, RUSLE model, and CROPWAT model in understanding watershed dynamics and agricultural water management.

Development of crop-water management strategies under changing climate in upper Tapi sub catchment

Agriculture, the largest water consumer, must meet the demands of a growing population amidst changing climatic conditions. The IPCC projects a global temperature increase of 1.5–4°C by 2100, with significant impacts on precipitation and hydrological cycles. Land use/land cover (LU/LC) changes exacerbate these issues by altering water balance and rainfall distribution. This study integrates hydrological modeling, LU/LC dynamics, and climate projections to develop sustainable crop-water management strategies under changing climatic conditions. The SWAT model was employed to assess runoff potential, calibrated (1994–2001) and validated (2007–2009) at the Burhanpur gauging station using SUFI-2 in SWAT-CUP 2019. Sensitivity analysis identified CN2.mgt as the most influential parameter. Several performance metrics confirmed model accuracy, while uncertainty analysis demonstrated its reliability. GIS-based weighted overlay analysis revealed 25.43% of the watershed as medium to very high suitability for rainwater harvesting. LU/LC projections using a hybrid CA-Markov model predicted forest (4,934.05 km²) and cropland (3,295.73 km²) as dominant classes by 2035, with built-up land increasing moderately to 221.29 km². Climate projections using a multi-model ensemble of 13 GCMs under SSP245 and SSP585 scenarios for 2035–2050 and 2075–2090 indicated rising trends in rainfall and temperatures. SWAT simulations showed significant increases in pre- and post-monsoon streamflow, with mixed trends during monsoon months. Crop water requirements were estimated for major Kharif (565.98–694.64 mm) and Rabi (416.70–487.76 mm) crops, with volumetric water demand ranging from 3,229.45–4,013.11 MCM. Analysis between water availability and demand emphasize optimizing irrigation systems and implementing sustainable water management strategies. This study provides insights for policymakers to ensure water sustainability and food security in the Upper Tapi Sub-catchment.

Study on water productivity of tomato under sensor-based irrigation scheduling

With rising global food demand and diminishing water resources, improving water productivity in agriculture is a pressing necessity. This study, "Study on Water Productivity of Tomato under Sensor-Based Irrigation Scheduling," conducted at the Centre for Protected Cultivation Technology (CPCT), ICAR-IARI, New Delhi, explored integrating sensor-based irrigation scheduling and mulching to enhance water productivity and tomato yield in open-field conditions. A randomized block design was used to compare mulched and non-mulched treatments under different irrigation schedules. Tensiometers monitored soil moisture at varying depths, providing real-time data for precise irrigation adjustments based on soil matric potential. Mulching, particularly silver poly-mulch, was employed to further conserve moisture and enhance plant performance. Key growth parameters, including plant height, leaf area, branch count, biomass, and fruit yield, were recorded to evaluate the impact of these interventions. Results showed that sensor-based irrigation significantly improved water productivity compared to conventional methods. Mulching amplified these benefits by retaining soil moisture, reducing evaporation, and regulating soil temperature, resulting in enhanced plant growth and yield. The highest water productivity recorded was 17.3 kg/m^3 for the Pusa Prasanskrit variety under mulched conditions, demonstrating the synergy between mulching and precise irrigation. The FAO AquaCrop model was used to simulate water productivity under varying irrigation scenarios and was validated against field data, showing a strong correlation. AquaCrop provided valuable insights into the relationship between irrigation practices and crop yield, serving as a reliable tool for water management strategies. This study underscores the potential of combining sensor-based irrigation scheduling with mulching to optimize water use, improve crop yield, and conserve resources, offering a sustainable solution for regions facing water scarcity.

Development of integrated sensing device for irrigation scheduling

Judicious irrigation scheduling enhances water productivity, but high-cost, advanced sensors for soil and plant monitoring remain inaccessible to small and marginal farmers. Keeping in view, the present study was undertaken to develop a low-cost Integrated Sensing Device for Irrigation Scheduling (ISDI). Field and laboratory experiments were carried out at the Water Technology Centre (WTC) and Centre for Protected Cultivation Technology (CPCT) of ICAR-IARI, New Delhi. The device was developed by integrating canopy temperature sensor (Melexis MLX90614 infrared), air temperature sensor and humidity sensor (DHT22), and soil moisture sensor (capacitive soil moisture sensor V1.2) and connected to a microcontroller with the coded software for the assessment of on-site microclimatic and soil-plant-atmosphere dynamics using a single robust system. The performance of the system was calibrated with gravimetric method and compared with TDR and handheld infrared thermometer. A series of field experiments involving maize in both net houses and open fields, wheat in open fields, and capsicum in greenhouses under different irrigation regimes were carried out to calculate crop water stress index (CWSI) using this developed system. To compute CWSI, the lower baseline and upper threshold for selected crops were developed by establishing a linear regression between the temperature difference between the canopy and air (Tc–Ta) and the vapor pressure deficit (VPD). The CWSI were integrated with soil moisture deficit up to a 0-30 cm soil depth under various irrigation regimes at regular intervals throughout the crop duration to optimize CWSI values for irrigation scheduling. The ISDI was calibrated using the gravimetric method with exhibiting promising accuracy (R^2: 0.68-0.81) for soil moisture measurement in comparison to TDR (R^2: 0.8-0.87). Calibration equations were unique for each field; however, device needs to be calibrated regularly. The performance of ISDI' infrared probes were at par hand held infrared thermometer. The developed lower baseline equation and upper threshold for CWSI computation were (Tc-Ta)ll= -1.86*VPD-3.44 (R2: 0.73) and -0.91 0C; respectively in net house maize and (Tc-Ta)ll= -1.58*VPD-3.74 (R2: 0.69) and -1.16°C in open field maize. In open field wheat, the developed lower baseline equation were (Tc-Ta)ll= -1.94*VPD-1.33, with R2=0.89 for pre-heading; (TcTa)ll=-1.30*VPD-2.37 with R2: 0.78 for post-heading and (Tc-Ta)ll=-1.97*VPD-1.43 with R2:0.86 for entire crop period and upper threshold of 1.93°C. Lower baseline equation and upper threshold for entire crop period of drip irrigated green house capsicum were (Tc-Ta)ll=-1.60*VPD-0.40, with R2:0.87 and 2.23°C; respectively. Overall, the results revealed unique baseline equations for specific crops. Based on CWSI approach of irrigation scheduling, it was recommended to schedule irrigation, when CWSI $\geq$ 0.51, 0.42, 0.35 and 0.28; respectively for net house maize, open field maize, open field wheat and green house capsicum experiment. Deficit irrigation impacted yield and water productivity, with a strong correlation between mean seasonal CWSI and yield attributes under diverse irrigation regimes. The Integrated Sensing Device for Irrigation Scheduling (ISDI) demonstrated reliable performance, aligning with FAO Penman-Monteith estimates for actual evapotranspiration. The ISDI can optimize irrigation scheduling for maize, wheat, and capsicum, with the potential for use in other crops after recalibration and crop-specific CWSI baseline development.

Modelling water and nutrient dynamics of mustard crop under deficit irrigation

The deteriorating state of agricultural water resources due to climate change, pollution, declining groundwater levels, and extreme weather events necessitates efficient irrigation practices. This study assessed water and nitrogen dynamics in the root zone and mustard crop yield under deficit irrigation conditions to improve water use efficiency. Irrigation was scheduled using the FAO Penman-Monteith (PM) method, estimating crop evapotranspiration (ETc) based on climate data and crop coefficients for different growth stages (initial, development, mid, and late). Three irrigation treatments—full irrigation (100%), 80%, and 60% of full irrigation—were tested with seven replications. Soil moisture content (SMC) and nitrogen dynamics were simulated using HYDRUS-1D. SMC was highest under full irrigation, followed by 80% and 60%. Nitrogen concentration fluctuated most under 60% irrigation, indicating reduced leaching but increased variability near the root zone. Greater irrigation levels resulted in higher nitrogen leaching, reducing root-zone nitrogen availability. The 80% irrigation treatment achieved the highest yield (22.3 kg/m^2), while the 60% treatment recorded the highest water productivity (1.04 kg/m^3). These results underscore the trade-offs between yield and water use efficiency under deficit irrigation. This study highlights the importance of understanding crop water use across growth stages and the interactions between water availability and nutrient dynamics. The findings provide valuable insights for optimizing irrigation scheduling and nutrient management in mustard cultivation, offering sustainable strategies for water-scarce regions. This approach can guide researchers, farmers, and policymakers in improving agricultural water resource management and enhancing productivity in water-limited environments.

Effect of hydrogel placement depths on crop and water productivity in vertisols

water scarcity poses a critical challenge in agriculture, particularly in arid and semiarid regions. Superabsorbent polymers (SAPs), such as hydrogels, have emerged as promising solutions for enhancing soil moisture retention and improving crop yield and water productivity in these environments. A comprehensive study, i.e. a one-year grow bag experiment and a two-year field trial conducted to evaluate the effects of hydrogel type and application depth on soil water distribution, water productivity, and crop growth. Two hydrogel types—polymer-based (Hydrogel-1) and small organic molecule-based (Hydrogel-2)—were applied at four depths: surface, 5, 10, and 15 cm. The grow bag study was implemented using a randomized block design, while the field study employed a split-plot design. The findings indicated that the water absorption capacity of polymer-based was negatively impacted by water salinity, whereas molecules-based hydrogel maintained consistent performance under saline conditions. Soil moisture retention improved with deeper hydrogel applications, with polymer-based hydrogel at 10 cm significantly extending irrigation intervals by 2–4 days as compared to the control. Hydrogel applications at 10 cm depth significantly enhanced spinach growth parameters, including plant height, leaf count, leaf area, root length, SPAD value, and shoot and root fresh and dry weight and yield. The highest yield (35.2 t/ha) and water productivity (20.3 kg/m^3) were achieved with Hydrogel-1 applied at 10 cm depth. Additionally, a 10-row seed-cum-hydrogel applicator was developed and tested for optimized application depth in spinach cultivation. The applicator demonstrated an effective field capacity of 0.37 ha/h, operating at 77% efficiency with a forward speed of 2.5 km/h. Economic analysis revealed the highest benefit-cost ratio (2.42) in the treatment combination H1D3 (Hydrogel-1 at 10 cm depth), followed by H2D3 (Hydrogel-2 at 10 cm depth) with a ratio of 2.13. The study concludes that hydrogel application at a depth of 10 cm optimizes resource use efficiency and water productivity in spinach cultivation on vertisols, while water has become a precious resource.

Theme 5: Precision Irrigation

Design and development of an iot-enabled depth-integrated type soil moisture monitoring system

Freshwater is a limited resource, with only 0.01% of the total water available for human use, and agriculture consumes up to 80% of it. This heavy consumption, combined with inefficient irrigation practices, contributes to potential water shortages, especially as global populations grow. Traditional irrigation methods often lead to issues like waterlogging, soil salinization, nutrient leaching, and reduced crop yields. Soil moisture plays a vital role in maintaining soil structure, transferring nutrients, and supporting microbial activity, all of which impact soil fertility and plant health. Accurate soil moisture monitoring is essential for efficient irrigation and optimal crop growth. To address this, recent research aimed to develop an affordable and user-friendly soil moisture sensing system capable of measuring moisture levels at different depths (20, 40, 60, and 80 cm) within the root zone. The system utilized capacitive sensors to provide real-time data for irrigation scheduling. Integrated with a Wireless Sensor Network (WSN) via a GSM module and managed by a microcontroller, this system alerts users via SMS when soil moisture falls below a specified threshold at any of the monitored depths. This technology offers a practical solution for rural farmers, reducing labour and enabling more efficient irrigation, nutrient management, and overall agricultural practices. The system provides a way to optimize water use while minimizing waste, which is critical for sustainable agricultural development.

Alleviating water stress in garlic crop through deficit irrigation and plant growth regulators in deccan plateau

Water scarcity is a critical issue for crop productivity, especially in the arid and semi-arid regions of the Deccan Plateau in peninsular India. In this context, deficit irrigation (DI) combined with exogenous foliar application of plant growth regulators (PGRs) has emerged as an effective strategy to enhance crop productivity and mitigate water stress. A field experiment conducted during the 2023–24 season focused on garlic cultivation under various deficit irrigation levels (100%, 75%, 50%, and 25% of evapotranspiration, ET) and foliar applications of PGRs, including irradiated chitosan (IC), seaweed extract (SWE), thiourea (TU), salicylic acid (SA), and nanourea (NU). The study found that water stress negatively impacted garlic growth, with total bulb yield (TBY) decreasing from 12.6 Mg ha−1 to 2.7 Mg ha−1 as irrigation levels reduced from 100% to 25% ET. However, the application of PGRs improved the yield by 4.9%–23.0%, enhancing photosynthesis, enzyme activity, plant water relations, and other physiological processes. Water productivity (WP) was optimized under PGR treatments, with the maximum average WP ranging from 3.98 to 4.65 kg m−3, indicating significant water savings (10.3%–39.4%) compared to the control. The results suggested that foliar application of IC and NU helped garlic crops tolerate water deficit better, with yield response factors (KIC and KNU) indicating greater drought resistance. While some physical quality traits, such as bulb weight and girth, declined under water deficit conditions, other quality attributes like harvest index, bulb firmness, and total phenol and flavonoid content improved. The total soluble solids (TSS) content initially increased with low water stress but declined under severe stress. Overall, the application of PGRs, especially IC, NU, and SWE, in combination with moderate deficit irrigation (50–75% ET), proved effective in enhancing garlic yield, quality, and water stress tolerance. These findings can be valuable for commercial garlic production in water-scarce regions of India.

Deficit Drip Irrigation (DDI) strategies and plant growth regulators (PGR) in high-density mango orchards

Mango (*Mangifera indica* L.) is an important fruit crop grown across tropical, subtropical, and semi-arid regions of India, where water scarcity is a significant challenge. Deficit irrigation (DI) is a key strategy to improve fruit crop yields in water-limited areas. The application of plant growth regulators (PGRs), partial rootzone drying (PRD), and deficit irrigation strategies have independently been shown to enhance mango productivity under such conditions. A field experiment conducted at ICAR-NIASM, Baramati, during 2023-24 investigated the combined effects of deficit drip irrigation, PRD, and PGRs on the yield, quality, and water use efficiency (WUE) of high-density mango (Cv. Kesar) grown in shallow basaltic soil. The study focused on three deficit irrigation levels (100%, 75%, and 50% of evapotranspiration, ET) along with foliar application of salicylic acid (SA) at 300 ppm and naphthalene acetic acid (NAA) at 40 ppm at different growth stages. Results showed that the DI 75% + SA + NAA treatment increased mango yield by 7.54% while saving 25% of water. The DI 50% + SA + NAA strategy improved WUE by 44.5%. The DI 75% + SA + NAA combination also resulted in higher ascorbic acid and total soluble solids content, as well as a 15% increase in fruit volume. Furthermore, the PRD 50% + SA + NAA treatment led to increased proline accumulation and flavonoid content. Several physiological and biochemical parameters, including Relative Water Content (RWC), Normalized Difference Vegetation Index (NDVI), Membrane Stability Index (MSI), Chlorophyll Content (SPAD), Canopy Temperature, and Chlorophyll Fluorescence (PSII), were assessed. Both DI 75% + SA + NAA and PRD 75% + SA + NAA treatments showed the highest RWC across growth stages, improving stress tolerance and water use efficiency. Higher NDVI values during fruit enlargement were observed under DI 75% + SA + NAA, indicating improved crop productivity and vigor. Overall, the study concluded that deficit irrigation strategies with 75% ET, combined with PGRs like SA and NAA, significantly enhanced mango yield, quality, and water use efficiency in high-density plantations grown in shallow basaltic soil. These optimized strategies offer valuable insights for sustainable mango production in water-scarce regions.

Theme 6: Quality Storage of Agricultural Produce

Development of hot air dryer coupled with biomass-fired steam heater

This study examines biomass-fired steam-assisted dryers as an innovative solution to improve agricultural drying processes, particularly for products like curry leaves. Traditional sun-drying methods are prone to weather-related risks and quality degradation, but controlled drying environments offer advantages such as reduced drying times, minimized losses, and enhanced product quality. Biomass-fired steam heating systems, which use local biomass, provide energy-efficient, scalable solutions that promote sustainability and economic growth, especially in off-grid rural areas. The study details the development and evaluation of a biomass-fired steam heating system integrated with a tray-type drying cabinet for drying curry leaves. The heating system consists of a concentric cylinder boiler, a copper-tube aluminium finned heat exchanger, thermostatic and non-return valves. The drying cabinet, designed with 10 perforated trays, provides an effective drying area of 2.7 m². Rigorous testing was conducted to ensure functionality and performance reliability. Practical tests compared the drying efficiency of the biomass-fired steam heating system with a conventional electric tray dryer under identical conditions. The experimental results demonstrated that the biomass-fired steam dryer achieved a maximum operating temperature of 70°C within 30 minutes, reducing the moisture content of curry leaves from 93% to 10.5% (wet basis) in 190 minutes. This drying duration was similar to that of the conventional tray dryer, which took 170 minutes. The biomass-fired dryer exhibited an overall thermal efficiency of 42%, surpassing the boiler's initial thermal efficiency of 33% when using firewood. The study highlights the potential of utilizing biomass resources for sustainable, efficient drying practices in agriculture, offering farmers increased access to higher-value markets and contributing to their income growth.

In-situ stabilization of rice bran with infrared heating of brown rice

A continuous infrared (IR) heat treatment system of 100 kg/h capacity for brown rice was developed. The IR heat treatment experiments were conducted by considering three independent variables including initial moisture content (MC)(10 %, 12 % and 14 %), distance of heater from brown rice surface (D) (40 mm, 60 mm and 80 mm) and heating time (HT) (30 s, 60 s and 90 s).The IR heat treated brown rice was further allowed to achieve room temperature followed by polishing for 20 s by Satakepolisher. The optimum values of IR heat treatment variables viz. MC, D and HT were 12 %, 60 mm and 60 s, respectively. The values of dependent variables viz. surface temperature, moisture loss, free fatty acids (FFA), peroxide value (PV), head rice yield, degree of polishing, broken rice percentage, total phenol content, total flavonoid content, and DPPH antioxidant activity were 67.5 °C, 0.33 %, 2.36 %, 1.60mEq/kg, 91.54 %, 6.92 %, 2.16 %, 734.68 mg GAE/100 g, 572.63mg QE/ 100 g and 95.13 %, respectively at the optimized processing condition. The amylose content of IR heat treated milled rice was in range of 12.18±0.22 to 14.43±0.07 %. The cooking time, solid loss and water absorption ratio of the IR treated milled rice were in range of 20.27±0.03 and 22.28±0.01 min, 3.01±0.03 to 4.52±0.12 % and 3.11±0.03 to 3.98±0.12 %, respectively. Storage study of raw and IR stabilized rice bran at storage conditions (ambient and refrigerated) and packaging materials (low density polyethylene, polypropylene and laminated aluminium pouches) revealed that, under refrigerated condition the FFA and PV of IR stabilized rice bran packed in laminated aluminium pouches were far below the accepted limit at the 7th week and at ambient condition, the FFA and PV were below the accepted limit for 7 weeks. Thus, the rice bran can be stabilized in-situ with infrared heat treatment of brown rice with storability of 7 weeks.

Theme 7: Value Addition of Agricultural Produce

Infrared pretreatment for milling quality improvement of Kodo millet (*Paspalum scrobiculatum*)

Kodo millet (*Paspalum scrobiculatum*), a nutrient-dense grain native to India, thrives in arid conditions and offers high levels of protein, vitamins, minerals, dietary fiber, and bioactive compounds. However, its small size, unique shape, and anti-nutritional factors like tannins and phytates hinder nutrient bioavailability and dehusking efficiency. Conventional hydrothermal treatments are labor-intensive and may cause off-flavors and reduced shelf life, prompting the exploration of infrared (IR) radiation as an energy-efficient alternative. This study evaluated IR treatment as a pretreatment for dehusking Kodo millet, focusing on dehusking efficiency, nutritional enhancement, and reduction of anti-nutritional factors. A laboratory IR setup was used, with variables including voltage (200–260 V), duration (30–210 s), and grain moisture content (10–16% w.b.). Optimal conditions were identified as 220 V, 90 s, and 12% w.b. Machine learning models predicted critical responses, with XGBoost outperforming others. A Discrete Element Modeling (DEM) study optimized screw geometry and rotational speed for efficient grain transport and exposure to IR heating. An IR applicator was fabricated with a capacity of 200 kg/h achieved a dehusking efficiency of 72.08%, head rice yield of 71.71%, and reduced operating costs (Rs 0.28/kg). IR-treated millet showed significant nutritional improvements, including increased protein (6.75% d.b.), fiber (0.95% d.b.), and ash content (1.06% d.b.). Tannins and phytates decreased by 86.76% and 25.47%, respectively, while antioxidant potential, phenolics (188.72 mg GAE/100 g DW), and flavonoids (1712.21 mg QE/100 g DW) significantly increased. Structural analyses confirmed enhanced dehusking efficiency due to surface roughening and micro-cracks. Compared to conventional treatments, IR-treated millet exhibited superior bioactive compound retention, lighter color, reduced cooking time (12.58 min), and better storage stability, particularly in HDPE packaging at 15°C. IR treatment enhances dehusking, nutritional quality, and storage stability, offering a sustainable solution to increase Kodo millet's commercial value.

Investigations on nano-micro surface modification of biomass-based carbon for supercapacitor electrode

This study focused on the synthesis of nanoporous carbon from chickpea stalk through chemical activation using potassium hydroxide (KOH). The synthesized nanoporous carbon was thoroughly characterized and applied in the field of energy storage. Activation of the chickpea stalk was performed under an inert nitrogen atmosphere at varying activation times (30, 60, and 90 minutes) and temperatures (750, 800, and 850 °C). Comprehensive characterization of the raw chickpea stalk and the prepared nanoporous carbon was conducted using TGA, kinetic analysis, proximate analysis, adsorption analysis, BET surface area analysis, SEM, XRD, and FTIR spectroscopy. Adsorption analyses revealed that the nanoporous carbon exhibited high microporosity and mesoporosity. Furthermore, the BET surface area analysis, confirmed by Type IV isotherm curves, showed that all the prepared nanoporous carbon samples possessed micro- and mesopores. The highest surface area (1239 m^2/g) and pore volume (0.60 cm^3/g) were recorded for sample CT-9. SEM imaging revealed interconnected micro- and mesopores in the prepared nanoporous carbon. FTIR analysis indicated functional groups such as alcohol group (O–H), estergroup (C–O), carbon dioxide (O=C=O), and carboxylic acid (O–H) significantly improved the interaction between the material and electrolyte ions. Electrochemical performance was evaluated using a three-electrode setup with 1M KOH as the electrolyte. Cyclic Voltammetry (CV), Galvanostatic Charge-Discharge (GCD), and Electrochemical Impedance Spectroscopy (EIS) were employed to analyze the nanoporous carbon as an electrode material. The results showed that the nanoporous carbon-based electrode exhibited a specific capacitance of 343.29 F/g at a current density of 1.0 A/g, an energy density of 48 Wh/kg, and a power density of 495 W/kg, along with excellent cycling stability. The equivalent series resistance was measured at 1.06 Ω. These findings indicate that chickpea stalk-derived nanoporous carbon is a promising bio-material for high-performance super capacitors and energy storage devices.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of student & roll no.	Degree	Title of thesis	Chairperson	Institute
1.	Shilpa S (21888)	M. Tech.	AI based crop growth modeling in vertical hydroponic system	Dr. Murtaza Hasan	ICAR-IARI, New Delhi
2.	Karale Omkar Sunil (21890)	M. Tech.	AI based nutrition modeling for vertical hydroponics farming	Dr. Murtaza Hasan	ICAR-IARI, New Delhi
3.	Ajay Mudgil (21891)	M. Tech.	Development of hot air dryer coupled with biomass-fired steam heater	Dr. Arun Kumar T V	ICAR-IARI, New Delhi
4.	Dera Vikas Reddy (21893)	M. Tech.	Development of non-destructive adulteration detention protocol for saffron using advanced imaging techniques	Dr. Roaf Ahmed Parray	ICAR-IARI, New Delhi
5.	Suryawanshi Vikesh Mangilal (21919)	M. Tech.	Study on water productivity of tomato under sensor-based irrigation scheduling	Dr. Dhirendra Kumar Singh	ICAR-IARI, New Delhi
6.	Biman Majumdar (21920)	M. Tech.	Design and development of an IoT-enabled depth-Integrated soil moisture monitoring system	Dr. Anil Kumar Mishra	ICAR-IARI, New Delhi
7.	Sajja Poojith (21965)	M. Tech.	Ergonomic assessment of powered cylindrical lawn mower for enhanced operator's comfort	Dr. Adarsh Kumar	ICAR-IARI, New Delhi
8.	Pratyasha Mishra (60142)	M. Tech.	Modelling water and nutrient dynamics of mustard crop under deficit irrigation	Dr. Santosh Sambhaji Mali	ICAR-IARI, New Delhi
9.	Saranya S (70020)	M. Tech.	Alleviating water stress in garlic crop through deficit irrigation and plant growth regulators in Deccan Plateau	Dr. Goraksha C Wakchuare	**ICAR-NIASM Baramati
10.	Subha Mondal (70021)	M. Tech.	Deficit Drip Irrigation (DDI) strategies and plant growth regulators (PGR) in high-density mango orchards	Dr. D. D. Nangare	**ICAR-NIASM Baramati
11.	Abhishek Upadhyay (11962)	Ph.D.	Development of a computer vision based disease management system for tomato crop	Dr. Narendra Singh Chandel	**ICAR-CIAE, Bhopal
12.	Bogala Pravallika (11391)	Ph.D.	In-*situ* stabilization of rice bran with infrared heating of brown rice	Dr. Saroj Kumar Giri	**ICAR-CIAE, Bhopal

13.	Pradeep Kumar (11682)	Ph.D.	Design and development of embedded system controlled site specific seed cum fertilizer applicator	Dr. H. L. Kushwaha	ICAR-IARI, New Delhi
14.	Manojit Chowdhury (11684)	Ph.D.	Design and development of crop canopy reflectance based real-time variable rate fertilizer application system	Dr. Tapan Kumar Khura	ICAR-IARI, New Delhi
15.	Manisha Hanumant Jagadale (10951)	Ph.D.	Ergonomic studies on hand cranking operation of women workers	Dr. Kamal Nayan Agrawal	**ICAR-CIAE, Bhopal
16.	Mude Arjun Naik (11685)	Ph.D.	Design and development of robotic pesticide applicator for greenhouse	Dr. Adarsh Kumar	ICAR-IARI, New Delhi
17.	Radhika Sahu (11194)	Ph.D.	Enhancing water productivity in Jargo medium irrigation project, U.P., under changing climatic conditions	Dr. Anil Kumar Mishra	ICAR-IARI, New Delhi
18.	Arti Kumari (10750)	Ph.D.	Development of integrated sensing device for irrigation scheduling	Dr. Dhirendra Kumar Singh	ICAR-IARI, New Delhi
19.	Edde Mounika (11677)	Ph. D.	Infrared pretreatment for milling quality improvement of Kodo millet (*paspalum scrobiculatum*)	Dr. Debabandya Mohapatra	**ICAR-CIAE, Bhopal
20.	Ravi Kumar Sahu (11965)	Ph.D.	Investigations on nano-micro surface modification of biomass based carbon for supercapacitor electrode	Dr. Sandip Gangil	**ICAR-CIAE, Bhopal
21.	Abhishek Patel (11189)	Ph. D.	Development of crop water management Strategies under changing climate in upper Tapi sub catchment	Dr. K V Ramana Rao	**ICAR-CIAE, Bhopal
22.	Deepak Sabaji Thorat (11400)	Ph. D.	Development of canopy volume based variable rate spraying system for pomegranate orchard	Dr. C. R. Mehta	**ICAR-CIAE, Bhopal
23.	Umashankar (11974)	Ph.D.	Effect of hydrogel placement depths on crop and water productivity in vertisols	Dr. K V Ramana Rao	**ICAR-CIAE, Bhopal

***Outreach institutes*

AGRICULTURAL PHYSICS

9

Prof. P. Krishnan

Starting from a small unit ‘Physics in Agriculture’ created in 1948, the Division of Agricultural Physics was established as a full-fledged teaching and research Discipline in 1962. Endowed with a mission to study Soil-Water-Plant-Environment Energetics for eco-friendly and sustainable exploitation of agricultural resources, the Division had initially four sub-disciplines: Soil Physics, Plant-Biophysics, Environmental Physics and Agricultural Meteorology at the time of its establishment. And today, all these form the major pillars of the edifice of Agricultural Physics as a Discipline. 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 of the Division since 1970 onwards. Ever since its inception, the Division has collaborated in Inter-Divisional, Inter-Institutional and International research projects. The achievements of the students are presented in following themes, as below:

Theme 1: Remote Sensing and Drone Technology

Drone-based water stress monitoring under different irrigation and nitrogen levels in wheat (*Triticum aestivum* L.)

Wheat crop growth relies on two crucial inputs: water and nitrogen. Drone-based thermal imagery can effectively monitor crop water stress, enabling real-time irrigation applications and optimized water. A field experiment was conducted during the Rabi season of 2023-24 at Indian Agricultural Research Institute, New Delhi with objectives to assess water stress through drone-based thermal remote sensing and to characterize water stress under different irrigation and nitrogen levels in wheat crops. Three irrigation levels (I1: no irrigation, I2: 2 irrigations, I3: 5 irrigations) and six nitrogen levels (N1-N6: 0-200 kg N ha-1) were evaluated in a split plot design. Thermal and multispectral images were acquired using a drone-mounted camera system, enabling the extraction of pure canopy temperature data. NDVI co-registration method effectively extracted pure canopy temperature, correlating well with ground truth data (R2 = 0.92). Drone thermal imagery then enabled the derivation of Simplified Crop Water Stress Index (CWSIsi) for water stress monitoring of wheat, showing strong correlations with relative leaf water content (RWC, R2 = 0.73), stomatal conductance (GS, R2 = 0.63), transpiration rate (Tr, R2 = 0.73), and moderate correlation with surface soil moisture (R2 = 0.56) at the reproductive stage. RWC, GS and Tr increased significantly from non-irrigated to irrigated treatments and with increasing nitrogen dose up to 120 kg N ha-1. Notably, CWSIsi was influenced by canopy temperature, increased with water stress in non-irrigated treatments and decreased with higher nitrogen doses, highlighting its sensitivity to water and nitrogen management-induced stress. CWSIsi index also showed strong negative correlations with grain yield (r = - 0.846*) and biological yield (r = - 0.848*), indicating its potential for yield prediction. The study demonstrated the potential of drone-based monitoring to accurately assess water stress in wheat, enabling data-driven irrigation management and nitrogen fertilization decisions. This approach can enhance crop water productivity and reduce environmental impacts in wheat production systems.

Evaluation of the effect of foliar nitrogen fertilization by drone and knapsack sprayer on growth and yield of wheat (*Triticum aestivum* L.)

Wheat (*Triticum aestivum* L.) is the principal crop of India. Optimal fertilization and nutrient supply at critical growth stages are crucial for maximizing yields. Foliar spraying is an effective method for delivering essential nutrients to wheat plants. The choice of sprayer is vital for enhancing the efficacy of foliar fertilization. A field experiment was conducted at the Indian Agricultural Research Institute, New Delhi to compare the effectiveness of drone and knapsack sprayers in foliar fertilization and to identify the most efficient method for promoting healthy wheat growth and yields. There were sixteen treatments including 75% and 50% RDN +2 foliar sprays of nano urea, prilled urea, and nano-DAP at two growth stages viz., tillering and jointing. Fertilizers were applied via foliar spray using a quadcopter drone and battery-operated knapsack sprayer. Performance was evaluated using water-sensitive papers, assessing parameters like droplet density, coverage, size distribution, relative span factor, and uniformity coefficient to compare the effectiveness of both sprayers. Results showed the drone sprayer outperformed in uniformity and most parameters, except coverage. No significant differences were found among nitrogen sources (Nano Urea, Prilled Urea, and Nano-DAP). Drone spraying also yielded significant improvements in vegetation indices (NDVI, NDRE, LCI, GNDVI, and NGRDI), highlighting its potential for enhanced plant growth. The foliar application of fertilizers via drones significantly impacted wheat growth and yield. The optimal treatment, T7, combining 75% RDN with 2 foliar sprays of Nano-DAP applied by drone, yielded the highest growth parameters and yield attributes. In this treatment, increased plant height of 83.9 cm and 98.8 cm, LAI of 4.52 and 2.75, dry matter of 1096.8 g/m2 and 1256.7 g/m2 , LNC (%) of 4.21 and 3.62% and SPAD value of 52 and 57 at 90, 120 DAS, were recorded. These improvements led to a substantial increase in grain yield (62.85 q/ha), and nitrogen use efficiency (55.7%). Future studies should focus on scaling up drone-based foliar fertilization, exploring its applicability to other crops, and integrating it with other precision agriculture technologies to enhance crop yields and resource efficiencies.

Artificially intelligent high-throughput phenotyping of wheat for water and nitrogen deficit stress tolerance using fluorescence and hyperspectral imaging

Growing population and diminishing soil fertility necessitates the accelerated crop improvement for yield sustainability and global food security. In this study was carried out for highthroughput phenotyping of wheat RILs for water and nitrogen deficit stress using chlorophyll fluoresce and hyperspectral imaging. It explores the concurrent assessment of chlorophyll fluorescence and plant growth responses using chlorophyll fluorescence (ChlF) image based high-throughput phenotyping (HTP) for nitrogen deficit stress on 176 RILs in a controlled environment phenotyping facility. Under nitrogen deficit stress conditions, recombinant inbred lines (RILs) displayed a diminished variable to maximum fluorescence ratio (Fv/Fm) compared to the control. However, stress-tolerant lines maintained higher Fv/Fm ratio and projected Fv/Fm area (PFA), mitigating stress-induced yield losses. Machine learning using support vector regression predicted wheat yield with R2 of 0.75. Further, QTL analysis identified major QTL for sensor derived traits like Fv/Fm and PFA for which major QTL was found on Area and Fv/Fm related sensor derived traits on chromosome number 11 (Area90_C), 12 (Area75_C, Area80_C), 15 (Area80_C) and 21 (PSII112_N). ML algorithms showed high accuracy for masking of hyperspectral images with F 1 score of 0.99 for Rf and XG Boost. The elbow method identified the optimum number of clusters as k=5, which captured the differential response of RIL to the nitrogen deficit stress component based on stress tolerance. The tolerance RILs showed higher absolute value of pixels as well as its proportional contribution for cluster 3 and 4 localized at top parts of the plant forming upper leaves and spikes. Similarly, in the water deficit stress experiment, simultaneous assessment of photosynthetic machinery and plant growth responses using chlorophyll fluorescence (ChlF) image based high-throughput phenotyping (HTP) for water deficit stress tolerance on 184 RILs in a controlled environment phenotyping facility. Under stress, recombinant inbred lines (RILs) displayed a diminished variable to maximum fluorescence ratio (Fv/Fm) compared to the control. Machine learning using K-Nearest Neighbor (KNN), Support Vector Classifier (SVC) and Random Forest (RF), classified wheat RILs intro stress tolerance classes using sensor derived parameters with high accuracy of 0.56, 0.58 and 0.60 respectively. This study demonstrates the full potential of ChlF image-based phenotyping for enhanced throughput, identifying underlying stress tolerance mechanisms and QTLs. It also demonstrated that hyperspectral sensors can be used in characterization and selection of RIL for water deficit stress tolerance. It emphasizes the importance of utilizing innovative data analytics techniques like PCA, clustering and machine learning to alleviate the data analysis bottleneck of HTP, for accelerating the pace of crop improvement for stress tolerance and sustainable food production.

Electrochemical method-based remediation of heavy metals from irrigation water

In the peri-urban areas of fast-growing cities, wastewater is being increasingly used for irrigation in crop production. The wastewater utilised by farmers is heavily contaminated with toxic heavy metals as a result of industrial discharge and other human activities. Consequently, the prolonged use of wastewater has detrimental impacts on both soil quality as well as crop health. The presence of heavy metals in the food chain is widely acknowledged as a major environmental route via which humans can be exposed to possible health hazards. However, there are very few easy, less time consuming, environment-friendly and cost-effective technique available to remove toxic heavy metals from wastewater. In this study our main objective was to quantifying heavy metals content in wastewater, designing and integrating an electrochemical system and analysing its efficiency to remove heavy metals from wastewater. With the help of ICP-OES heavy metal content in wastewater was quantified. An electrochemical system using graphite electrode was developed to remove heavy metals (Cd, Zn, Co and Mn) from wastewater. Efficiency of the developed electrochemical system was calculated. Optimization of the different parameter i.e. voltage, initial concentration and operating time was done using response surface methodology (RSM). From this study we observed that applying 10V of voltage and 60 min of operating time, highest removal efficiency was found for cadmium (Cd) and zinc (Zn) and after 90 min of operating time highest removal efficiency was found for cobalt (Co) and manganese (Mn). The highest obtained metal removal efficiency of the developed electrochemical system using graphite electrode for cadmium (Cd), zinc (Zn), cobalt (Co), and manganese (Mn) were 94%, 85%, 91% and 99% respectively. It was found that energy consumption and hence the operating cost of the developed electrochemical system increased with increase of voltage and operating time. These findings implies that graphite can be used as electrode in an electrochemical system to remove heavy metals from wastewater. Furthermore, the cost effectiveness of the developed electrochemical system should be studied and efforts should be made to standardize electrochemical system to apply this technique at community level.

Effect of zinc oxide green-nanoparticles to enhance moisture stress tolerance in wheat (*T. aestivum* L.)

The physiological attributes of both wheat varieties, namely, absolute growth rate, varied significantly within the treatments, with notable enhancements in the growth rates for treatments using 20 nm ZnO-NPs at a 40 ppm concentration for HD 3226 and 60ppm concentration for HD 3298. The relative growth rate also showed an elevation in both wheat varieties when ZnO-NPs were applied, with a major significant difference identified between treated plants and controls. Moreover, leaf photosynthetic rates were positively influenced, displaying the highest values in plants treated with 20 nm ZnO-NPs. Stomatal conductance and transpiration rates similarly exhibited significant improvements under various nanoparticle applications when they were compared to control groups, thereby indicating that ZnO-NPs could alleviate moisture stress. Chlorophyll 'a', chlorophyll 'b', and total chlorophyll contents reflected significant increase across treatments, emphasizing the effect of ZnO-NP application in enhancing photosynthetic efficiency and overall plant health under moisture stress. Root morphological attributes, such as total root length, surface area, diameter, and volume, also improved significantly when ZnO-NPs were utilized, pointing towards enhanced root development, which is crucial for water uptake in moisture stress conditions.Treatments with ZnO-NPs led to increased biochemical attributes such as protein, proline, superoxide dismutase, peroxidase, and catalase contents, highlighting their beneficial role in stress mitigation and enhancing moisture stress tolerance mechanisms in the wheat varieties. In the third section, yield attributes such as plant height, panicle length, the number of productive tillers, filled grains per plant, grain weight, and dry biomass significantly increased, particularly under the effects of the 20 nm ZnO-NPs at 40 ppm and 60 ppm for HD 3226 and HD 3298 wheat cultivars, respectively. These findings claim that these nanoparticles not only improve physiological processes but subsequently enhance yield as well. Finally, the study investigated the micronutrient profile of the wheat varieties, revealing that ZnO-NP application significantly influenced zinc concentration in grains, roots, and leaves. However, a non-significant enhancement was observed in iron content in various plant parts of both wheat cultivars, which exhibited heightened zinc nutrient levels when treated with ZnO-NPs, emphasizing their potential role in addressing micronutrient deficiencies in wheat crops.

Effect of magnetic treatment of seeds on biophysical parameters and yield characteristics of wheat grown under different irrigation conditions

Experiments were conducted with an aim to study the effect of pre-sowing wheat (Var. HD-3086) seed treatment to standardized static magnetic field. Wheat seeds were treated to magnetic field of 50 mT to 250 mT in steps of 50 mT for ½ hour and 1 hour in all the field strengths by electromagnetic field generator "Testron EM-20". Results showed that magnetic field application enhanced seedling shoot length, seedling root length, seedling dry weight, seedling vigour I and seedling vigour II over control. Seed treated by 150 mT for ½ h followed by 100 mT for ½ h was found best among all the ten magnetic treatments. Seeds treated by 150 mT for ½ hour and 100 mT for ½ hour were sown in the field along with untreated control under five, three and two irrigations.The plants raised from seeds treated by 150 mT for ½ hour and 100 mT for ½ hour showed enhancement in bio-physical parameters, root characteristics, yield characteristics, yield radiation use efficiency and water productivity as compared to control in five, three and two irrigation. The value of leaf area index, chlorophyll concentration, shoot length, biomass and seed yield was reduced in three and two irrigations respectively as compared to five irrigations in plant raised from seed treated by magnetic field as well as control. Plant raised from seed treated by magnetic field had significantly higher value of total root length, root surface area, root volume, root average diameter,gravimetric soil moisture content (SMC) photosynthesis rate, stomatal conductance and transpiration rate relative water content, radiation use efficiency, IPAR and fIPAR, Water productivity as compared to corresponding value in control in all irrigation levels. was found to be higher in plant raised from seed treated by magnetic field as compared to corresponding value in control in all irrigation levels. Plant raised from seed treated by magnetic field 150 mT for ½ hour performed better than plant raised from seed treated by magnetic field 100 mT for ½ hour in all irrigation levels. Hence it may be concluded from this study that seeds treated by magnetic field 150 mT for ½ hour and 100 mT for ½ hour improved germination characteristics.

Theme 2: Soil Physics

Soil quality index for enhanced productivity under conservation agriculture based rice-wheat cropping system

Principal Component Analysis (PCA) based global Soil Quality Index (SQI) was developed using the data on different spatial scale published in literature. Wheat crop yield was predicted by multi-linear regression (MLR) and four machine learning approaches (i.e., artificial neural network (ANN); support vector machine (SVM), classification and regression tree (CART); and random forest (RF)) using soil health indicators. Meta data analysis showed that there was overall decrease in soil bulk density (BD) irrespective of depths, climates, textures and duration of the study under CA based management practices.There was significant % increase in soil organic carbon (SOC) content of the soil. There was significant increase in mean weight diameter (MWD) in 0-20 cm of soil layer (45.68%) and in sub-tropical climate (49.79%), under loamy soil (56.20%) and for 4-10 years duration of the study (58.28%). Change (%) in wheat yield (t/ha) in CA over CT at climates, textures and overall, there was 9.1% increase in wheat yield under CA based agricultural practices. The parameters most sensitive to global SQI were available soil P, SOC, pH, DHA and EC for productivity goal. Developed SQI was positively related with the crop yield. Stepwise forward regression showed that among these 5 parameters pH, DHA and SOC have significant effects on wheat yield. In the combined dataset, ANN with 3 hidden layers performed better than another model in prediction of wheat crop yield ad target variable and soil health indicators as predictor variables. Available P was the only common soil health indicators affecting SQI at field level and SQI developed from meta data. Relationship of wheat yield and SQI from the field experiment data showed positive relation with a R^2 value of 0.58. SQI developed from meta data set was validated with the field data and the calculated SQI showed a positive relation with R^2 value of 0.89.

Quantification and mapping of soil ecosystem services under conservation *vis-a-vis* conventional agriculture

Two field experiments were conducted in wheat crop during the *rabi* season, in 2021-2022 and 2022-2023, under long-term conservation agriculture practice at IARI Experimental Farm and existing conservation agriculture (CA) and conventional tillage (CT) fields in different villages of Karnal and Kaithal district of Haryana. Four different types of ecosystem services, i.e., provisioning, regulating, supporting and cultural services were quantified from different soil health indicators, crop yield and by-product using standard methodologies. Ecosystem dis-services like greenhouse gas emission and soil erosion were quantified. Based on the observed result study proposes an ecosystem service sustainability index (ESSI) using nine significant services. Result showed that significantly higher wheat yield was recorded in PBB+R (6.12 t ha^{-1}) compared to CT (4.88 t ha^{-1}). Over all, the retention of crop residues has significantly improved the grain yield by ~13%. Approximately, 15.7% increase in grain yield was reported under CA in Karnal district and in Kaithal districts. Retention of crop residues had significantly improved the SOC concentration in the top 0–15 cm soil layer by ~40%. The total SOC stock in the 0–30 cm soil layer enhanced by ~27% in plots with residue retention compared to nonresidue plots.In Karnal and Kaithal districts, CA showed 46 and 37% improvement in value of SOC stock over CT.Grain yield (t/ha) was strongly (positive) corelated with soil available N ($R^2 = 0.84$), soil available P ($R^2= 0.76$), SOC stock ($R^2 = 0.53$) and negatively correlated with bulk density ($R^2 = 0.36$).Gain in provisioning service in the whole study area ranged between 0.55 – 0.77 t/ha with an average of 0.63 t/ha. The total provisioning ES value for food and by-products under wheat ES ranged from ₹122733 ha^{-1} (CT) to ₹152452 ha^{-1} (PBB+R) with a mean value of ₹137171 ha^{-1}. The economic value of food in Karnal district recorded a 16% increase in CA over CT. CA treatment in Karnal and Kaithal districts had shown a 16 and 13% decrease in total GHG emissions over CT.Above all, CA had significantly improved MES and NMES over CT (16 and 47%) in the Karnal district. The Ecosystem Service Sustainability Index (ESSI) could help to delineate the areas with degraded, vulnerable, sustainable and hot spot areas of ecosystem services in wheat agroecosystem.By adopting sustainable practices and valuing ecosystem services, agriculture can contribute to a healthier planet and a more secure food future.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1	Supriyo Dhara (21804)	M.Sc.	Drone-based water stress monitoring under different irrigation and nitrogen levels in wheat *(Triticum aestivum L.)*	Dr. Rajeev Ranjan	ICAR-IARI, New Delhi
2	Swagata Das (21910)	M.Sc.	Effect of magnetic treatment of seeds on biophysical parameters and yield characteristics of wheat grown under different irrigation conditions	Dr. Ananta Vashisth	ICAR-IARI, New Delhi
3	Animesh Panda (21929)	M.Sc.	Soil quality index for enhanced productivity under conservation agriculture based rice-wheat cropping system	Dr. Pragati Pramanik Maity	ICAR-IARI, New Delhi
4	Pritam Chanak (21948)	M.Sc.	Electrochemical method-based remediation of heavy metals from irrigation water	Dr. Monika Kundu	ICAR-IARI, New Delhi
5	Shreya Sharma (21966)	M.Sc.	Effect of zinc oxide green-nanoparticles to enhance moisture stress tolerance in wheat (*T. aestivum* L.)	Dr. Achchhelal YadaV	ICAR-IARI, New Delhi
6	Abithaa P (21974)	M.Sc.	Evaluation of the effect of foliar nitrogen fertilization by drone and knapsack sprayer on growth and yield of wheat (*Triticum aestivum* L.)	Dr. Rajeev Ranjan	ICAR-IARI, New Delhi
7	Sunny Arya (11201)	Ph.D.	Artificially intelligent high-throughput phenotyping of wheat for water and nitrogen deficit stress tolerance using fluorescence and hyperspectral imaging	Dr. R N Sahoo	ICAR-IARI, New Delhi
8	Ms. Nandita Mandal (11706)	Ph.D.	Quantification and mapping of soil ecosystem services under conservation vis-a-vis conventional agriculture	Dr. Pragati Pramanik Maity	ICAR-IARI, New Delhi

AGRONOMY

10

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 research 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. The research work carried out by the students of the Division during 2023-24 can broadly be classified into following five themes, for which the significant findings are presented below.

Theme 1: Nutrient Management

Performance of nitrogen sources and zinc fertilization on productivity and nutritional quality of wheat-rice sequence

A field experiment was conducted during 2021–22 and 2022–23 at ICAR-IARI, New Delhi, to evaluate the impact of nitrogen (N) and zinc (Zn) fertilization on the wheat-rice cropping sequence. Using a split-plot design, nitrogen sources (0, 65, 97.5, and 130 kg N/ha with nano urea or prilled urea foliar sprays) were assigned to main plots, and Zn treatments (no Zn, 0.5% $ZnSO_4.7H_2O$, 0.1% nano-ZnO, and cyanobacterial BF1) to subplots. Key findings showed that 130 kg N/ha significantly improved growth parameters, yield attributes, and yields of wheat and rice. Wheat and rice yields increased by 27.7% and 26.6%, respectively, compared to the control. The highest system productivity was 13.59 t/ha (2021–22) and 12.82 t/ha (2022–23), 25.48% and 27.94% higher than the control. Nano-ZnO (0.1%) foliar spray further enhanced wheat and rice yields by 5.0 and 5.1%, respectively. N use efficiency was highest with 65 kg N/ha + nano urea foliar spray, achieving partial factor productivity (65.0–65.9 kg grain/kg N) and agronomic efficiency (8.6–9.4 kg grain increase/kg N). Nutrient concentrations and uptake (N, P, K, Zn, Fe) were maximized with 130 kg N/ha and 0.1% nano-ZnO. Economic analysis showed significantly higher gross returns, net returns, and benefit-cost ratios with 130 kg N/ha. Lower nitrogen doses (65 kg N/ha + nano urea) reduced wheat and rice yields by 9.2–15.5% and 6.9–9.1%, respectively, compared to 130 kg N/ha. In conclusion, applying 130 kg N/ha and 0.1% nano-ZnO foliar spray at critical stages is recommended for maximizing productivity and profitability in the wheat-rice cropping system of the Indo-Gangetic plains.

Nutrient management in baby corn-based intercropping systems

A field experiment was conducted during the *rabi* season of 2023-24 at ICAR-IARI, New Delhi, to evaluate the effects of nutrient management practices on baby corn-based intercropping systems. The factorial randomized block design (FRBD) included three nutrient management practices—N_1 (Inorganic fertilization: 150:60:60 kg NPK/ha), N_2 (Integrated Nutrient Management (INM): 75% NPK + 5 t FYM/ha + biofertilizer consortia), and N_3 (Organic fertilization: FYM (20 t/ha), biofertilizer consortia, PROM, *Panchgavya* @ 3%)—and four intercropping systems: sole baby corn, baby corn + cabbage, baby corn + carrot, and baby corn + spinach. INM significantly improved plant growth, yield attributes, and yield compared to inorganic and organic management practices. Cob yield with and without husk peaked under INM (13.66 t/ha and 3.26 t/ha, respectively) and green fodder yield reached 26.37 t/ha, slightly outperforming inorganic treatment. Intercropping systems did not significantly affect baby corn and fodder yield, but the baby corn + cabbage system under INM recorded the highest baby corn equivalent yield (10.26 t/ha) and profitability (gross return: ₹668 × 10^3/ha, net return: ₹577 × 10^3/ha, net B:C 6.38). Nutrient uptake was highest under INM with sole baby corn showing the greatest N, P, and K uptake. Organic management excelled in enhancing soil microbial properties. The baby corn + cabbage intercropping system under INM or organic management can be recommended for maximizing yield, profitability, and soil health in *rabi* season cultivation.

Precision nitrogen management in maize using android-based mobile app

Real-time Nitrogen (N) management tools like GreenSeeker™ (GSTM), SPAD chlorophyll meter, and leaf colour chart (LCC) predict crop N requirements. Still, their high costs and limitations hinder widespread use among Indian farmers. To address this, data from maize field experiments (2020-22) on the dark green color index (DGCI), NDVI, SPAD, LCC, and N concentration (%) were analyzed. DGCI at 35 and 45 days after sowing (DAS) had the strongest correlation with N concentration (%), outperforming NDVI, SPAD, and LCC. Calibration curves based on 35 DAS data were used to predict leaf N concentration at 45 DAS, identifying DGCI as the most accurate predictor ($R^2 = 0.69$, MAPE = 16.96%, RMSE = 0.31). A "Pusa N Doctor" app, developed using DGCI-based calibration, to estimates potential yield without additional fertilization and recommends N splits at 35 and 45 DAS. In a 2023 *kharif* maize field validation, treatments with 50 kg N basal and app-based splits (N_{50}PK+App) showed comparable yields and grain protein to GSTM and RDF-based treatments, reducing N use by 18.7%. N_{50}PK+App achieved 22.9% higher agronomic efficiency, 23% greater partial factor productivity, and 22.1% improved N recovery efficiency over the RDF. It also reduced CO_2 emissions by 11.1% compared to RDF and recorded the lowest N loss (44.9 kg/ha). The app-based strategy optimizes N use, enhances the farm economy, and minimizes environmental impact, supporting SDG 12 (responsible consumption and production) by promoting sustainable, resource-efficient practices.

Response of maize to nutrients sources in acidic soil of upper Assam

This study evaluated the effects of organic and inorganic nutrient sources on maize growth, yield, and soil health in acidic soils during the *kharif* season of 2023. The experiment was conducted at ICAR-IARI, Assam in a split-plot design with three organic treatments (control, FYM @ 10 t/ha, and vermicompost @ 2.5 t/ha) and four inorganic treatments (control + lime @ 300 kg/ha, 50% RDF (NPK) + lime, 75% RDF (NPK) + lime, and 100% RDF (NPK) + lime). The soil was characterized with high acidity (pH 4.84), sandy loam texture, and low available nitrogen (197.6 kg/ha), which posed challenges for crop productivity. Results showed that FYM @ 10 t/ha significantly improved crop growth, grain yield (4.37 t/ha), and net returns (₹71,040/ha), outperforming vermicompost @ 2.5 t/ha (4.19 t/ha) and control (3.3 t/ha). The FYM application resulted in 4.29% and 32.42% higher yields compared to vermicompost and control, respectively. Inorganic nutrient management with 100% RDF (NPK) + Lime @ 300 kg/ha provided the highest grain yield (4.43 t/ha) and profitability (net B:C 1.7), yielding 33% more than the control. The combined application of FYM @ 10 t/ha and 100% RDF (NPK) + lime achieved the highest productivity (4.84 t/ha) and net returns (₹80,040/ha), highlighting its potential for sustainable maize production. Treatments integrating FYM or vermicompost with reduced RDF and lime were cost-effective options for maximizing maize yield.

Response of organic and inorganic nutrient management in finger millet under alluvial soils of Assam

Finger millet (*Eleusine coracana L.*), a staple crop in semi-arid and tropical India, is valued for its nutritional content, drought resilience, and ability to thrive in marginal soils. This study was conducted during the *kharif* season of 2022-23 at IARI, Assam, aimed to optimize nutrient management strategies for finger millet on Assam's variable alluvial soils to enhance productivity and sustainability. The experiment used a split-plot design with three organic treatments (organic manure @ 1 t/ha, biofertilizers, and FYM @ 5 t/ha) in main plots and five nitrogen (N) levels (0, 20, 40, 60, and 80 kg/ha) in sub-plots. The combined impact of these treatments on growth, yield, and soil properties was assessed. Results showed that FYM @ 5 t/ha combined with 80 kg N/ha delivered the best performance, achieving the highest grain yield, straw yield, and total biological yield. This treatment demonstrated the synergistic effects of integrating organic and inorganic nutrient sources, significantly improving growth parameters, productivity, and soil health. The highest grain yield was recorded under this treatment along with enhanced soil organic carbon content, better soil structure, and increased nutrient availability. These findings highlight the potential of combining FYM and optimal nitrogen inputs to boost finger millet productivity while maintaining soil health. This integrated approach offers a sustainable solution for addressing the challenges of farming in Assam and similar agro-ecological regions.

Analyzing the yield gap of rice in a hilly ecosystem using bio-physical modelling for different nitrogen levels

The North Eastern Hill (NEH) region of India faces significant rice yield variability due to suboptimal fertilizer use, erratic rainfall, acidic soils, and socioeconomic constraints. A study conducted during the *kharif* season of 2023 at ICAR-NEH, Umiam, Meghalaya, aimed to address these challenges using field experiments and crop simulation models. Field trials with two rice varieties @ Shahsarang and Mendri, revealed that applying 125% of the recommended nitrogen dose (RDN) produced the highest grain yields 4354 kg/ha for Shahsarang, and 3484 kg/ha for Mendri. Yields under 100% RDN (4199 kg/ha for Shahsarang and 3224 kg/ha for Mendri) were statistically comparable. Net returns increased by 20–157% and 23–117% for 125% and 100% RDN, respectively, with the highest marginal returns at 100% RDN (₹623 for Shahsarang and ₹362 for Mendri). Long-term simulations using APSIM optimized sowing windows and assessed yield gaps and soil organic carbon (SOC) dynamics. Early sowing improved yields by up to 30% compared to late sowing, while supplemental irrigation (50 mm) mitigated yield losses during delayed sowing by 7–16%. Future climate projections (RCP8.5) indicated yield advantages for Shahsarang of 363 kg/ha (2050) and 632 kg/ha (2080). Yield gaps due to nitrogen limitations were 2.8 t/ha for Shahsarang and 1.63 t/ha for Mendri under rainfed conditions. Integrated nutrient management (75% RDN + 5 t/ha FYM) outperformed 100% RDN in yield and SOC stability, especially in low-carbon soils. High-carbon soils showed limited response to additional nutrient inputs. Over 33 years, irrigation during drought years improved yields by 11–17% for Shahsarang and 5.5–9.6% for Mendri. This study highlights the importance of integrated nutrient management, irrigation, and early sowing in enhancing productivity and resilience while maintaining soil health in the NEH region. Insights gained could guide sustainable rice production and climate adaptation strategies.

Biochar and solid digest effects on productivity and nutrient use efficiency in mungbean under mungbean-wheat system

A study was conducted during the *kharif* season of 2023 at ICAR-IARI, New Delhi, to evaluate the impact of biochar (BC) and solid digest (SD) on mungbean productivity, soil properties, and resource use efficiency. A randomized complete block design with 11 treatments, including combinations of BC, SD, and inorganic nutrients, was implemented. Key findings showed that the application of 100% RDF + 2 t/ha SD and 100% RDF + 3 t/ha BC significantly improved crop growth parameters, yield attributes, and yield. Economic yield increases of 37.5% and 29%, respectively, were observed compared to 100% RDF alone, and yield improvements reached 131.6% and 117.2% over the control. Economic analysis revealed that 100% RDF + 2 t/ha SD provided 48.9% higher net returns than 100% RDF alone. The highest benefit-cost (B-C) ratio was recorded for 75% RDN + Full P&K + 25% N (SD), which also achieved the highest agronomic and apparent recovery efficiencies. Meanwhile, 100% RDN + SD resulted in the highest physiological efficiency, highlighting its long-term nutrient potential. Soil nutrient improvements were also notable, with the maximum available N and P recorded in 100% RDF + 2 t/ha SD, and the highest available K in 100% RDF + 3 t/ha BC, attributed to the nutrient composition of the amendments. This study underscores the potential of biochar and solid digest, used alone or integrated with inorganic fertilizers, to enhance mungbean productivity, profitability, and soil health sustainably.

Response of wheat (*Triticum aestivum* L.) to chemical fertilizers under FYM and biofertilizer integration

A field experiment was conducted during the *rabi* season of 2023–2024 at ICAR-NBPGR, New Delhi to assess the effects of integrating farmyard manure (FYM), biofertilizers, and chemical fertilizers on the growth and yield of wheat (*Triticum aestivum* L.). The study employed a split-plot design with 20 treatment combinations replicated three times. Main plot treatments included control, FYM @ 5.0 t/ha, FYM @ 5.0 t/ha + Consortia 1, and FYM @ 5.0 t/ha + Consortia 2. Sub-plot treatments consisted of various chemical fertilizer levels: Control, 50%, 75%, and 100% of the recommended dose, as well as 75% N + 100% PK with two nano-urea sprays. Results demonstrated significant improvements in growth attributes (plant height, tiller numbers, leaf area, dry matter) and yield parameters (number of ear-bearing tillers, spike length, grains per spike, grain weight per spike, and test weight) with FYM and biofertilizer integration. The highest grain yield was achieved using 75% of the recommended chemical fertilizer dose combined with FYM @ 5.0 t/ha + biofertilizer. The integration of FYM and biofertilizers reduced fertilizer doses with improved soil health, recovery efficiency, and nutrient productivity. These treatments also enhanced the harvest index, 1000-grain weight, and overall biological yield compared to the control. This study highlights the potential of integrating organic and inorganic nutrient management practices to enhance wheat productivity and sustainability. Combining FYM with optimal fertilizer levels offers a viable solution to improve crop yields and soil health, addressing key challenges in wheat cultivation.

Nitrogen and crop residue management in maize under subsurface drip fertigated maize-wheat-greengram cropping system

The effects of subsurface drip fertigation (SSDF) and crop residue incorporation on maize (Pusa HQPM-1) growth, yield, nitrogen use efficiency (NUE), economics, and water budgeting under different nitrogen (N) levels, and residue treatments were evaluated in a field experiment at ICAR-IARI, New Delhi, during the *kharif* seasons of 2022 and 2023. In the main plot, treatments included 100%, 75%, and 50% recommended dose of nitrogen (RDN) applied in 3 (3S) or 4 splits (4S) with a control (no-N) and conventional cultivation. Subplot treatments involved residue incorporation or no residue. Results showed that growth parameters, physiological traits, yield attributes, and yields were significantly higher in 100% RDN-4S and 75% RDN-4S treatments compared to the control and conventional cultivation. Grain yields in 100% RDN-4S were 6.73 t/ha (2022) and 6.53 t/ha (2023), significantly higher than conventional cultivation (5.46 t/ha). Incorporating crop residue also increased yields by 4-6% compared to no-residue treatments. Fertigation increased yield by 68-123% over control, with 100% RDN-4S yielding 20-25% more than conventional practices. Protein content and yield were highest with 100% RDN-4S (10.58%, 714 kg/ha). SSDF improved water-use efficiency (IWUE), and was found highest with 75% (4S) (86.4 kg ha/mm), whereas in conventional it was 37.42 kg ha/mm during 2022. Water saving of 48.7 and 33.5% in 2022 and 2023, respectively was achieved with SSDF. Nitrogen distribution and use-efficiency were higher in 50% and 75% RDN treatments, with significant economic benefits. Net returns and benefit-cost ratios were highest with 100% RDN-4S (INR 163,773/ha). Residue incorporation also improved net returns by 6.4-10.9% over no-residue plots. Soil biological properties *viz.*, urease, SMBC, SMBN, and DHA were significantly improved with higher doses of N (100 and 75 % RDN). Retaining of crop residue @ 3 t/ha improved crop productivity, profitability, and soil chemical and biological properties. SSDF of 75% RDN-4S saved 25% nitrogen while maintaining yield and profitability, and demonstrating the potential for optimizing N use and crop productivity.

Tillage, residue and nutrient management for enhancing productivity, profitability and resource use efficiency in maize-wheat system

The effects of crop establishment practices (CEPs) and nitrogen placement methods (NPMs) on the maize-wheat system were evaluated in sandy loam soil of ICAR-IARI, New Delhi, during 2022-23 and 2023-24. The treatments included zero tillage with residue retention (ZT+R), zero tillage without residue retention (ZT), and conventional tillage (CT) as main plots, and control, recommended dose of nitrogen (RDN), improved RDN (subsurface band placement), and improved 80% RDN as sub-plots. ZT+R significantly outperformed with CT in growth parameters, with enhancements in plant height, dry matter, leaf area index, and crop yields. In maize, ZT+R increased grain yield by 8.87%, stover yield by 8.23%, and biological yield by 9.43% over CT. Wheat yields also showed a similar increase. Improved RDN significantly increased crop growth and yield attributes over RDN, with 3.28% higher grain yield in maize and 2.82% in wheat. The 80% RDN treatment provided similar results to full RDN, saving 20% nitrogen. ZT+R improved soil health, physical properties of soil were remarkably improved with lower bulk density (10.36%) and penetration resistance (12.25%) than under CT. Improved 80% RDN had significantly higher partial factor productivity, and agronomic efficiency, with the highest apparent nitrogen recovery of 57.38 and 59.89% in maize and wheat, respectively. Reducing bulk density and penetration resistance, and enhanced soil microbial activity. Energy use efficiency and carbon sustainability index improved by 22.81% and 14.05%, respectively, under ZT+R. Economic analysis showed that ZT+R had a BC ratio of 1.98 with higher gross and net returns over CT. This study demonstrates that ZT+R with improved RDN is a sustainable, eco-friendly practice that boosts productivity, soil health, and economic returns while minimizing environmental impact in the maize-wheat system.

Nitrogen management in rice-wheat system under various crop establishment protocols

The rice-wheat system (RWS) is crucial for food security in South Asia particularly in India, where it spans 14 million hectares and contributes significantly to foodgrain production. The study was conducted at ICAR-IARI, New Delhi during the *kharif* and *rabi* seasons of 2022-23 and 2023-24, to investigate the effects of precision nitrogen (N) management including nano-urea on productivity and N uptake in rice and wheat crop under various crop establishment methods. The results indicated that leaf colour chart (LCC)-guided balanced N application led to higher grain yield and N uptake for both crops across all establishment techniques. The highest rice yield and N uptake were observed in puddled transplanted rice (PTR) in both years (4.5 t/ha and 109.3 kg/ha in the first year), followed by Vattar direct-seeded rice (VDSR) and dry direct-seeded rice (DDSR). PTR outperformed VDSR and DDSR by 5.6% and 11.1% in grain yield, respectively, and 8.1% and 17.7% in N uptake. In wheat, zero till-wheat (ZTW) with rice residue at 3 t/ha achieved the highest yield (4.5 t/ha) and N uptake (131.9 kg/ha) during the first year, which was comparable to conventional till-wheat (CTW) with residue. ZTW and CTW with residue showed an 8.1% and 5.3% increase in grain yield and a 13.1% and 9.1% increase in N uptake over CTW without residue. The study highlighted the importance of optimized N management for improving crop productivity and nutrient uptake in the rice-wheat system.

Productivity and resource budgeting of rice-based production systems under different irrigation methods and nitrogen management

To address sustainability challenges in South Asia's rice-based cropping systems a study was conducted at the International Rice Research Institute-South Asia Regional Centre, Varanasi (2022-24). Field trials compared various crop establishment techniques and irrigation methods *viz*., flood-irrigated PTR, flood-irrigated DSR, surface drip irrigated (SD) DSR, and subsurface drip irrigated (SSD) DSR in rice-wheat (RW) and rice-maize (RM) systems, with two nitrogen management levels of 100% and 75% of the recommended dose. Results showed SSD-based systems consistently outperformed PTR systems, closing the 15% yield gap observed in flood-irrigated DSR. The SSD systems increased dry matter accumulation and nitrogen uptake (14-20% higher), with a 70% reduction in water use and 3-4 times higher irrigation water productivity. Economic analysis showed 24-29% higher net returns from SSD-based systems, with DSR combined with SSD being the most profitable. Meta-analysis revealed DSR systems reduced methane (CH_4) emissions by 69.9%, global warming potential (GWP) by 36.7%, and carbon footprint (CFP) by 34.4%, but increased nitrous oxide (N_2O) emissions by 84.6%, with an ~11% yield penalty in dry DSR systems. The DNDC model validated these findings, showing substantial CH_4 reductions (75-83%) and improved water and nitrogen balances under SSD systems. The study highlights SSD integration with DSR as a sustainable, water-saving, profitable solution for rice-based cropping systems in North-Eastern India and South Asia, with environmental benefits.

Theme 2: Conservation Agriculture

Crop establishment methods, residue retention and nitrogen effects on weeds, productivity and resource-use efficiency in a wheat-cotton system under conservation agriculture

The effects of conservation agriculture (CA) practices and nitrogen management on a wheat-cotton system were studied in a field experiment at ICAR-IARI, New Delhi during 2021-22 and 2022-23. The experiment compared CA with conventional tillage (CT), and included treatments based on crop establishment methods (Permanent narrow-bed (PNB), permanent broad-bed (PBB), Zero-till flat-bed (ZTFB) and nitrogen application (75% N and 100% N). The experiment was conducted in the 12th and 13th year of a long-term CA experiment. Results showed that CA-based practices, particularly PBBR100N, reduced weed biomass by 45.2% in wheat and 41.9% in cotton during 2021-22, with similar reductions during 2022-23. PBBR100N increased wheat grain yield by 13.9% and cotton seed yield by 35.6% in the first year, and by 17.9% and 32.2% in the second year, compared to CT. System productivity was 29% higher in the first year and 28.1% higher in the second year with PBBR100N. This treatment also resulted in 27.4% higher gross returns and 35.1% higher net returns than CT. CA practices improved soil health, with higher soil organic carbon (SOC), microbial biomass, and water retention, along with reduced bulk density and penetration resistance. CA-based practices resulted in 10.6-16.9%, 12.5-32.1%, and 9.8-22.4% savings of irrigation water in wheat, cotton, and system, respectively. The 75% N application had higher partial factor productivity of N in both wheat and cotton crops than 100% N, indicating saving of 25% N in long term CA. The treatment PBBR100N led to 23.2% and 22.5% higher output energy than CT during 2021-22 and 2022-23, respectively in wheat-cotton system. CA-based practices also reduced GHG emissions, with lower CO_2 and N_2O emissions under PBB and ZTFB treatments. CA practices with 100% N in early years and 75% N thereafter are recommended for sustainable intensification of wheat-cotton systems in the Indian IGP and similar agro-ecologies.

Productivity, resource use efficiency and greenhouse gases emission in pigeon pea-wheat system under different production scenarios

Productivity, resource use efficiency, greenhouse gas (GHG) emissions, and soil health in a pigeon pea-wheat system under conservation agriculture (CA), conventional tillage (CT), and organic agriculture (OA) systems were studied at ICAR-IARI, New Delhi during 2022-24. Treatments included CA, CA-Permanent narrow-bed (PNB), CA-Permanent broad-bed (PBB), CA-Permanent flat-bed (PFB), CT, conventional tillage-based organic (OA-CT), and zero-tillage-based organic (OA-PNB, OA-PBB, OA-PFB). Results showed that CA systems, especially CA-PBB and CA-PFB, outperformed CT and OA systems on crop growth, yield, system productivity, irrigation water productivity (IWP), total water productivity (TWP), and nutrient use efficiency (NUE). CA-PBB was the most profitable, offering higher gross returns and lower cultivation costs compared to CT and OA. Zero-tillage organic systems (OA-PNB, OA-PBB, OA-PFB) were more cost-effective and energy-efficient than CT and CA, achieving higher net energy and energy productivity. GHG emissions were highest with CA-PFB (N_2O) and OA-CT (CO_2), with OA-PNB showing the lowest emissions. Soil health improvements were seen in CA systems, with higher soil organic carbon (SOC) content, carbon accumulation, and sequestration, especially under CA-PFB. OA systems enhanced nutrient availability, particularly N, P, and K, compared to CT. Soil bulk density was lower in CA systems, and carbon mineralization rates were higher in zero-tillage OA systems.Conventional tillage-based OA systems showed the highest Q10 values, indicating greater temperature sensitivity of carbon mineralization. The study highlights the potential of CA and zero-tillage-based organic systems for improving productivity, efficiency, and soil health, while reducing GHG emissions in pigeon pea-wheat systems.

Theme 3: Crop Diversification

Effect of land configuration and cereal-legume integration on system productivity, resource use efficiency and soil health

A field experiment was conducted in 2023-24 at ICAR-IARI, New Delhi to evaluate the effects of land configuration and cereal-legume integration on system productivity, resource efficiency, and soil health in maize-wheat rotations. The study was conducted in sandy loam soil and a split-plot design with flat-bed and permanent raised bed (PRB) configurations in the main plots, and four cereal-legume integrations in sub-plots: maize-wheat, maize + blackgram + soybean-wheat + chickpea, maize + cowpea + soybean-wheat + lentil, and maize + cowpea + soybean-wheat + mustard. Results showed significantly higher growth, yields, and system productivity under the PRB system. Maize grain yield (5.15 t/ha) and wheat grain yield (2.39 t/ha) were maximized with the PRB system. Among integrations, maize + cowpea + soybean-wheat + lentil recorded the highest maize yield (5.60 t/ha), system productivity (18.29 t/ha), and net benefit-cost ratio (NBCR, 2.81). Soil health parameters, including organic carbon, microbial biomass, and enzyme activities, were superior under PRB and the maize + cowpea + soybean-wheat + lentil system. Cereal-legume integration improved system productivity, energy use efficiency, and carbon sequestration (2-3 times) while reducing the carbon footprint (2.5-3 times) compared to the maize-wheat system. The PRB system exhibited a 21.89% higher NBCR and 5.39% higher production efficiency than the flatbed. Additionally, PRB reduced the water footprint and enhanced water productivity. These findings establish PRB and cereal-legume integration as sustainable approaches for improving productivity, profitability, and soil health in the Indo-Gangetic Plains.

Theme 4: Weed Management

Integrated weed management in lentil

A field experiment was conducted during the *rabi* season of 2023-24 at the Division of Agronomy, IARI, New Delhi, to evaluate integrated weed management strategies for lentil production. The randomized block design experiment comprised ten treatments, including herbicidal, manual, and cultural practices: pendimethalin @ 1000 g/ha (PE), pendimethalin @ 750 g/ha + imazethapyr 50 g/ha (PE), pendimethalin @ 750 g/ha (PE) + hand weeding at 30 days after sowing (DAS), pendimethalin @ 750 g/ha (PE) + maize straw mulching (4 t/ha), imazethapyr @ 50 g/ha (20 DAS), quizalofop-ethyl @ 50 g/ha (20 DAS), and weedy and weed-free checks. The pendimethalin @ 750 g/ha (PE) + hand weeding at 30 DAS achieved the highest weed control efficiency, reducing weed density and dry weight and increasing grain yield by 92.95% over the weedy check. The pendimethalin @ 750 g/ha (PE) + maize straw mulching (4 t/ha) also recorded lower weed density and dry weight at 30 DAS. The quizalofop-ethyl post-emergence treatments were less effective. Weed-free conditions maximized growth parameters, yield attributes, and yields, comparable to pendimethalin @ 750 g/ha (PE) + hand weeding at 30 DAS. Herbicide treatments improved yield by 36.61 to 92.95% over the weedy check. The pendimethalin @ 750 g/ha (PE) + hand weeding at 30 DAS recorded the highest net return (₹62,200/ha) and B:C ratio due to higher gross returns (₹92,000/ha) compared to cultivation costs (₹29,800), followed by Pendimethalin @ 750 g/ha (PE) + maize straw mulching (₹55,600/ha).

Theme 5: Irrigation Management

Moisture conservation and potassium management in the pearl millet-wheat cropping system

The effects of moisture conservation and potassium management in a pearl millet-wheat cropping system were studied. The study utilized crop establishment methods (no residue mulching (C0), crop residue mulching (C1), and crop residue mulching with Pusa Decomposer (C2)) and potassium management strategies (control (K0); 40 kg K_2O/ha (K1); 40 kg K_2O/ha with potassium-solubilizing bacteria (KSB) (K2); 30 kg K_2O/ha with KSB (K3); and 20 kg K_2O/ha with KSB (K4) for the pearl millet crop and 60 kg K_2O/ha (K1); 60 kg K_2O/ha with KSB (K2); 45 kg K_2O/ha with KSB (K3); and 30 kg K_2O/ha with KSB (K4) for wheat crop). Results showed that crop residue mulching significantly improved the growth and yield of both crops. C2 treatment, followed by C1, resulted in the highest grain yields for both crops, with pearl millet yields increasing by 16.0% and 17.6% in 2021 and 2022, respectively, and wheat yields increasing by 14.7% and 16.4%. Stover yield was also highest under C2. Nutrient content in grain (N, P, K, Zn, Fe, Mn, Cu) was higher under C2, followed by C1. Gross and net returns were higher under C2 and C1, with C2 providing the highest returns. Energy-use efficiency was highest in C0 for wheat. Potassium management strategies (K2 and K3) significantly improved growth, yield, and irrigation water productivity with the highest yields and returns. Soil potassium availability was highest under K2. Overall, combining 3 t/ha crop residue mulching (with or without decomposer) and 30/40 kg K_2O/ha + KSB for pearl millet and 45/60 kg K_2O/ha + KSB for wheat resulted in enhanced productivity, economic returns, potassium use efficiency, and soil health.

Moisture management and Zn fertilization effects on productivity and resource use efficiency of pearl millet–mustard cropping system

The effects of moisture management practices and zinc (Zn) fertilization on the productivity and nutritional quality of a pearl millet-mustard cropping system were assessed in a field experiment at ICAR-IARI, New Delhi, during 2020-21 and 2021-22. The treatments included moisture management practices (no mulch, straw mulch, Pusa hydrogel at 2.5 and 5 kg/ha) and zinc application methods (soil application of $ZnSO_4 \cdot 7H_2O$ at 12.5 kg/ha, with foliar sprays at critical growth stages). Results showed that Pusa hydrogel (5 kg/ha) significantly improved growth metrics and yields, with 21.2% higher pearl millet yield and 18.6% higher mustard yield compared to no-mulch. Zinc application (12.5 kg/ha soil + foliar spray at the maximum tillering stage in pearl millet and the maximum vegetative growth stage in mustard) also enhanced growth, yield, and nutritional quality, increasing protein and zinc concentrations in both crops. The application of hydrogel at 5 kg/ha increased protein content by 13.0–13.4% and grain zinc concentration by 17.8–17.9% in pearl millet, and enhanced protein by 13.0–15.1%, seed zinc concentration by 12.9–13.3%, and oil content by 12.7–12.9% in mustard, compared to the no-mulch treatment. Rainwater use efficiency was improved by 18.9-22.4% in pearl millet and 16.6-20.4% in mustard with hydrogel at 5 kg/ha. Economic analysis showed that hydrogel at 2.5 kg/ha offered a cost-effective alternative, with a 7.7–8.5% higher net B:C ratio in pearl millet and 3.37–5.34% higher in mustard. The combination of hydrogel and $ZnSO_4 \cdot 7H_2O$ significantly enhanced economic returns. The study recommended using hydrogel at 2.5 or 5 kg/ha and $ZnSO_4 \cdot 7H_2O$ at 12.5 kg/ha as a soil application, followed by a 0.5% foliar spray at the maximum tillering stage in pearl millet and the maximum vegetative growth stage in mustard for improved productivity and economic sustainability in the pearl millet–mustard system in Western India.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of student & roll no.	Degree	Title of thesis	Chairperson	Institute
1.	Aastika Pandey (21826)	M.Sc.	Effect of land configuration and cereal-legume integration on system productivity, resource use efficiency and soil health	Dr. Subhash Babu	ICAR-IARI, New Delhi
2.	Sayantika Sarkar (21827)	M.Sc.	Precision nitrogen management in maize using android-based mobile app	Dr. Pravin Kumar Upadhyay	ICAR-IARI, New Delhi
3.	Rimjhim Chaudhary (21828)	M.Sc.	Nutrient management in baby corn-based intercropping systems	Dr. Y. V. Singh	ICAR-IARI, New Delhi
4.	Hamesh Kumar Meena (21829)	M.Sc.	Integrated weed management in lentil	Dr. Rajvir Sharma	ICAR-IARI, New Delhi
5.	Navneet Kumar (21830)	M.Sc.	Response of wheat (*Triticum aestivum* L.) to chemical fertilizers under FYM and biofertilizer integration	Dr. Ishwar Singh	ICAR-IARI, New Delhi
6.	Shubham Yaduwanshi (21832)	M.Sc.	Biochar and solid digest effects on productivity and nutrient use efficiency in mungbean under mungbean-wheat system	Dr. S.S. Rathore	ICAR-IARI, New Delhi
7.	Sneha Bharadwaj (50096)	M.Sc.	Analyzing the yield gap of rice in a hilly ecosystem using bio-physical modelling for different nitrogen levels	Dr. C.M. Parihar	#ICAR-IARI, Assam

8.	Chandrakant Yadav (50097)	M.Sc.	Response of organic and inorganic nutrient management in finger millet under alluvial soils of Assam	Dr. Kapila Shekhawat	#ICAR-IARI, Assam
9.	Huchchappa Jamakhandi (50098)	M.Sc.	Response of maize to nutrients sources in acidic soil of upper Assam	Dr. Shiva Dhar	#ICAR-IARI, Assam
10.	Arjun Singh (10984)	Ph.D.	Nitrogen and crop residue management in maize under subsurface drip fertigated maize-wheat-greengram cropping system	Dr. Anchal Das	ICAR-IARI, New Delhi
11.	Madam Vikramarjun (11455)	Ph.D.	Moisture management and Zn fertilization effects on productivity and resource use efficiency of pearl millet–mustard cropping system	Dr. S.L. Meena	ICAR-IARI, New Delhi
12.	Gunturi Aekhya (11721)	Ph.D.	Crop establishment methods, residue retention and nitrogen effects on weeds, productivity and resource-use efficiency in a wheat-cotton system under conservation agriculture	Dr. T.K. Das	ICAR-IARI, New Delhi
13.	Kadapa Sreenivasa Reddy (11722)	Ph.D.	Performance of nitrogen sources and zinc fertilization on productivity and nutritional quality of wheat-rice sequence	Dr. Y.S. Shivay	ICAR-IARI, New Delhi
14.	Ashok Kumar (11923)	Ph.D.	Moisture conservation and potassium management in the pearl millet-wheat cropping system	Dr. K.S. Rana	ICAR-IARI, New Delhi
15.	Priyanka Saha (12000)	Ph.D.	Productivity, resource use efficiency and greenhouse gases emission in pigeonpea-wheat system under different production scenarios	Dr. T.K. Das	ICAR-IARI, New Delhi
16.	K Srikanth Reddy (12001)	Ph.D.	Productivity and resource budgeting of rice-based production systems under different irrigation methods and nitrogen management	Dr. C.M. Parihar	ICAR-IARI, New Delhi
17.	Akshay Glotra (12003)	Ph.D.	Tillage, residue and nutrient management for enhancing productivity, profitability and resource use efficiency in maize-wheat system	Dr. S.L. Jat	ICAR-IARI, New Delhi
18.	G.D. Sanketh (12005)	Ph.D.	Nitrogen management in rice-wheat system under various crop establishment protocols	Dr. Kapila Shekhawat	ICAR-IARI, New Delhi

#IARI off-campus

ENVIRONMENTAL SCIENCES

11

Prof. Dinesh Kumar 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. These are likely to threaten the food security and livelihoods of millions of people in India. To sustain the food and nutritional security of the country, urgent need is to make Indian agriculture more resilient to environmental degradation and climate change. To address these challenges Division of Environmental Sciences, a multi-disciplinary Division was established at Nuclear Research Laboratory Building, ICAR-Indian Agricultural Research Institute, New Delhi. 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. The achievements of the students are presented in following themes:

Theme 1: Climate Change

Field and simulation studies on the interactive effect of elevated carbon dioxide and temperature on *aestivum* and *durum* wheat

Climate change is an impending threat affecting the biological system on earth. Increase in atmospheric CO_2 concentration and rise in temperature can significantly affect crop growth and soil processes. The following study was undertaken at experimental field of Division of Environmental Sciences, ICAR-IARI, New Delhi for two consecutive years that is 2020-2021 and 2021-2022 during the *rabi* season (November to April) to study the interactive effect of elevated CO_2 and temperature on *aestivum* and *durum* wheat by field and simulation studies. Two varieties of *Triticum aestivum* (HD 3226, HD 3086) and two varieties of *Triticum durum* (HI 8663 and HI 8627) were grown inside the open top chambers (OTC). Inside the OTCs, two levels of CO_2 concentration were maintained *i.e.,* the ambient level of 410 ppm and the increased level of 550 ± 25 ppm. Days to maturity also reduced in elevated temperature and elevated *CQi* plus temperature treatment. Two temperature levels were also maintained within the OTC i.e. chamber control and elevated temperature. Wheat varieties matured early in high temperature treatment. Rise in temperature by 2.0-2.1° C reduced grain yield in *aestivum* varieties by 9.5-12.1% while in *durum* varieties reduction in grain yield due to temperature rise ranged from 5.0-7.5%. Yield reduction in *durum* varieties were less as compared to *aestivum* varieties under elevated temperature condition. Elevated CO_2 concentration of 550 ppm was able to compensate yield loss due to temperature rise by 5.1-7.1% in *aestivum* varieties and by 1.3-4.0% in *durum* varieties. Simulated results showed reduction in yield and N uptake in *aestivum* and *durum* wheat under elevated CO_2 and temperature condition in north-western and central India. The study on differential response of *aestivum* and *durum* wheat to changes in climatic variables may help in development of climate smart agricultural technologies in future.

Effectiveness of modified urea fertilizers in reducing ammonia and nitrous oxide losses and increasing the nitrogen use efficiency in rice

This study comprehensively investigated the efficiency of modified urea fertilizers in enhancing rice production while minimizing environmental impacts. Various nitrogen fertilizer treatments were employed, including prilled urea (PU), neem oil-coated urea (NCU), karanji oil-coated urea (KCU), phosphogypsum-coated urea (PCU), sulfur-coated urea (SCU), and urea coated with both neem oil and Limus (DI). The coated urea significantly reduced GHG emissions and NH3 volatilization, demonstrating values up to 22% lower global warming potential and 30% reduced NH3 emissions. Coated urea application enhanced soil nitrate-N and ammoniacal-N compared to PU. The application of coated urea enhanced microbial biomass carbon (60–74%) and microbial biomass nitrogen (28-48%). Additionally, dehydrogenase activity increased by 40 50%, while nitrate reductase activity decreased by 20-57%. The urease activity peaked during the flowering phase, showing highest values in PU but significantly lower in coated urea treatments. Different treatments demonstrated significant variations in tillers per hill, total biomass, grain yield, nitrogen uptake, and NUE. Coated urea, particularly PCU and SCU, generally outperformed PU. Notably, DI exhibited the highest harvest NUE at 51.6% in 2019 and PCU at 52.7% in 2020. Overall, coated urea application strategies show promise for enhancing rice productivity and NUE. The economic feasibility of 144 each treatment was evaluated through benefit-cost (B:C) ratio analysis. Coated urea treatments, especially PCU, SCU and KCU (1%), demonstrated higher gross and net returns compared to PU. B:C was consistently higher for coated urea, with PCU exhibiting the highest B:C ratio in both years. Thus, this study emphasized the significant role of modified urea fertilizers not only in optimizing rice production systems via improving productivity and reducing environmental impacts but also in enhancing economic viability. Continued research and the widespread adoption of coated urea technologies are imperative for advancing sustainable agricultural practices and safeguarding food security amidst pressing global environmental challenges.

Life cycle assessment of maize and wheat products

To evaluate GHG mitigation options, a study was conducted in laboratory conditions comparing eight novel coated urea fertilizers to neem-coated urea (NCU) and prilled urea and found that coated ureas effectively reduced greenhouse gas emissions and ammonia volatilization. Prilled urea had the highest N_2O and CO_2 emissions, while coatings like NCU, Tagetes-coated urea (TCU), and polymer-coated urea (PCU) controlled emissions and favoured steady nitrogen release. 188 Treatments with reduced emissions were selected (TCU1, CCU2, PCU2.5) to be used in the field experiment on maize and wheat crops. The field study showed that coated urea treatments, especially Neem-Coated Urea with compost and neem compost (NCU+C+N) and Polymer-Coated Urea (PCU), were highly effective in reducing greenhouse gas emissions, ammonia volatilization, and nitrogen leaching compared to prilled urea. Prilled urea had the highest emissions and volatilization losses, whereas NCU+C+N and PCU achieved the lowest GWP and ammonia losses. NCU+C+N consistently resulted in the highest crop yields and nitrogen retention, demonstrating improved nitrogen use efficiency. After life cycle inventory, the inventory analysis and impact assessment were done. Impact assessment study found that conventional milling had a generally lower environmental impact than industrial milling for wheat flour, while maize flour showed mixed results across categories. In fertilizer treatments, Neem-Coated Urea NCU and PCU were most effective in reducing greenhouse gas emissions and overall environmental impacts for both crops. Combining nitrogen with organic matter (NCU+C and NCU+C+N) provided additional benefits in minimizing eutrophication but resulted in higher greenhouse gas emissions. Electricity production and fertilizer manufacturing were identified as major emission hotspots in all treatments. Coated urea fertilizers, especially in conjunction with organic sources, are promising GHG mitigation strategies in cereal crops. Given the unique agroclimatic diversity in India, the study emphasizes the need for primary data to accurately reflect regional farming practices.

Greenhouse gases and particulate matter emission due to sugarcane residue burning using measurements and remote sensing

The study was conducted in the Shamli district in Uttar Pradesh. A field survey was conducted in five locations (60 farmers) in the district to know the cropping pattern, the method of sugarcane harvesting, cane and biomass yield and various usage of residue, to estimate the harvest index (HI), Residue to crop ratio (RCR), fraction of biomass burned and moisture content in the residue. The average concentration of various GHGs, CH_4, CO_2, and N_2O monitored on-farm was 2.79 ± 0.13 ppm, 652.33 ± 39.52 ppm, and 394.98 ± 45.21 ppb, respectively. The emission factors calculated in the present study were 1358.66 ± 43.48, 2.98 ± 0.48, 0.24 ± 0.04, 110.19 ± 27.11, 1.82 ± 0.75, and 2.74 ± 1.18 g/kg dry biomass for CO_2, CH_4, N_2O, CO, and PM2.5, respectively. The total amount of biomass burned in the district was estimated as 499.8 thousand tons in scenario 1 and 456.2 thousand in scenarios 2 and 3. The total amount of biomass burned in the district was estimated as 166.5 thousand tons in scenario 4. Approximately, 51.66% of N and almost 99% of carbon is lost in the environment due to on-farm burning of sugarcane residue. The study revealed that the burning of sugarcane residue resulted in the release of a significant amount of GHGs and air pollutants into the atmosphere, resulting in global warming and poor air quality. The estimates of burnt area in the particular region once identified can be further used by policymakers to take the necessary measures, formulate alternate management solutions, and devise new policies to promote sustainable residue management practices.

Theme 2: Environmental Pollution/Waste Management

Phosphorus dynamics under different tillage and residue management practices in maize-wheat cropping system

In present study, soil samples were collected at various stages for different treatment of both maize and wheat crops at 0-5, 5-15 and 15-30 cm soil depth during 2018-19 and 2019-20. The result revealed that no tillage (NT) and crop residue mulch (CRM) treatment had significantly higher SOC at 0-5 and 5-15 cm soil depth in both crops. Dehydrogenase (DHA), acid phosphatase (ACP), and alkaline phosphatase (ALP) activities were significantly higher under NT and CRM treatments. The findings indicated that a higher amount of soluble and loosely-bound P (SL-P) was observed in the NT and CRM treatments among the inorganic P fractions. In contrast, iron-bound P (Fe-P), aluminium-bound P (Al-P), reductant soluble P (RES-P), and calcium-bound P (Ca-P) were higher under conventional tillage (CT) and no mulch treatments at 0-5 and 5-15 cm soil depth in both years. Among the organic (Po) fractions, labile Po, fulvic acid Po and residual Po were significantly increased under NT and CRM at 0-5 and 5-15 cm soil depth. In contrast HCl-associated Po and humic associated Po were insignificant in both years. Available P in soil and aggregates-associated available P were significantly increased under NT and CRM treatment at 0-5 and 5-15 cm soil depth during both years of experiment. Phosphorus fixation and adsorption were significantly higher under CT and no mulch treatment at 0-5 and 5-15 cm soil depth during both years of experiment. The grain and biomass yield of maize and wheat crops were found significantly higher under NT, CRM and 150% RDN level during both years of experiment. This study suggest that farmers can successfully adopt NT with 5 t ha^{-1} crop residue mulch with 150% RDN to attain better soil health and higher grain and biomass yield under the maize-wheat cropping system.

Preparation and performance analysis of bioplastics synthesized using titanium dioxide nanoparticles with corn cob

The study aimed to extract cellulose from corn cobs and prepare biodegradable plastics with the help of produced titanium dioxide nanoparticles. Bioplastics were made with a constant starch: cellulose ratio of 3:1, and several procedures like alkalization, exposure of fiber, and xanthation were done, and bioplastics with several compositions were prepared. FTIR, XRD, and SEM of cellulose and TiO_2 were performed to identify their functional groups, morphological characters, and crystal structure. Zetasizer was used to measure the particle size of the TiO_2 nanoparticles. Physical characteristics like bioplastic film thickness, density, moisture content, solubility, and tensile strength of the bioplastics films made with different ratios of cellulose: plasticizers: nanoparticles were measured, and two of the bioplastics which showed better results were taken for further analysis like FTIR, XRD, SEM, TGA, DTA, biodegradability. The FTIR, XRD, and SEM results of cellulose and TiO_2 confirmed the presence of functional groups of cellulose and TiO_2. The absorption bands in different wave numbers of FTIR spectra of cellulose and TiO_2, morphological analysis by obtained images through SEM, and the obtained peaks in the specific 2ɵ value in XRD analysis were compared with several other studies that got similar results. The bioplastic samples made with cellulose: plasticizers: nanoparticles ratio of 6:6:1 and 4:6:1 showed maximum tensile strength and better physical properties. In the thermogravimetric analysis, the ultimate residue after a breakdown is 17.73% for Sample B and 20.98% for Sample A, Bioplastics A, and B, with cellulose: plasticizers: nanoparticles ratios of 6:6:1 and 4:6:1, respectively, were analyzed for continuous biodegradation over 30 days. The findings indicate that plasticizers promote biodegradation, perhaps making bioplastic with the ratio 4:6:1 more ecologically friendly for breakdown and disposal.

Chitosan/ zeolite urea nanocomposite to improve nitrogen use efficiency in wheat

In the present study, the synthesis and application of Chitosan/zeolite Urea Nanocomposite on wheat crop and its effect on plant growth, nitrogen losses, and soil health will be studied. Chitosan-Urea NC and Zeolite-Urea NC were synthesized and characterized. The growth and yield parameters are high in the treatment T5 followed by T3. Result from this study is revealed that RAE of the Chitosan-Urea and Zeolite-Urea were 55% and 49% higher as compared to urea, respectively. The highest MBC was observed in the treatment with T3 (298mg/kg) followed by T2 (278mg/kg). The highest MBN was observed in the treatment with T3(17.4 mg/kg) followed by T7(15.3 mg/kg). The highest soil dehydrogenase activity was observed in the treatment T5(58 µg TPF /g of soil/h) followed by T3(56.64 58 µg TPF /g of soil/h). The highest soil urease activity was observed in the treatment with T6(52 mg urea /g of soil/h) followed by T7(49 mg urea /g of soil/h). The earthworm toxicity test was conducted as per the OECD guidelines for testing the eco-safety of the nano-fertilizers. The range of % survival of earthworms varied from 90% to 100% both at 7 days and 14 days. The 100 % survival of earthworms was observed in all the treatments with synthesized NC at 7 days. Both the synthesized Zeolite-Urea and Chitosan-Urea NC aid in the delayed release of nitrogen, ensuring that nitrogenous fertilizer given to the soil is used effectively. So, the application of Chitosan-Urea NC beads and Zeolite-Urea NC are eco-safe and efficient alternative to conventional urea.

Study on reactive nitrogen losses from tomato cultivation under open field and polyhouse condition

The present study, conducted from November 2023 to May 2024 at two experimental sites, viz. Polyhouse, Vegetable Science Division, and Open Field, Environmental Sciences Division, IARI, New Delhi, aims to quantify the reactive nitrogen losses from tomato cultivation under different nitrogen management practices in open field and polyhouse conditions. The key findings reveal that the bulk density of soil in the open field ranged from 1.43 to 1.45 g/cm³, while in the polyhouse, it ranged from 1.38 to 1.41 g/cm³. Biological activities, such as dehydrogenase and urease, were significantly higher in polyhouse soils, attributed to the controlled environment favouring microbial growth. Cumulative N_2O emissions were 21.22% higher in polyhouse cultivation than open field treatments, which indicates more significant greenhouse gas emissions under protected conditions. Ammonia volatilization was highest from T2 plots (RDF @ 120 kg N/ha) in both environments, with emissions being 30.7% greater in polyhouses. Moreover, NH_4^+ and NO_3^- leaching losses were recorded 12.93% and 14% higher, respectively, in open fields than in polyhouses, suggesting better nitrogen retention in polyhouse conditions. Overall, total reactive nitrogen losses were 24.03% higher in polyhouse cultivation. The study concludes that while polyhouse cultivation may lead to higher reactive nitrogen losses compared to open-field cultivation, it also provides a more controlled environment that can reduce certain forms of nitrogen loss and enhance crop yields. To maximize the benefits and minimize environmental impacts, careful management of nitrogen inputs is essential in polyhouse systems. This research offers valuable insights for farmers and policymakers aiming to balance agricultural productivity with environmental sustainability.

Isolation, characterization of biosurfactant and their effect on hydrocarbons' degradation in different soils

In present study, biosurfactant was optimized on the basis of surface tension and results showed that 27°C, 150 rpm, 72 h was optimum condition and minimum surface tension was achieved as 37.4 mN m^{-1}. Critical micellar concentration was recorded as 0.1 g L-1. 56.4-86.6% reduction in oil area showed the effectiveness of good dispersant. Fragmentation of oil into small droplets make biosurfactant as good option for providing oil as food substrate for microbes. With increase in temperature and addition of biosurfactant in oil-water emulsion leads to decrease in viscosity that leads to use its role as lubricant. Foaming (40-70%) indicates its role as detergent. Biosurfactant was found to be stable at different temperature (25, 35 and 45°C), salt concentration (0.5, 1, 3 and 5%) and pH (3, 5, 7, 9, 11). Surface tension and oil dispersion was almost stable till 24 h. An analytical method for detection and quantification of naphthalene (220 nm), fluorene (210 nm), Phenanthrene and pyrene (246 nm) were developed. The detection limit and quantification limit for all four PAHs varied from 0.086-0.094 and 0.26-0.29 mg L-1, respectively. Recovery of all 68 PAHs varied from 85.4-94.5% in Delhi soil and 82.3-98.1% in Jharkhand soil. Results showed that degradation followed the first order kinetics and degradation of PAHs mixture was faster in Delhi soil as compared to Jharkhand soil. Further, there was no much effect of double dose of biosurfactant on degradation. Among different formulations, soluble liquid (PSL2) based formulation was found to be effective for degradation of PAHs in soil. Isolated biosurfactant was tested against whitefly using leaf dip assay and median dose lethal mortality (LC50) was observed as 0.0437%. Metabolite profiling showed the abundance of Serinolamide A type of compounds.

Elevated temperature responsiveness of soybean genotypes

The present study, conducted at ICAR-NIASM, Baramati, aimed to evaluate the effects of elevated temperature on 15 soybean genotypes, including five control varieties (both tolerant and susceptible checks). The trial was designed to expose these genotypes to controlled (29°C) and elevated temperature conditions (35°C and 37°C) for seven days during the R1 stage (flowering). The results of the study showed significant differences in physiological, biochemical, and yield parameters between the genotypes when exposed to higher temperature. Genotypes EC-396067, PS-1024, RSC 10-52, and EC-389399 showed a higher relative water content (RWC), indicating a better ability to store water and a greater tolerance to heat stress. These genotypes also exhibited a greener canopy, higher membrane stability index (MSI) and improved photosynthetic efficiency, indicating their potential for sustained growth and productivity under elevated temperature. In addition, RSC 10-52 and EC-396067 showed increased proline content, an important Osmo protectant that supports plant resistance to heat stress. For yield parameters such as number of pods per plant, number of seeds per plant, and seed weight per plant, RSC 10-52 and EC-396067 performed better than the other genotypes under elevated temperature conditions, highlighting their resilience and potential for breeding programs. The results of the study suggest that RSC 10-52 and EC-396067 are particularly promising candidates for breeding programs focused on developing heat-tolerant soybean varieties. These genotypes have the potential to play critical role in future agricultural strategies by ensuring food security by maintaining soybean productivity in the face of rising temperature. This research underscores the importance of further investigating the specific responses of different genotypes to climate change. Such studies are crucial for the development of resilient crop varieties that can withstand the challenges of rising global temperature.

Nitrogen and water footprints of tomato cultivation under different irrigation and nitrogen management practices

A field experiment was conducted to quantify nitrogen losses, nitrogen foot print and water footprint from tomato under different irrigation and nitrogen treatments.The cumulative emission of N_2O was significantly higher in ridge & furrow (1.55 kg/ha) compared to DI (1.24kg/ha). Within ridge and furrow, furrow showed 47.9% reduction in N_2O emission. The seasonal accumulated flux of NH_3-N was 6.58kg/ha in ridge & furrow and 2.9kg/ha in DI. NH_3-N emission reduced by 81.3% in furrow compared to ridge. The seasonal accumulated flux of NH_3-N emission was maximum in farmers practice (9.07 kg/ha) and minimum in no N control treatment (0.20 kg/ha). DI showed negligible leaching losses of nitrate-N, ammoniacal-N and total mineral N from soil compared to ridge and furrow method. Leaching losses of nitrate N ranged from 0.04 to 1.68 kg/ha, ammoniacal N losses from 0.34 to 2.36 kg/ha, and total mineral N losses from 0.38 to 4.04 kg/ha under different N treatments. The average GWP of DI (329.6±24.8 kg CO_2 eq/ha) was significantly lower than ridge & furrow method (411.2±22.2 kg CO_2 eq/ha). The lycopene content ranged from 3.25 mg/100g to 5.61 mg/100g among different irrigation and N treatments. The Lycopene content was statistically at par in RDF and CF2 treatments. DI was able to reduce the nitrogen and water footprint by 68.55% and 43% compared to ridge & furrow method. RDF, CF1 and CF2 reduced N footprint by 28%, 35 % and 43%, respectively compared to farmer practice treatment. No N control showed highest green and blue water footprint 26.33 m3/t and 368 m3/t, respectively. Present study revealed that customized fertilizer 2 with drip irrigation can substantially lower nitrogen losses and thus N footprint and also water foot print.

Effect of microbial and non - microbial bio-stimulants for increasing the chickpea resilience to dry spell

Chickpea, a cool-season crop, often encounters higher temperatures and drought during its late life cycle, which negatively affects basic physiological processes, ultimately limiting yield levels (Rani et al., 2020). To address climate risks and mitigate abiotic stresses, the use of biostimulants has emerged as a promising, cost-effective, eco friendly, and productive approach. Biostimulants, which include substances or microorganisms of natural origin such as enzymes, proteins, amino acids, micronutrients, and other compounds, enhance crop conditions without causing harmful side effects, offering a sustainable solution for improving agricultural resilience. The study focused on the effect of the HFS complex and *T. asperellum* on chickpea physiological, biochemical, and yield attributes and was measured in phytotron and field conditions. In Phytotron and field experiments, eight treatments were followed (four treatments in irrigated and four in dry spell conditions). In Phytotron we gave 8 days' dry spell and 17 days in field condition. The results showed that the combination of *T. asperellum* and HFS complex consistently showed superior performance, enhancing germination, root length, and plant height in controlled environments. In field conditions, the combined treatment significantly increased plant growth, and physiological, and gas exchange parameters. The combination treatment also reduced oxidative stress markers such as proline content (32.5%) and superoxide dismutase (45%) activity, indicating improved dry spell tolerance. Biological yield increased by 13.6% under dry spell conditions which was highest in plots treated with both T. asperellum and HFS complex. Overall, the study suggests that combining microbial and non-microbial biostimulants significantly enhances chickpea resilience to dry spells, offering the potential for sustainable agricultural practices under climate stress conditions.

Impact assessment of plant biostimulant and phenolic compound for water stress mitigation in wheat crop

The global agriculture sector is increasingly challenged by climate change, particularly affecting wheat (*Triticum aestivum* L.), a crucial staple food. This study investigates the potential of seaweed extracts (SWE), phenolic compounds (PHC) and their combination for enhance the tolerance of wheat crop under water stress condition. Water stress, a major limiting factor for wheat production, triggers various physiological and biochemical changes leading to reduced yields. Drought affects critical growth stages, particularly flowering, and induces oxidative stress, resulting in lower grain yields. Conventional breeding methods face limitations in addressing multidimensional stress tolerance, making alternative strategies necessary. Biostimulants, such as microbial inoculants and plant extracts, offer promising solutions to improve plant resilience. This research explores the efficacy of SWE and PHC in mitigating water stress in wheat. Pomegranate peel extract, rich in phenolic compounds, was combined with SWE to evaluate its impact on plant growth and stress responses. Results indicate that the SWE+PHC combination significantly improved various growth parameters under both irrigated and water stressed conditions. Specifically, this combination increased plant height by 14.86% under irrigated conditions and 19.78% under water stress. Additionally, the number of tillers, dry weight, and grain yield were enhanced, with increases of up to 42.86%, 24.18%, and 65.7%, respectively, under optimal conditions. Under water stress, similar improvements were observed, with reductions in proline content and lipid peroxidation by up to 11.2% and 51.2%, respectively. Further, SWE+PHC treatment led to the highest membrane stability, total chlorophyll content. The combination also increased the number of spikes per hill, spike length, amylose content, protein content, and starch content. Overall, the SWE+PHC treatment mitigated the negative effects of water stress, providing significant improvements in wheat productivity and resilience.

Mapping of variation in soil organic carbon stock within IARI- Jharkhand farm

This study investigated SOC stock across different research blocks (A, B, C, D, E, F and N blocks) of IARI-Jharkhand farm along with key soil properties and their relationship with SOC stock. The study area showed significant topographical variation ($p < 0.001$) with elevation ranging from 388-406 m. Upland was present in A, B, D and F blocks of the farm while medium land was found in D, B and E blocks and lowland in N, C and E blocks. These differences in topography influenced SOC stock distribution across the studied blocks. The studied block showed significant variation in SOC stock ($p<0.001$). The total soil carbon stock (TSOCS) ranged from low SOC stock (3.19 g/ kg soil) to medium (5.32 g/kg soil) SOC stock. The SOC stock was found highest in Block-N (4.76 ± 0.32 g/kg soil) and lowest in Block A (3.82 ± 0.18 g/kg soil). The map developed by IDW interpolation clearly showed spatial variation in soil carbon stock within the study area with high SOC content in low laying area followed by medium and upland areas. Among all the extracted SOC fractions, the most labile fraction was found dominant (42-48%) in all the land form and research blocks. The TSOC stock was found significantly correlated with very labile, less labile and non-labile carbon along with land elevation, soil bulk density, available soil N content and soil pH at 0.01 significant levels. A strong negative correlation was found between SOC stock and bulk density (r = -0.772) and sand content while positive correlation (r = 0.097) was found between SOC stock and available nitrogen (r = 0.427 and clay content.

Theme 3: Ecosystem Services

Quantification of soil ecosystem service from Kole wetland: a coastal agrarian wetland in Kerala

The present study quantified some ecosystem services like paddy and straw production, nutrient cycling, soil erosion prevention, carbon sequestration, and ground water recharge from Kole wetland in Kerala. The economic value of paddy and straw production, nutrient cycling, soil erosion prevention, carbon sequestration, and groundwater recharge from Kole wetland was ₹1,82,228/ha, ₹17,243/ha, ₹29,913/ha, ₹10,833/ha and ₹19,2097/ha respectively. The total value of these ecosystem services from whole Kole wetland was found to be ₹552,63,04,448. Due to anthropogenic activities like unjudicial use of agrochemicals, nearby industries and domestic wastes resulted in entering of many heavy metals into Kole wetland. The mean concentration of the heavy metals in soils varied over a wide range, in the following decreasing sequence Fe > Zn > Cr > Mn > Cu > Cd > Pb. The accumulation of heavy metals in paddy was within the acceptable limits given by FAO/WHO, except for Cd and Cr, which showed greater contamination in all sites. The Cd and Zn concentration in irrigation water was higher than the WHO limit. The health risk associated with the contaminated paddy was estimated by calculating EF, TF, BAF, HRI, and HI. The enrichment factor of heavy metal was in the decreasing order of Cr>Zn>Cd>Cu>Fe>Mn>Pb. Translocation factor of heavy metal from root to shoot and shoot to grain revealed that Cd and Zinc having high TF. The HRI of heavy metals for adult and children was in the order of Cd > Zn > Cu > Cr> Pb. The HI of Cd, Cr, Pb, Cu, and Zn for adult and children was 0.87 and 0.81 respectively, indicating minor health risk. But heavy metal intake through paddy for longer period may cause health risk.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Rajdeep Das (21814)	M.Sc.	Preparation and performance analysis of bioplastics synthesized using titanium dioxide nanoparticles with corn cob	Dr. Renu Singh	ICAR-IARI, New Delhi
2.	Anjaly M. (21949)	M.Sc.	Quantification of soil ecosystem service from Kole wetland: a coastal agrarian wetland in Kerala	Dr. D. K. Sharma	ICAR-IARI, New Delhi
3.	Pavan Kalyan, (21978)	M.Sc.	Chitosan / Zeolite urea nanocomposite to improve nitrogen use efficiency in wheat	Dr. Manoj Shrivastava	ICAR-IARI, New Delhi
4.	Asmaul Hossain, (21812)	M.Sc.	Study on reactive nitrogen losses from tomato cultivation under open field and polyhouse condition	Dr. Sandeep Kumar	ICAR-IARI, New Delhi
5.	Ashwini Yadav (60124)	M.Sc.	Isolation, characterization of biosurfactant and their effect on hydrocarbons' degradation in different soils	Dr. Ashish Khandelwal	#ICAR-IARI Jharkhand
6.	Nisha Khatri (21950)	M.Sc.	Greenhouse gases and particulate matter emission due to sugarcane residue burning using measurements and remote sensing	Dr. Niveta Jain	ICAR-IARI, New Delhi

7.	Reenu Verma (70024)	M.Sc.	Elevated temperature responsiveness of soybean genotypes	Dr. Ajay K. Singh	**ICAR-NIASM, Baramati
8.	Ashwariya Laxmi (21913)	M.Sc.	Nitrogen and water footprints of tomato cultivation under different irrigation and nitrogen management practices	Dr. Niveta Jain	ICAR-IARI, New Delhi
9.	Anju Choudhary (21813)	M.Sc.	Effect of microbial and non - microbial bio-stimulants for increasing the chickpea resilience to dry spell	Dr. Anita Chaudhary	ICAR-IARI, New Delhi
10.	Arun Meena (21815)	M.Sc.	Impact assessment of plant biostimulant and phenolic compound for water stress mitigation in wheat crop	Dr. Anita Chaudhary	ICAR-IARI, New Delhi
11.	Ramakrishna Panda (60131)	M.Sc.	Mapping of variation in soil organic carbon stock within IARI- Jharkhand farm	Dr. Dipak K. Gupta	#ICAR-IARI Jharkhand
12.	Ankita Paul (11024)	Ph.D.	Effectiveness of modified urea fertilizers in reducing ammonia and nitrous oxide losses and increasing the nitrogen use efficiency in rice	Dr. Arti Bhatia	ICAR-IARI, New Delhi
13.	Shravani Sanyal (11491)	Ph.D.	Field and simulation studies on the interactive effect of elevated carbon dioxide and temperature on aestivum and durum wheat	Dr. Bidisha Chakrabarti	ICAR-IARI, New Delhi
14.	Alesh Kumar (11025)	Ph.D.	Phosphorus dynamics under different tillage and residue management practices in maize-wheat cropping system	Dr. Manoj Shrivastava	ICAR-IARI, New Delhi
15.	Helen Mary Rose (11026)	Ph.D.	Life cycle assessment of maize and wheat products	Dr. Niveta Jain	ICAR-IARI, New Delhi

 # IARI off-campus
***Outreach institute*

MICROBIOLOGY

12

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

Insights into the genome of extreme Halophilic Archaea: Prospecting agriculturally important (salinity tolerance) genes

This study investigated the potential of halophilic archaea from the Rann of Kutch to alleviate salinity stress in wheat. These archaea, tolerant to up to 4.5 M salinity, possess plant growth-promoting traits, solubilizing phosphorus (14-61 mg L-1), potassium (37-78 mg L-1), and zinc (8-17 mg L-1), and producing IAA (17.30 to 49.3 µg mL-1). Five wheat cultivars (two salt-tolerant, three salt-susceptible) were grown in 8 dSm-1 EC soil. Halophilic archaea inoculation significantly increased wheat protein (46%), sugar (27%), and chlorophyll (31%) levels. It also enhanced proline (31.51%) and total carbohydrate (27.85%) accumulation, while reducing antioxidant enzyme activity (SOD, catalase, peroxidase by 57-76%). Growth improvements were more pronounced in susceptible cultivars. To understand the mechanisms behind salt tolerance, a differential gene expression analysis of *H. pelagica* CDK2 was conducted under 8% and 26% NaCl, revealing 406 genes with altered expression. At high salt (26% NaCl), the archaeon upregulates genes for transport of amino acids, potassium, and glycine betaine, helping maintain cellular balance. It also increases expression of genes for stress response, specifically universal stress proteins, which aid in coping with challenging conditions, as well as genes for energy and metabolism necessary for functioning in a high-salt environment. At low salt (8% NaCl), *H. pelagica* CDK2 increases expression of detoxification genes, namely ATPases that remove heavy metals, which can become more toxic in low salt conditions. In silico analysis of the differentially expressed genes provided further insights into the proteins they encode, including protein properties like size, charge, and stability in the intracellular environment; protein function, such as roles in transport, catalysis, and other cellular processes; and protein interactions, identifying partnerships that contribute to overall cellular function. This combined transcriptomic and in silico approach revealed the complex strategies employed by *H. pelagica* CDK2 to thrive in varying salt concentrations. These findings highlight its potential for developing microbial inoculants to improve crop growth in saline soils. The identified genes, such as those involved in transport and stress response, may also be valuable targets for future genetic engineering efforts aimed at enhancing salt tolerance in crops.

Interactive effect of water-deficit stress and osmotolerant bacteria on nutrient uptake and biomass accumulation in mustard

Drought is a major environmental constraint limiting mustard production globally, negatively impacting critical growth stages and yield. This study investigated the potential of the osmotolerant bacterium *Bacillus sp.* strain MRD-17 to enhance mustard growth and nutrient uptake under water-deficit conditions. The research employed a multi-faceted approach, encompassing hydroponic experiments to assess seedling responses and pot experiments to evaluate whole-plant performance under drought stress.Hydroponic studies revealed that MRD-17 inoculation significantly improved seedling growth, root architecture, and nutrient uptake in both drought-sensitive and tolerant mustard varieties subjected to osmotic stress induced by polyethylene glycol (PEG). The bacterium's beneficial effects were particularly pronounced under combined osmotic and nutrient stress, highlighting its ability to alleviate the detrimental impacts of multiple stressors. Furthermore, MRD-17 inoculation enhanced the accumulation of osmolytes and antioxidant enzymes, contributing to improved stress tolerance in mustard seedlings.Interestingly, even bacterial volatile organic compounds (VOCs) released by MRD-17 positively influenced seedling growth and physiological attributes under stress conditions. VOCs exposure led to increased seedling biomass, enhanced root development, and improved osmotic adjustment, suggesting a novel mechanism through which beneficial bacteria can promote plant growth.Pot experiments further confirmed the positive effects of MRD-17 inoculation on mustard performance under drought stress. Drought significantly reduced plant growth, photosynthetic capacity, and yield, while increasing stress indicators like proline and antioxidant enzyme activity. However, MRD-17 inoculation mitigated these negative impacts, leading to improved plant water status, nutrient uptake, and ultimately, higher seed yield. The bacterium's beneficial effects were attributed to its ability to enhance root growth, improve nutrient acquisition, and alleviate oxidative stress. This study provides compelling evidence that *Bacillus sp.* strain MRD-17 can effectively enhance mustard growth and productivity under water-limited conditions. The bacterium's ability to improve nutrient uptake, promote stress tolerance, and mitigate drought-induced yield losses highlights its potential as a valuable tool for sustainable agriculture in arid and semi-arid regions. Further research is warranted to explore the underlying mechanisms of MRD-17's beneficial effects and to evaluate its efficacy under field conditions

Theme 2: Plant-Microbe Interaction for Crop Growth Promotion

Developing synthetic microbials (SMs) based novel biostimulants for improved crop growth and nutrient use efficiency

This study explored the potential of synthetic microbial communities (SMs) as novel biostimulants to improve crop growth and nutrient use efficiency. The research focused on harnessing beneficial plant-microbe interactions, such as nitrogen fixation and phosphorus solubilization, to enhance crop nutrition. From a pool of microbial isolates, those exhibiting significant plant growth-promoting traits (PGPts) and community-forming traits (CFts) were selected. These isolates demonstrated diverse capabilities, including nitrogen fixation (1.43 to 9.16 µmol of ethylene mg protein^{-1} hr^{-1}), phosphorus solubilization, potassium solubilization, zinc and calcium solubilization, and phytohormone production (IAA and GA3). Additionally, isolates displayed biocontrol traits like siderophore production, HCN, ammonia production, and antagonistic activity.Synthetic microbial communities were constructed based on genomic data and abundance, with key genera including *Klebsiella varicola*, *Enterobacter cloacae*, *Stenotrophomonas sp.*, *Pseudomonas sp.*, and various *Bacillus* species. Isolates were combined based on positive interactions, demonstrated by enhanced growth, biofilm formation, and EPS production facilitated by quorum sensing. This led to the development of three core communities: SM1 (PGPt isolates), SM2 (CFt isolates), and SM3 (both PGPt and CFt isolates). A fourth community, SM4, included isolates with both types of traits but lower abundance based on genomic data.These SMs were then integrated with non-microbial biostimulants, humic acid (HA) at 0.2% and seaweed extract (SWE) at 1%, to create SynBio formulations. Under controlled conditions, SMs and SynBio formulations significantly improved plant growth parameters, with SM3+HA showing the greatest increase in shoot length (24.43 to 46.97 cm), root length, flag leaf length, and plant dry matter (432.64 mg/plant). Gene expression analysis revealed upregulation of nutrient transporter genes in SynBio-treated plants.Field experiments further validated the positive effects on wheat productivity. SM and SynBio treatments significantly increased shoot length, flag leaf length, productive tillers, earhead length, plant dry matter, and chlorophyll content. SM3+HA consistently showed the greatest improvements, leading to a 56.83% increase in seed yield compared to the uninoculated control. Metagenome analysis of rhizospheric soil indicated shifts in microbial diversity with the application of SMs.This study highlights the potential of synthetic microbial communities combined with non-microbial biostimulants as a sustainable approach to enhance plant growth, nutrient uptake, and soil health, ultimately leading to significant increases in crop productivity.

Development and evaluation of cyanobacterial formulations for nutri-fertigation of vegetable crops

This study investigated the potential of cyanobacteria as biofertilizers for vegetable crops, particularly focusing on their use in nutri-fertigation strategies for protected cultivation. A set of cyanobacterial strains were screened for plant growth-promoting and bio-fertilizing attributes, and their metabolite profiles were analysed using GC-MS. The analysis revealed a predominance of beneficial organic compounds, including sugars, amino acids, and their conjugates, highlighting the cyanobacteria's role in carbon and nitrogen enrichment. To evaluate their effects on vegetable crops, cyanobacterial culture extracts were used to prime seeds and raise seedlings of tomato and spinach varieties. Tomato varieties NS2533 and NS4266 showed superior performance, while Pusa All green spinach responded better than Mulayam, exhibiting 15-20% higher seedling trait values. Further experiments focused on the application of formulations from promising cyanobacteria – *Anabaena laxa* (C11), *Nostoc carneum* (BF2), and *Anabaena doliolum* (BF4). Soil drench application at pre-flowering and fruiting stages significantly improved growth, productivity, and fruit quality in tomato variety NS4266 under protected cultivation. In spinach, seed coating and soil drenching with a mix of *Anabaena laxa* C11, *Nostoc carneum* BF2, and *Anabaena laxa* RPAN8 enhanced yield and quality traits, including ascorbic acid, β-carotene, and leaf iron content. Path coefficient analysis revealed positive correlations between these traits and available nitrogen, PEPCase activity, nitrate reductase activity, chlorophyll a, carotenoids, and leaf area. To assess their potential as biopriming agents, spinach seeds coated with individual cyanobacterial formulations were stored for twelve months. Coated seeds demonstrated significantly higher germination indices, fresh/dry weight, leaf enzymatic activities, and micronutrient content, with *Anabaena laxa* C11 and *Anabaena laxa* (RPAN8) showing the most consistent and robust performance. This study demonstrates the potential of cyanobacterial formulations as valuable and resource-efficient biofertilizers for vegetable crops. Their ability to enhance plant growth, yield, and quality, along with their positive impact on soil health and nutrient availability, makes them a promising tool for sustainable agriculture, particularly in protected cultivation systems.

Analyses of the nutrient mobilization potential of cyanobacteria and their biofilms in maize (*Zea mays* L.)

This study investigated the potential of cyanobacteria-based bioinoculants to improve maize growth and nutrient use efficiency, specifically under varying water availability. A consortium of four nitrogen-fixing cyanobacteria (BF1-4), consisting of *Anabaena torulosa*, *Nostoc carneum*, *Nostoc piscinale*, and *Anabaena doliolum*, and a novel cyanobacteria-fungal biofilm (An–Tr) composed of *Anabaena torulosa* and *Trichoderma viride* were tested on two elite maize genotypes, V6 (HKI323PV) and V7 (HKI161PV), known to require high doses of chemical fertilizers. Preliminary studies on the An–Tr biofilm cultures revealed significant increases in chlorophyll content, indole-3-acetic acid (IAA) production, exopolysaccharides (EPS), and glomalin-related soil proteins (GRSP), indicating enhanced growth promotion potential. Nitrogenase activity also improved markedly in the An–Tr biofilm cultures, suggesting more efficient nitrogen fixation, while elevated glutamine synthetase (GS) and nitrate reductase (NR) activities pointed to stimulated nitrogen assimilation pathways.The bioinoculants were evaluated through a series of pot, mesocosm, and field experiments under both moisture-sufficient and deficit conditions (75% and 50% water holding capacity, respectively) to simulate moderate and severe moisture stress at both seedling and flowering stages. Comprehensive physiological, biochemical, microbiological, and molecular assessments were conducted to capture a holistic understanding of the cyanobacteria/biofilm's impact on maize. Results illustrated enhanced yields and a 25% reduction in nitrogen fertilizer requirements.In both controlled mesocosms and field conditions, maize plants treated with BF1-4 and An–Tr displayed superior germination rates, enhanced root and shoot growth, and increased biomass accumulation, even under water-limited conditions. Elevated microbial biomass carbon and dehydrogenase activity in the rhizosphere of biofilm-inoculated plants indicated improved nutrient availability, fostering an environment conducive to sustained plant growth. Phospholipid fatty acid (PLFA) analysis revealed shifts in microbial community structure towards beneficial groups, including arbuscular mycorrhizal fungi and Gram-negative bacteria. Principal component analysis (PCA) further highlighted important relationships between soil biochemical parameters and plant nutrient attributes, such as nitrogen and micronutrient levels.The expression patterns of key nitrogen assimilation genes, *ZmGOGAT1* and *ZmGS1;1*, were analysed using real-time PCR to evaluate their transcriptional responses under different bioinoculant treatments and plant developmental stages. Differential upregulation of these genes was observed across roots, shoots, and reproductive tissues. Notably, at flowering, the An–Tr biofilm significantly enhanced shoot-level nitrogen metabolism, signifying a tissue- and stage-specific effect.In summary, merging *Anabaena torulosa* and *Trichoderma viride* into a biofilm yielded synergistic effects, leading to more effective plant–microbe interactions, improved plant vigor, and enhanced drought tolerance. This approach offers a sustainable agricultural option for reducing chemical inputs, enhancing soil fertility, and developing stress-resilient cropping systems.

Prospecting exopolysaccharides for plant growth stimulation

This study explored the potential of exopolysaccharides (EPS) produced by plant-associated bacteria to stimulate crop growth. EPS are natural polymers with diverse biological activities that can benefit plant health and productivity.Initially, 86 bacterial strains isolated from pearl millet seeds were screened for EPS production. Promising strains were then evaluated for their effects on wheat germination and seedling growth. Inoculation with selected strains significantly enhanced seed germination rates and vigor indices, indicating their potential as biostimulants. Further analysis revealed that EPS extracted from these strains had a direct growth-promoting effect on wheat seedlings.The study also investigated the influence of EPS concentration and bacterial growth conditions on EPS production and efficacy. Optimal EPS production varied among strains, highlighting the importance of strain-specific optimization strategies. Characterization of the EPS revealed diverse structural and functional properties, including water absorption capacity and antioxidant activity.Overall, this research demonstrated the potential of EPS-producing bacteria as sustainable biostimulants for enhancing crop growth. The identified strains, *Atlantibacter hermannii* MPT27, *Bacillus subtilis* subsp. *subtilis* PC7N47, and *Bacillus subtilis* subsp. *subtilis* PC7T5, showed promising plant growth-promoting activities and represent valuable candidates for further development as biofertilizers or biopesticides. This study contributes to the growing body of knowledge on the application of microbial metabolites in sustainable agriculture, offering eco-friendly alternatives to conventional chemical inputs.

Bio-stimulant assisted mycorrhizal donor plant in vitro culture system for enhanced colonization and efficacy

This study developed an efficient in vitro system for producing arbuscular mycorrhizal fungi (AMF) inoculum using tomato plants as hosts (Mycorrhizal Donor Plants, MDPs). The system fostered AMF colonization and extraradical mycelium growth under autotrophic conditions, with plant shoots photosynthesizing under high light and roots colonized by AMF in the dark. A modified M solution (mMS-1) lacking sucrose, vitamins, and agar was used.Effective surface sterilization of inoculum was achieved using Chloramine T/Tween 20 and streptomycin sulfate. Dual inoculation with AMF spores and root inoculum maximized root colonization and growth. Molecular analysis confirmed the presence of the target AMF species, and trap cultures validated inoculum efficacy. Phytohormone application enhanced colonization, with a combination of auxin and cytokinin, particularly BAP at 2 mg/L, proving most effective. Among phenolic compounds tested, catechin increased colonization, while flavonoids like apigenin, genistein, and rutin stimulated colonization at low concentrations.Combining phytohormones and secondary metabolites further improved colonization and biomass. The in vitro system yielded a high abundance of infective propagules (3300 per gram of MDP product). This novel method efficiently produces AMF inoculum for biofertilizer applications, confirmed by successful re-infection of indicator plants in a polyhouse setting.

Biocontrol potential of AMF associated bacteria against common root rot in wheat

This study investigates the biocontrol potential of bacteria associated with arbuscular mycorrhizal fungi (AMF) against common root rot in wheat, a disease caused by *Bipolaris sorokiniana*.Out of 29 bacterial isolates initially screened for the irantimicrobial activity,three isolates—SS13, SS17, and SS20—demonstrated significant pathogen inhibition, with inhibition rates of 62.50%, 53.15%, and 46.85%, respectively. These isolates were further assessed for their defensive mechanisms, including the production of siderophores, hydrogen cyanide (HCN), and lytic enzymes like cellulase and chitinase. Microscopic observations revealed the disruption of *B.sorokiniana* mycelia following treatment with crude extracts from these bacterial isolates, indicating their strong antifungal activity. Additionally, antioxidant enzyme activities in the pathogen were significantly reduced. Pot trials further confirmed the efficacy of these isolates, with SS13 showing the highest control efficacy, reducing disease incidence by68.34%. A subsequent trial demonstrated that co-inoculation of SS13 with AMF not only enhanced disease control efficacy to 72.75% but also significantly improved root architecture and overall plant biomass, highlighting the synergistic benefits of combining AMF with biocontrol bacteria. This study concludes that the integration of AMF with the SS13 represents a potent biological control strategy against *Bipolaris sorokiniana*-induced common root rot in wheat. The dual inoculation approach offers an eco-friendly and sustainable alternative to conventional chemical treatments, promoting healthier crops, enhanced resistance to pathogens, and improved agricultural productivity.

Theme 3: Bioprospecting Microorganisms for Value Added Products, C-sequestration and Bioremediation

Co-digestion of paddy straw and wastewater grown microalgae and assessment of its manurial potential in rice crop

This study explored the potential of integrating microalgal cultivation with agricultural wastewater treatment and anaerobic co-digestion for biofuel production and nutrient recycling. Nine microalgal species were screened for their biomolecule production and phyco remediation capacity in agricultural wastewater. *Coelastrella* sp., *Desmodesmus* sp., and *Phormidium* sp. exhibited the highest potential, effectively reducing wastewater pollutants (EC, BOD, COD, nitrate, ammoniacal-N, phosphate, TDS, and TSS) while increasing pH and dissolved oxygen. Optimal growth and phyco remediation were achieved at a 10% inoculation rate in undiluted wastewater.To address the low carbon-to-nitrogen (C/N) ratio of microalgal biomass for anaerobic digestion, paddy straw was used as a co-substrate. Co-digestion of microalgae and paddy straw significantly enhanced methane yield compared to mono-digestion.The resulting digestate, rich in nitrogen, phosphorus, and potassium, was evaluated for its manurial potential in a rice crop pot experiment. Application of digestate at 25% of the recommended fertilizer dose, in combination with 75% chemical fertilizer, resulted in comparable or superior rice growth and soil quality compared to the sole use of chemical fertilizer.This integrated approach demonstrates the potential of cultivating microalgae in agricultural wastewater for bioremediation and biomass production. Co-digestion of microalgal biomass with paddy straw enhances biogas production and generates nutrient-rich digestate, offering a sustainable strategy for waste valorization and nutrient recycling in agriculture.

Process optimization for enhanced biomass and lipid accumulation using *Dunaliella tertiolecta* for exploring biodiesel potential

The commercial cultivation of microalgae is rapidly expanding due to their diverse biotechnological and industrial applications. *Dunaliella tertiolecta*, a halotolerant green microalga, is widely cultivated for biodiesel and carotenoid production. This study investigated growth rate and lipid productivity in *D. tertiolecta* using metabolic engineering and cultivation temperature optimization, employing a one-variable-at-a-time (OVAT) approach.Optimized nutrient concentrations (0.32 g/L KNO_3, 0.2 g/L KH_2PO_4) and sea salt (36.5 g/L), coupled with a cultivation temperature of 28 ºC, yielded maximum growth and lipid productivity of 11.52 mg/L/d and 15.33 mg/L/d, respectively. To reduce costs, the conventional nutrients were replaced with the fertilizer Suphala, resulting in a biomass production of 1127.43 µg/ml, a lipid content of 18.10%, and a lipid productivity of 14.58 mg/L/d.Response surface methodology (RSM) was further employed to optimize the nutrient media for enhanced biomass and lipid production. Central composite design (CCD) identified sea salt stress and NPK fertilizer as key factors influencing biomass, lipid, and carotenoid production. The RSM model demonstrated strong predictive capability (R^2 values of 0.9999, 0.9993, and 0.9593 for biomass, lipid, and carotenoid production, respectively).Overall, optimization resulted in a 15.20% increase in lipid production, with a notable increase in palmitic and linolenic acids. Additionally, the optimized conditions led to the production of myristic, stearic, and oleic acids. Extra polymeric substances (EPS) and poly-β-hydroxybutyrate (PHB) were also produced at 77 µg/ml and 6.21 µg/mL, respectively.Techno-economic analysis indicates the potential for economically viable biofuel production from *D. tertiolecta*, particularly when integrated with the production of carotenoids, EPS, and PHB in a biorefinery model.

Phyllosphere methylotrophs of major cereals and pulse crops as a source of recalcitrant soil carbon

Microbial methane oxidation by plant-associated microorganisms is crucial for reducing atmospheric methane from agriculture. This study investigated the potential of methylotrophs (methane-consuming bacteria) living on plant leaves (phyllosphere) to convert methane into microbial necromass (dead microbial cells) and contribute to soil carbon storage. Total of 26 methylotrophic communities from different crop plants were analysed and found significant variations in their ability to utilize methane-derived carbon. The resulting necromass was characterized by spectrophotometric and FTIR analysis. The E4/E6 ratio ranged from 5.48-2.42 and the presence of functional groups reported in spectral studies are a broad band at 3600–3200 cm^{-1} corresponding to H-bonded OH groups of alcohols, phenols and organic acids, as well as H bonded N-H groups are peaks at 2800–3000 cm^{-1} indicated the high degree of homology of necromass carbon with that of the soil humic substances. The observed E4/E6 ratio indicated a highly degree of aromatic and condensed carbon biomolecules presents in the necromass, similar to soil humic substances, indicating its potential for long-term stability in soil.In a soil experiment, adding this necromass increased microbial biomass carbon content over the control by ranging from 189.02-2963 µg/gm of soil. Walkley Black carbon increased by 1.078% - 0.123%; phenol oxidase activity increased (8.7-0.88 µmol/gm of soil) as compared to control soil not receiving phyllosphere methylotrophs microbial communities. Input of necromass derived PMMC from the different crop species in the soil mesocosm experiment resulted in significant gain in Soil Microbial Biomass Carbon (SMBC) ranges from 436.77%-65.7%; Phenol oxidase activity (POX) 691.3%-19.70% compared to unamended; Walkley Black carbon 1.078%-0.123 % but a significant decline was noticed in the β-glucosidase activity reduced 46.6% over the control not receiving necromass carbon.This study highlights the dual role of phyllosphere methylotrophs: mitigating methane emissions and contributing to soil carbon sequestration by forming stable necromass. This finding suggests a potential strategy for enhancing soil health and climate change mitigation by promoting these microbial communities.

Standardizing process for bioethanol production from corn stover using both hemicellulosic and cellulosic fractions

The escalating global energy crisis and climate change necessitate a transition to renewable energy sources. Lignocellulosic biomass, such as corn stover, presents a sustainable alternative for bioethanol production.This study focuses on standardizing a process for bioethanol production from corn stover, utilizing both hemicellulosic and cellulosic fractions.A sequential pretreatment method was employed, involving alkaline treatment followed by acid treatment. This approach enriched the glucan content to 75-80% while recovering 50% lignin from the alkaline extracts. Despite significant dry matter loss (42.5-50%), the process yielded acid hydrolysates containing 0.9-1% xylose. Subsequent saccharification achieved 85-90% efficiency, generating concentrated sugar syrups with ~7% total reducing sugars. Fermentation using *Candida tropicalis* and *Saccharomyces cerevisiae* resulted in complete glucose conversion and ethanol yields up to 2.66%.This study demonstrates the potential of sequential alkali-acid pretreatment for efficient fractionation of corn stover, enhancing cellulose enrichment and bioethanol yields. The results highlight the viability of corn stover as a sustainable feedstock for biofuel production, contributing to energy security, agricultural sustainability, and greenhouse gas mitigation efforts.

Strain identification and characterization of exopolysaccharides producing cyanobacteria

This study focused on the identification and characterization of exopolysaccharide (EPS)-producing cyanobacteria. Ten strains of *Nostoc* and *Anabaena* with high EPS production potential were selected from the CCUBGA culture collection at ICAR-IARI, New Delhi. A promising strain, based on EPS accumulation at 15 and 30 days of growth, was further investigated under varying light quality, light intensity, and magnesium sulfate ($MgSO_4$) and calcium sulfate ($CaSO_4$) concentrations.Red light significantly enhanced carbohydrate and protein content at both 15 and 30 days of growth, while uronic acid content was maximized under white and red light, respectively. Optimal light intensity for EPS production was 5400 lux. Maximum EPS synthesis occurred at 0.1 g/L $MgSO_4$, with the highest carbohydrate, protein, and uronic acid content observed at 0.15 g/L $MgSO_4$. Increasing $MgSO_4$ concentration beyond the recommended level in BG-11 medium further enhanced EPS yield. Peak bioflocculation activity was observed at 0.072 g/L $CaSO_4$ at 15 days and 0.1 g/L $CaSO_4$ at 30 days.This study identified a promising *Anabaena* sp. strain capable of high EPS production. Furthermore, it demonstrated the influence of environmental and nutritional factors on EPS yield. This strain holds potential for scaled-up EPS production for applications in agriculture, pharmaceuticals, and cosmetics.

Understanding the response of cyanobacterial biofertilizer strains to Atrazine

This study investigated the impact of the herbicide atrazine on four cyanobacterial strains (*Nostoc muscorum*, *Tolypothrix tenuis*, *Anabaena variabilis*, and *Aulosirafertilissima*) individually and in consortia. Physiological, biochemical, and ecological responses were evaluated across varying atrazine concentrations (0.5, 1.0, and 2.0 mg L^{-1}). At low concentrations (0.5 mg L^{-1}), cyanobacteria exhibited adaptive responses, including increased carotenoid production, enhanced antioxidant enzyme activity (catalase and SOD), and improved metabolic function, although species-specific differences were observed. Higher atrazine concentrations (2.0 mg L^{-1}) induced oxidative stress, inhibiting growth, pigment synthesis, enzymatic activities, and overall metabolic performance. Variations in antioxidant activities and indole-3-acetic acid (IAA) production among strains and consortia resulted in differential responses to atrazine exposure.Atrazine removal efficiency varied among strains, with *Anabaena variabilis* and cyanobacterial consortia exhibiting the highest removal rates. Soil-based experiments demonstrated that cyanobacterial inoculation mitigated atrazine toxicity by enhancing soil enzymatic activities (urease, dehydrogenase, and alkaline phosphatase), nutrient cycling, and wheat crop growth.Combined atrazine and cyanobacteria treatments further improved plant height, seed vigor, and soil health compared to atrazine alone.This study highlights the dose-dependent effects of atrazine on cyanobacteria, with lower concentrations triggering adaptive mechanisms and higher concentrations causing physiological and ecological suppression. Cyanobacterial consortia demonstrated significant potential for atrazine bioremediation, promoting soil and crop health. These findings underscore the potential of cyanobacteria as sustainable biofertilizers for managing herbicide contamination in agricultural systems.

List of contributing students and Chairpersons of their advisory committee

S. No	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Ujwalgowda H S (21940)	M.Sc.	Standardizing process for bioethanol production from corn stover using both hemicellulosic and cellulosic fractions	Ms. Anju Arora	ICAR-IARI, New Delhi
2.	Kamali R (21904)	M.Sc.	Prospecting exopolysaccharides for plant growth stimulation	Dr. Minakshi Grover	ICAR-IARI, New Delhi
3.	Abhijit Pal (21927)	M.Sc.	Bio-stimulant assisted mycorrhizal donor plant in vitro culture system for enhanced colonization and efficacy	Dr. Subrata Nath Bhowmik	ICAR-IARI, New Delhi
4.	Sarthak Patil (21905)	M.Sc.	Strain identification and characterization of exopolysaccharides producing cyanobacteria	Dr. Onkar Nath Tiwari	ICAR-IARI, New Delhi
5.	Balamurgan N (21791)	M.Sc.	Phyllosphere methylotrophs of major cereals and pulse crops as a source of recalcitrant soil carbon	Dr. Geeta Singh	ICAR-IARI, New Delhi
6.	Prajwal K H (21906)	M.Sc.	Understanding the response of cyanobacterial biofertilizer strains to Atrazine	Dr. Pranita Jaiswal	ICAR-IARI, New Delhi
7.	Deepak (21941)	M.Sc.	Biocontrol potential of AMF associated bacteria against common root rot in wheat	Dr. Seema Sangwan	ICAR-IARI, New Delhi

8.	Mayur Giridhar Naitam (11061)	Ph.D.	Insights into the genome of extreme Halophilic Archaea: Prospecting agriculturally important (salinity tolerance) genes	Dr. Rajeev Kaushik	ICAR-IARI, New Delhi
9.	Lavanya A K (11062)	Ph.D.	Interactive effect of water-deficit stress and osmotolerant bacteria on nutrient uptake and biomass accumulation in mustard	Dr. Sangeeta Paul	ICAR-IARI, New Delhi
10.	Vikas Sharma (11064)	Ph.D.	Analyses of the nutrient mobilization potential of cyanobacteria and their biofilms in maize (*Zea mays* L.)	Dr. Radha Prasanna	ICAR-IARI, New Delhi
11.	Anil Kumar (11286)	Ph.D.	Process optimization for enhanced biomass and lipid accumulation using *Dunaliella tertiolecta* for exploring biodiesel potential	Dr. Sunil Pabbi	ICAR-IARI, New Delhi
12.	Krutika Patil (11541)	Ph.D.	Co-digestion of paddy straw and wastewater grown microalgae and assessment of its manurial potential in rice crop	Dr. Sunil Pabbi	ICAR-IARI, New Delhi
13.	Devashish Pathak (11812)	Ph.D.	Developing synthetic microbials (SMs) based novel biostimulants for improved crop growth and nutrient use efficiency	Dr. Archana Suman	ICAR-IARI, New Delhi
14.	Nivedha R M (11814)	Ph.D.	Development and evaluation of cyanobacterial formulations for nutri-fertigation of vegetable crops	Dr. Radha Prasanna	ICAR-IARI, New Delhi

SOIL SCIENCE AND AGRICULTURAL CHEMISTRY

13

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; soil test crop response correlation studies; advice to the farmers on soil test-based fertilizer recommendations. Since its existence, it has made outstanding contributions both of theoretical and practical value in many fields extending over the various aspects of soil science and agricultural chemistry. The post graduate research findings have been grouped under various themes as under:

Theme 1: Synthesis and Evaluation of Novel Fertilizer Products

Evaluation of urea loaded nano-clay biopolymer composites and biosolubilizers for enhancing nutrient availability and nitrogen use efficiency in rice and wheat

Nitrogen (N) is essential for plant growth, but its inefficient use in agricultural systems, particularly in rice-wheat cropping systems (RWCS) in India, causes environmental issues like nitrate leaching and greenhouse gas emissions. Conventional fertilizers, especially urea, have poor utilization efficiency, with only 30-65% of applied N being absorbed. Slow-release fertilizers (SRFs) and controlled-release fertilizers (CRFs), such as nano-clay biopolymer composites (NCBPC), offer a solution by optimizing N release. This study evaluated the potential of NCBPC in conjunction with biosolubilizers to enhance nitrogen use efficiency (NUE) and nutrient availability in RWCS.NCBPC was synthesized and characterized using XRD, FTIR, and SEM, confirming its exfoliated structure and slow-release properties. Incubation studies under different soil types and moisture conditions showed gradual nitrogen release. A greenhouse experiment in rice and wheat with 10 treatments, including 75% N from NCBPC in conjunction with biosolubilizers for phosphorus (P), zinc (Zn), and iron (Fe), was conducted alongside control treatments and recommended fertilizer doses. Results indicated that NCBPC, especially with triple biosolubilizers, significantly improved agronomic parameters like plant height, tiller number, grain yield, and root biomass in rice and wheat compared to conventional fertilizers. Nutrient concentrations of N, P, Zn, and Fe, as well as chlorophyll content, were higher. Agronomic nitrogen use efficiency and apparent N recovery efficiency improved significantly, reaching 17.77 g/g and 58.76% in rice, and 21.80 g/g and 68.61% in wheat. Post-harvest soil analysis showed increased levels of available P, Zn, Fe, microbial biomass carbon, and dehydrogenase activity. These findings suggest that NCBPC with biosolubilizers is a sustainable alternative to conventional fertilizers, improving productivity and minimizing nitrogen losses in RWCS.

Effect of urea and nitrification inhibitors loaded nanoclay biopolymer composite on nitrogen use efficiency in maize-wheat cropping system

Nitrogen (N) is a vital nutrient for plant growth, influencing crop yield and quality as a key component of chlorophyll, amino acids, and nucleic acids. While N fertilizers are essential for food grain production, only 30–50% of applied nitrogen is utilized by plants, leading to significant losses. These inefficiencies contribute to environmental issues, such as nitrate leaching, eutrophication, ammonia volatilization, groundwater contamination, and nitrous oxide emissions, collectively creating a nitrogen cascade. To address these challenges, a nanoclay biopolymer composite (NCBPC) was developed as a sustainable fertilizer alternative to improve nitrogen use efficiency (NUE). The NCBPC was synthesized using acrylic acid and maize flour, with 20% acrylamide monomer substitution and nano-bentonite served as a diffusion barrier. Free radical polymerization, crosslinking agents, and nitrification inhibitors (DCD and Schiff bases) enhanced its properties. Characterization using FTIR, XRD and SEM confirmed successful polymerization and nanoscale dispersion of bentonite layers. Field trials on maize and wheat were conducted to compare NCBPC (at 0%, 50%, 75%and 100% of the recommended 150 kg ha^{-1} dose) with conventional urea. Results showed that NCBPC with 75% N and 3% DCD improved soil nitrogen retention, sustaining higher ammonium levels while reducing nitrate leaching. This treatment enhanced leaf chlorophyll content, root growth, grain and straw yields, and soil health, achieving superior performance compared to 100% N through urea. The NCBPC formulation increased apparent nitrogen recovery (40.43% in maize and 40.60% in wheat) and agronomic NUE (36.20% and 37.10%), while reducing nitrous oxide emissions by 27.69% and 30.47%, respectively. By reducing nitrogen requirements by 25% without compromising yields, NCBPC offers a sustainable solution to enhance NUE, mitigate greenhouse gas emissions and support environmentally friendly maize and wheat production.

Theme 2: Soil and Residue Management Strategies to Enhance SOC Sequestration and Soil Quality

Carbon mineralization kinetics of different crop residues with Pusa decomposer in soil

India annually generates~869 million tonnes of crop residues (CRs), posing management challenges. This study evaluated the efficiency of a microbial consortium, Pusa Decomposer (PD), in degrading Rice, Maize, Cotton, and Pigeon pea CRs. Results indicated that the C/N ratio of CRs followed the order: Rice >Maize >Cotton >Pigeon pea. Maize showed the highest holocellulose content, while Pigeon pea had the lowest. Lignin content followed the order: Cotton >Rice >Pigeon pea >Maize. Incubation experimentswere conducted at 25 and 35°C to measure cumulative C mineralization (C_t). Microbes showed a preference for CRs with lower lignin and higher holocellulose. Maize residues exhibited maximum C_t despite having higher C/N, likely due to lower lignin and higher holocellulose. Lignin and polyphenol content proved to be better indicators of CR decomposition than C/N ratio alone. Pusa decomposer efficiently decomposes all the CRs, performing better for extended periods at lower temperatures. At 25°C, Maize had higher C_{Labile} owing to a high saccharide content. Cotton residues showed the highest C_{Recal} and lowest K_{Recal} owing to high contents of polyphenol and lignin. The PD addition, at higher temperatures, enhanced K_{Recal} and K_{Labile} values and shifted C from the labile to the recalcitrant pool, particularly in Rice CR. The results indicated a positive priming effect (PE) for Rice, Cotton, and Pigeon pea CRs, while Maize showed initial negative PE. The PE was positively impacted by a rise in temperature, whereas, PD addition diminished PE, through possible enhancement in the lability of CR-C. The additions of different CR, along with PD benefit the labile soil C pools tremendously. In a nutshell, the addition of PD enhanced CR decomposition, reduces PE, and promotes soil C sequestration, thus necessitating its' inclusion along with CR addition in sustainable regenerative agricultural practices.

Assessment of enhanced rock weathering for carbon sequestration and reclamation of an acid soil from Assam

Enhanced rock weathering (ERW) is one of the potential Negative Emission Technologies (NETs) that aims to hasten the natural geological process of atmospheric CO₂ removal by applying finely ground rock dust to agricultural soil and also is capable of ameliorating soil acidity through the production of carbonate and bicarbonates. In the present study, two incubation experiments and detailed characterization of the Rock Mineral Poder (RMP), obtained from the Saurashtra region were performed. The results showed the presence of various silicate minerals, dominated by feldspars in the RMP. The RMPs increased the pH of the acid-aqueous solutions. The release of Ca and Mg from the RMP was almost instantaneous, accompanied by a late release of K. The cumulative C emissions (C_t) from the treatments containing only RMPs were statistically similar to that from the control, almost throughout the incubation period irrespective of temperatures. Treatments with higher doses of RMP *i.e.,* Organic Manure (OM)+RMP_5, OM+$RMP_{10,}$ and OM+RMP_{25} registered significantly lower C_t than those with OM. The OM+RMP treatments registered a sharp increase in pH in the initial period. Irrespective of the temperature, the treatments containing only RMPs and the control registered similar C_t and pH across the incubation period. Noticeable effects were obtained on the soil CEC, labile SOC, and dehydrogenase activities. From the study, it was found that the application rate of RMPs might be recommended @ 8 t ha^{-1} along with organics @10 t ha^{-1} with a carbon dioxide removal (CDR) potential of 356 Kg ha^{-1}, which if extrapolated for potential use in pan-India acid soils results in CDR potential of 0.32 Gt. These indicate the potent application of RMPs and organics as a C-neutral reclamation measure in India's acid soils.

Impact of natural farming on carbon fractions and properties in an Alfisol under rice-rabi maize system

Natural farming offers a sustainable alternative, but its effectiveness compared to organic and integrated crop management (ICM) practices, especially in regions like Jharkhand, is not well-studied. The study titled "Impact of natural farming on carbon fractions and properties in an Alfisol under rice-rabi maize system" aimed to evaluate the impact of natural farming on soil carbon fractions, properties, and rice grain quality. The study was conducted at Birsa Agriculture University, Ranchi, Jharkhand, with five treatments: control, natural farming, organic farming, ICM-1, and ICM-2. Soil samples from depths of 0-15 and 15-30 cm and rice grain samples were collected during the rice harvest. Study revealed that organic and natural farming plots had significantly higher total carbon and total organic carbon (TOC). Organic farming showed the highest levels of very labile and labile carbon fractions and the best carbon management index. While bulk density and water holding capacity were similar across treatments, organic farming had higher mean weight diameter (MWD) and aggregate fractions. pH and electrical conductivity (EC) were similar across treatments, though surface soils had lower pH and higher EC. Organic farming increased soil organic carbon by 13.6% over natural farming treatments. In natural farming plots, available nitrogen (N) and phosphorus (P) decreased, while potassium (K) increased compared to ICM-1 and ICM-2, but decreased compared to organic farming. Natural farming exhibited higher micronutrient availability (except iron) and better microbial functions and enzymatic activity, but it did not match organic farming or ICM-1 in terms of grain quality, yield, and nutrient uptake. Although natural farming improved soil carbon fractions and biological properties compared to ICM treatments, rice grain quality and yield were lower than in organic and ICM treatments. The performance of natural farming may be influenced by agro-climatic and soil-specific factors. Therefore, it should be studied further across different regions with varying cropping systems.

Soil carbon and nitrogen pools under different cropping systems of the eastern plateau and hills region

Agricultural systems in the Eastern Plateau and Hills Region (EPHR) of India are challenged by low yields due to erratic rainfall, acidic soil, nutrient deficiencies, low soil organic carbon and inadequate residue recycling in soil. This study was conducted at the ICAR Research Complex for Eastern Region, Ranchi, and aimed to identify how various cropping systems affect soil organic carbon and nitrogen pools and soil biological properties. The treatments included: an uncultivated control; cropping systems of rice-chickpea, rice-linseed, maize+pigeonpea-chickpea, finger millet-fallow, groundnut-fallow, and a guava orchard, where soil samples were collected from 0–15, 15–30, 30–45, and 45–60 cm depths. The guava orchard recorded the highest carbon sequestration rate, total soil organic carbon stock, active and passive pools of carbon, carbon pool index (CPI), lability index (LI) and carbon management index (CMI). The carbon fractions followed the order: very labile > labile > non-labile > less labile. Guava orchards recorded the highest total nitrogen stock, potentially mineralizable nitrogen (PMN), nitrogen pool index (NPI) and nitrogen management index (NMI). The highest microbial biomass carbon, activities of dehydrogenase, fluoresceine diacetate, β-Glucosidase and N-Acetyl-β-D-glucosaminidase were also observed in the guava orchard. It can be concluded that cultivation of guava orchards and cereal-legume-based double cropping systems enhance soil organic carbon, nitrogen and microbial activity, whereas fallow land and monocropping degrade soil health. Thus, adoption of perennial guava orchards in upland and cereal-legume systems in medium and low land might be able to increase soil carbon sequestration, soil carbon and nitrogen pools and maintain better soil health in the rainfed ecosystems of Eastern Plateau and Hills Region of India.

Soil organic carbon sequestration in rice-wheat cropping system under conservation agriculture

Although conservation agriculture (CA) has been promoted for sustainable agriculture, limited information is available on the long-term effect on CA on carbon stabilization, soil aggregation, temperature sensitivity of soil organic carbon (SOC) decomposition and carbon cycling enzyme activities in rice (*Oryza sativa* L.) – wheat (*Triticum aestivum* L.) cropping system. Hence, a nine year CA field experiment was selected with seven treatments namely, zero tilled direct seeded rice (ZTDSR) –zero tilled wheat (ZTW), wheat residue (WR) + ZTDSR – rice residue (RR) + ZTW, WR + ZTDSR + brown manuring (BM) – RR + ZTW, ZTDSR – ZTW – ZT mungbean (MB), mungbean residue (MBR) + ZTDSR – RR + ZTW – WR + ZTMB, puddled transplanted rice (TPR) – ZTW, TPR – conventionally tilled wheat (CTW) laid out in a randomized block design with three replications. In the topsoil (0-5 cm), the MBR+ZTDSR-RR+ZTW-WR+ZTMB plots had ~23.0% more total SOC stock than CT plots (6.07 Mg C ha^{-1}). The MBR+ZTDSR-RR+ZTW-WR+ZTMB had ~27.9% higher labile C and~35.5% higher recalcitrant C than TPR-CTW plots in bulk soil. The highest C_t value was recorded in the MBR+ZTDSR-RR+ZTW-WR+ZTMB plots in all the three temperatures (27°, 32° and 37°C) for bulk soil, macroaggregates and microaggregates. The Q_{10} values revealed that SOC in TPR-CTW plots was more sensitive to temperature changes than ZT plots with residue retention (CA plots). The MBR+ZTDSR-RR+ZTW-WR+ZTMB plots showed maximum C stabilization (2.42 g C/1000 g bulk soil) within iPOM_mM which was 95% higher than TPR-CTW plots in top soil. About 0.183 Mg C ha^{-1} yr^{-1} was stabilized inside microaggregates within macroaggregates in the MBR+ZTDSR-RR+ZTW-WR+ZTMB over control. These findings revealed that under long-term CA, the physical stabilization of SOC in microaggregates within macroaggregates was the major mechanism of carbon sequestration in rice-wheat cropping system in an Inceptisol. Thus MBR+ZTDSR-RR+ZTW-WR+ZTMB can be a viable option for rice-wheat cultivation in the Indo-Gangetic plains that can enhance carbon sequestration and carbon stabilization in soils by mitigating climate change.

Impact of residue management on carbon dynamics in a Typic Haplustept under wheat-based cropping systems

Managing substantial crop residues from cereal-cereal-based cropping systems is a critical challenge globally. This study evaluates the long-term effects of residue management practices (RMPs) including biochar (BC) application, crop residue incorporation (CRI), on-farm residue burning (CRB), and complete residue removal (CRR) on carbon dynamics in a Typic Haplustept under wheat-maize/pearl millet/rice cropping systems (WMCS/WPCS/WRCS).WMCS enhanced macroaggregate (>0.25 mm) formation in surface layers, with BC emerging as the most effective practice for improving soil structure. In the 0–15 cm layer, BC-treated plots exhibited the highest geometric mean diameter (GMD), surpassing CRI, CRB, and CRR by 2.77%, 8.82%, and 10.4%, respectively. BC also enhanced aggregate-associated total organic carbon (TOC), glomalin, carbohydrates, and polysaccharides, particularly in WMCS and WPCS. Canonical discriminant analysis identified macroaggregates, TOC within aggregates, polysaccharides, glomalin, and carbohydrates as key variables for soil stability. BC improved SOC stability, evidenced by higher activation energy and Q10 values, especially in macroaggregates across depths. It also promoted labile carbon availability, supporting microbial activity and nutrient cycling, while CRB and CRR resulted in lower SOC stability and labile C content. BC application yielded the highest SOC build-up, with WMCS-BC achieving the greatest SOC content, whereas CRR had the lowest accumulation. A regression model ($y = 0.0636x + 0.6513$) revealed a positive correlation between carbon inputs and SOC dynamics.This study underscores the potential of BC and CRI in enhancing soil aggregation, SOC sequestration, and soil health in wheat-based systems. WMCS and WPCS proved more effective in sustaining C dynamics, while CRB and CRR practices had adverse effects, highlighting the need for sustainable residue management strategies.

Development of novel soil organic carbon-based protocols for soil quality assessment

Sustainable residue management and adopting appropriate cropping systems play a significant role in enhancing soil quality. A long-term study was conducted to evaluate the long-term effects of four contrasting residue management practices on soil quality changes under three wheat-based cropping systems: maize-wheat (MW), pearl millet-wheat (PW), and rice-wheat (RW) in an Inceptisol of Delhi. The four residue management practices involved crop residue incorporation (CRI), residue converted into biochar (BC), crop residue burning (CRB), and crop residue removal (CRR). The study indicated that most of the SQ indicators were significantly higher in plots with CRI, followed by BC. In contrast, CRB and CRR had negative impacts on SQ. Among the cropping systems, the maize-wheat (MW) system outperformed the other two. Assessing SQ is challenging because traditional methods, such as the conceptual framework (CF) and principal component analysis (PCA), require a large numbers of physical, chemical, and biological SQ indicators. These methods are tedious, time-consuming, and costly due to the need for reagents and equipment. Soil organic carbon (SOC), particularly its labile fractions, has historically been considered a key SQ indicator because of its sensitivity to management practices and its role as an early indicator of changes in SQ. Therefore, in this study, several SOC-based indicators were hypothesized as surrogate measures of SQ indicators, including labile pools of SOC fractions, dissolved organic carbon (DOC), $KMnO_4$-C, particulate organic carbon (POC), soil polysaccharides, soil carbohydrates, CO_2 flush, and β-glucosidase. The results showed that these SOC-based indicators were highly correlated with traditional conceptual framework (CF) based SQ indicators. Among them, $KMnO_4$-C, DOC, total organic carbon (TOC), and the enzyme β-glucosidase had the highest correlation coefficients (ranging from 0.95 to 0.98), making them reliable for developing an SOC-based soil quality index (SQI). The SQI derived from SOC, PCA, and CF methods were comparable. For example, under CRI, the SQI was the highest across all approaches, with values of 0.71, 0.65, and 0.80, respectively. To broaden the applicability, a similar SOC-based SQI was tested under the All India Coordinated Research Project (AICRP) on Long-Term Fertilizer Experiments (LTFEs) across different soil orders like Alfisol, Mollisol, Vertisol, and Inceptisol. Finally, a web-based decision support system (DSS) was developed to provide rapid and feasible SQ assessments using both the conceptual framework and SOC-based surrogate approaches.

Soil carbon and nitrogen stock, quality and stability under diverse land use systems in north eastern region of India

This study examines the impact of diverse land use systems on soil carbon and nitrogen stocks, quality, and stability in Tripura, North Eastern Region of India. Different physicochemical parameters of soil such as pH, EC, CEC, BD, major soil micronutrients and SOC were analyzed across bamboo plantations, tea plantations, mango orchards, lemon orchards, rice-rice, wheat-millets, okra-onion, and uncultivated lands. The findings reveal significant variations in soil properties among land use systems, with forest and plantation systems demonstrating higher SOC and total nitrogen (TN) stocks compared to agricultural and uncultivated lands. Tea plantations exhibited the highest SOC stock (31.8 Mg ha^{-1}) and TN stock (2.65 Mg ha^{-1}), followed by mango orchards and bamboo plantations. Available nitrogen, phosphorus, and potassium contents were significantly higher in tea, mango, and bamboo systems, while uncultivated land had the lowest values. Tea land use also recorded the highest microbial biomass carbon (760 mg kg^{-1}) and nitrogen (136 mg kg^{-1}) in macroaggregates, indicating enhanced microbial activity and nutrient cycling. Labile carbon pools and oxidizable carbon fractions were notably higher in tea and mango land use systems, reflecting their superior soil quality and stability. The study highlights the critical role of macroaggregates in storing SOC and TN, with tea land use showing the highest macroaggregate-associated carbon (20.5 g kg^{-1}) and nitrogen concentrations. Humic acid analysis revealed higher carbon content in plantation and horticulture systems, while agricultural systems showed lower soil quality.Cumulative carbon mineralization (Ct) under varying temperatures indicated significantly higher rates in tea soil macroaggregates compared to other systems, particularly at elevated temperatures, emphasizing the potential of tea land use for carbon sequestration under changing climatic conditions. Sustainable land management practices such as agroforestry, organic farming, and reduced tillage can enhance soil carbon and nitrogen sequestration, mitigate soil degradation, and promote biodiversity conservation.

Quality and stability of soil organic carbon in maintaining soil health and crop productivity in long term experiment under different agro-ecological regions of India

The current scenario of escalating climate change, land degradation and indiscriminate use of chemical fertilizers has led to a perilous decline in soil organic carbon quality and its enduring stability; compromising soil health and jeopardizing the sustainability of agricultural production. The present study aimed to evaluate the quality and stability of soil organic carbon (SOC) as influenced by long-term fertilization, covering four major soil orders and predominant cropping system of the country namely Mollisol (rice-wheat), Vertisol (sorghum-wheat), Inceptisol (rice-mustard-sesame) and Alfisol (maize-wheat) located in Pantnagar, Akola, Gayeshpur and Ranchi, respectively. The soil samples, collected from the long-term field experiments (0-15, 15-30 and 30-45 cm) underwent analysis of various quality and stability parameters of SOC. Prolonged application of manures and fertilizers increased SOC content by 72% in NPK+Zn foliar spray+FYM (NPKZnF) of Mollisol, 89% in NPK+FYM (NPKF+) of Vertisol, 65% in FYM+Biofertilizer (FB) of Inceptisol and 69% in the FYM treatment of Alfisol over the control. All the labile and stabilized pools of C were followed the similar trend. The study identified SOC, C_{mic}, BGA and $KMnO_4$-C as the primary organic carbon-based indicators and interpretative classes were established as a function of Relative yield (RY) of crops in each site. The SOC stock, build up, carbon sequestration potential and efficiency were remarkably greater under integrated use of nutrients across the experimental sites. Balanced fertilization with added manures (FYM) maintained the maximum level of SOC, carbon sequestration, improved soil microbial and physical properties. Thus, integrated use of chemical fertilizers in combination with organic manures/amendments *i.e.,* NPKZnF, NPKF+, FB, FYM/NPK+lime (NPKL) in Mollisol, Vertisol, Inceptisol and Alfisol, respectively could sustain the soil ecosystem by balancing the carbon addition and loss across the experimental sites. Therefore, these management practices might be recommended for maintaining soil health, enhancing carbon sequestration and sustaining crop productivity under the respective agro-ecological regions of India.

Theme 3: Dynamics of Nutrients and Their Interactions in Soil

Aggregate associated phosphorous fractions and enzyme activities in an Inceptisol under conservation agriculture-based maize-wheat system

Soil aggregation are essential for and soil health as well as phosphorus (P) availability, yet their relation under conservation agriculture (CA) in maize-wheat cropping systems on Indo-Gangetic Inceptisols remain understudied. This study investigated the impact of CA on P fractions, arbuscular mycorrhizal fungi (AMF), and P cycling enzymes using soil samples from a 16-year CA experiment at IARI, New Delhi. The experiment involved three depths (0-5, 5-15, 15-30 cm) in a split-plot design with tillage/nitrogen management (ZTRN125, ZTRN100, CTRN125) and phosphorus fertilization (P100, P75, P0). ZTRN125+P100 consistently outperformed CTRN125+P0, showing higher soil organic carbon and nutrient availability. ZTRN125 had the highest soil aggregate stability, with a 25% increase in macroaggregate proportion and significantly higher labile (H_2O-P, $NaHCO_3$-P_i), moderately labile (NaOH-P_i), and organic P fractions over control. Labile P, moderately labile P, and non-labile P were significantly higher in ZTRN125 and P100 over CTRN125 and P0 for both macro and microaggregates, with labile P higher in macroaggregates. ZTRN125 had 54% more H_2O-P in macroaggregates and 28.2% more in microaggregates, while P100 increased H_2O-P by 52.4% in macroaggregates and 54.5% in microaggregates over P0. ZTRN125 showed 37.2% more NaOH-Pi and 20% more NaOH-Po than CTRN125, while P100 increased NaOH-Pi by 11.7% and NaOH-Po by 7.6% over P75. ZTRN125 achieved the highest total Pi and Po in both aggregate types, with P100 outperforming P75 and P0, though residual P in microaggregates showed no significant differences. ZTRN125 with P75 exhibited the highest AMF spore count, microbial diversity indices, glomalin content, and phosphatase activity. Macroaggregates under ZTRN125 accumulated more stable P, while microaggregates, with lower P adsorption, released P faster. P75 optimized AMF diversity, glomalin, and phosphatase activity, suggesting reduced P fertilizer needs. Therefore, ZT with residue retention and N125, combined with P75, is recommended as a P fertilizer protocol for Inceptisols in maize-wheat systems.

Determination of minimum silicon dose for enhancing phosphorus availability in diverse soils

The Indian government heavily subsidizes phosphorus (P) fertilizers to ensure affordability for farmers. However, only 15-20% of applied P is utilized by plants, resulting in inefficiency and significant financial losses. Additionally, the rapid depletion of rock phosphate, essential for P fertilizer production, has escalated costs annually. Addressing this inefficiency by mobilizing fixed soil P can help reduce input requirements. Soluble silicon (Si) has potential in mobilizing P through ligand exchange between phosphate (PO_4^{3-}) and silicate (SiO_4^{4-}), warranting further research into Si-P interactions across diverse soils.This study examined twenty soils categorized as non-acidic alluvial (ten), acidic alluvial (four), red and lateritic (four), and black (two). Two incubation experiments were conducted using sodium silicate: one assessed P release over 2, 4, 7, and 14 days at 250 mg kg^{-1} Si, while the other evaluated varying Si doses (0-500 mg kg^{-1}) over 4 days. Soil analysis revealed variations in texture, pH, cation exchange capacity, organic carbon, and iron/aluminum oxides. Results showed soluble Si initially increased and later declined, with maximum P availability observed 4 days after Si application. Soluble Si positively correlated with pH. Minimum Si doses to significantly increase soluble P varied across soils viz.115 mg kg^{-1} for non-acidic alluvial soils, 125 mg kg^{-1} or >500 mg kg^{-1} for acidic alluvial soils, 375 mg kg^{-1} for black soils, and ~438 mg kg^{-1} for red and lateritic soils. Silicon was most effective in non-acidic soils with high calcium-bound P but less effective in acidic, clay-rich soils with elevated iron and aluminum oxides. The study highlights soluble Si's potential to mobilize fixed P in soils. Generally, Si was more effective in non-acidic soils with higher calcium-bound P and less effective in low pH soils or those with high clay, iron, and aluminum oxides.

Thermodynamic approach for assessing plant available potassium in soils

Soil potassium (K) availability is assessed using the standard free energy of exchange (ΔG^0) of calcium and magnesium against K^+, derived from quantity-intensity (Q/I) relationships. ΔG^0 reflects the driving force for K release and plant uptake. Along with ΔG^0, the non-exchangeable K (NEK) pool also influences plant K availability. However, no studies in India have integrated ΔG^0, soil K pools, K fixation capacity, and other properties to predict plant K availability. This study addressed this gap by examining twenty five soils with diverse properties, including acidic, neutral, alkaline, sodic, calcareous, red, lateritic, and black soils. The research analyzed soil physicochemical properties, K fractions, K fixation capacity, and Q/I parameters. A greenhouse experiment measured wheat biomass yield, K concentration, and K uptake at the vegetative stage. Results showed significant variations in soil texture, pH (4.34–9.11), cation exchange capacity (5.02–40.4 cmol[p^+] kg^{-1}), exchangeable Ca + Mg (0.98–39.1 cmol [p^+] kg^{-1}), and organic carbon (0.25–0.90%). NH_4OAc-K ranged from 25.6 to 712 mg kg^{-1}, covering low to high available K. NEK varied widely, with sodium tetraphenyl borate (NaTPB) extraction emerging as a better plant-available K indicator than NH_4OAc or boiling HNO_3 (21.4 – 1427 mg kg^{-1}). ΔG^0 values ranged from –4198 to –2443 cal mol^{-1}, influenced by soil K saturation and NaTPB extractable K. Soil pH, cation exchange capacity, and NaTPB extractable K explained 66% of ΔG^0 variability. NaTPB extractable K and ΔG^0 predicted plant K concentration and uptake with 74% and 67% accuracy, respectively. A simplified two-point method accurately predicted ΔG^0 ($R^2 = 0.95$, $p < 0.001$), offering a practical alternative for estimating soil K availability. These findings establish ΔG^0 and NaTPB extractable K as robust predictors of soil K availability for plants.

Fungus inoculated rice straw biobed for enhancing phosphorus availability in soils

Phosphorus (P) availability in soils is a key determinant of crop productivity, but its bioavailability is often limited due to fixation in soil within the minerals. On the other hand, crop residue generation especially rice straw is also becoming a menace. It is because the farmers do not have any management solution for these agro-waste and thus resort to stubble burning. So, the study was aimed to develop and characterize a rice straw-based biobed inoculated with phosphorus-solubilizing fungi (PSF) to enhance phosphorus availability in soils with the utilization of agrowaste. Three biobeds were prepared with different ratios of Reese's mineral medium (RMM) to rice straw and compared for phosphorus solubilization capacity, N- acety lglucosamine production, and phosphatase enzyme activities. Biobed-2, containing a 1:4 ratio (w/v) of rice straw to RMM, demonstrated the highest phosphorus solubilization and enzyme production capacity which was therefore selected and characterized using different techniques. Biobed-2 was mass multiplied to understand its behaviour in increasing phosphorus availability in soil. Incubation studies were conducted with the application of biobed with and without PSF inoculation to different soils at 1% and 1.5% of the soil. Results showed that PSF-inoculated biobed significantly improved phosphorus availability. It was found that irrespective of dose application, PSF-inoculated biobed showed improvement in different soil parameters. The effects were most pronounced up to 60 days of incubation, with the 1.5% PSF-inoculated biobed demonstrating superior results across both soil types. So, it can be concluded that PSF inoculated biobed applied at a particular dose can effectively enhance phosphorus solubilization and improve soil health, highlighting its potential as a sustainable solution for phosphorus management in agriculture. In future, field validation is required to confirm these findings.

Identification of response-based nutrient deficiencies in Assam lemon grown on acid soil

The field experiment was conducted for identification of response-based nutrient deficiencies in Assam lemon grown on acid soil located at Rodali Krishi Farm, Lakhimpur, Assam, from October 2023 to April 2024. This study aimed to evaluate the impact of different nutrient applications on soil fertility, leaf nutrient composition, microbial activity in soil and fruit, fruit yield and quality of Assam lemon and also to determine critical nutrient levels required for optimal productivity through soil and leaf analysis. The experiment was laid out in Randomized Complete Block Design with twelve treatments replicated three times in 7-year-old Assam lemon trees with a total of thirty-six plants. Among all the treatments, treatment T_{12} (NPK+Ca+Mg+Zn+B) showed highest fruit length, diameter, juice percentage with minimum peel thickness and also resulted in maximum plant height, canopy spread, tree girth and canopy volume. Treatment T_{12} resulted in about 144.62%, 69.3% and 44.1% increase in fruit yield, number of fruits per plant and fruit weight respectively over control. Soil fertility, indicated by increased availability of N, P, K, Ca, Mg, Zn and B, along with improved leaf concentrations of N, P, K, Fe, Mn, Zn and Cu, were significantly enhanced through the treatment T_{12}as compared to control. A larger proportion of bacterial colonies in soil were observed under treatment T_{12}. The critical limits of leaf N, P, K, Fe, Mn, Zn and Cu wereobserved as 2.65%, 0.14%, 2.35%, 171.5, 53.5, 25.5 and 6.35 mg kg^{-1} respectively with a maximum of 80% relative fruit yield. And critical levels of plant available N, P, K, Ca, Mg, Fe, Mn, Zn, Cu and B were observed as 238.4 kg ha^{-1}, 21.7 kg ha^{-1}, 260 kg ha^{-1}, 172, 111, 77.5, 7.54, 0.61, 0.72 and 0.50 mg kg^{-1} respectively.

Development of optimum soil fertility and leaf nutrient standards in relation to fruit yield of Assam lemon

The field experiment was conducted for development of optimum soil fertility and leaf nutrient standards in relation to fruit yield of Assam lemon in orchards of Lakhimpur district of Assam. The study was aimed to identify nutrient constraints in Assam lemon orchards, develop optimum soil fertility and leaf nutrient standards in relation to fruit yield of Assam lemon using Diagnosis and Recommendation Integrated System (DRIS) norms. Fourteen Assam lemon orchards were identified. The soil and leaf samples, fruit yield and quality were analysed and the data, were subjected to development of nutrient norms using DRIS. The optimum value of soil available nutrients was: N 224- 252 kg ha^{-1}, P 22.9-27.4 kg ha^{-1}, K 117- 134 kg ha^{-1}, Ca 16.3- 20.4 meq kg^{-1}, Mg 10.2- 12.2 meq kg^{-1}, Fe 152-210 ppm, Mn 8.3-12.6 ppm, Cu 0.72- 0.94 ppm, Zn 0.99- 1.20 ppm and B 0.53-0.64 ppm in relation to fruit yield of 22.2- 34.6 kg tree^{-1}. The DRIS norms identified based on soil analysis showed that the most deficient nutrient wascalcium followed by magnesium, zinc, boron, phosphorous, nitrogen and potassium.The most excessive nutrient was Fe followed by Mn and Cu as the DRIS indices were positive. The optimum values of leaf nutrients were: 1.93- 2.24% N, 0.12- 0.14%P, 1.83- 2.01% K, 240-289 ppm Fe, 20.2- 29.6 ppm Mn, 4.90-6.80 ppm Cu and 26.3-32.4 ppm Zn in relation to same fruit yield. Leaf analysis -based DRIS norms identified the most deficient nutrient in leaf was P followed by Zn, K and N showing negative DRIS values. The most excessive nutrient was Cu followed by Fe and Mn evident from positive DRIS indices. These optimum values of plant available nutrients and leaf nutrients corroborated well with high performing orchards of Assam lemon, displaying the good predictability of DRIS-model.

Impact of conservation agriculture on dynamics of potassium in a Typic Haplustept under maize-based cropping systems

Intensive conventional tillage has degraded soil quality and reduced potassium (K) availability in maize-growing areas of India, leading to declining maize productivity. A 2018-2019 field study, part of an ongoing long-term experiment started in 2008. The experiment was laid out in split plot design with three levels of tillage practice as main plots: permanent raised bed (PB), zero tillage flat (ZT-flat), and conventional tillage (CT-flat) and in subplots as four different cropping systems viz. maize-wheat-mungbean (MWMb), maize-chickpea-sesbania (MCS), maize-mustard-mungbean (MMuMb), and maize-maize-sesbania (MMS). Soil samples were collected from different depths of 0-5 cm, 5-15 cm, and 15-30 cm after the summer crop harvest. Soil K pools, quantity-intensity relationship (Q/I), K release kinetics and crops residue decomposition pattern with subsequent K release along with grain yield and K uptake were studied. The higher content of water-soluble K, exchangeable K, and non-exchangeable K were recorded in PB and ZT-flat over the CT-flat and among cropping systems MCS and MWMb as compared to other cropping systems. Among Q/I parameters, potential buffering capacity (PBC^K) was maximum and activity ratio (AR^K) and labile K (K_L) were minimum under PB and ZT-flat and MCS as well as MWMb cropping system than the CT-flat and other cropping systems at different depths of soil. This study showed that cereal crop residues, with higher K content and C/N ratio, can supply more potassium (K) for longer periods. In contrast, legume residues, with lower K content with a lower C/N ratio, releases K more quickly, benefiting short-term nutrient availability. Comparatively less depletion in overall K-supplying capacity of soil were recorded under PB and ZT-flat to CT-flat as well as MCS and MWMb cropping systems. The study thus underlined the necessity of adequate K input for the sustenance of soil health, inherent K-supplying capacity and crop productivity.

Impact of long-term fertilization on phosphorus dynamics in Inceptisol and Vertisol

Understanding long-term impact of fertilization and manuring on soil phosphorus (P) dynamics is crucial for sustainable P fertilizer management for optimum crop yield. Hence, two long-term fertilizer experiments have been selected under Inceptisol (Bhubaneswar) and Vertisol (Parbhani) to study transformation of P fraction of applied and native P, P adsorption and desorption behaviour and role of aggregates in P distribution and availability. For this, soil samples have been collected from seven treatments *viz*. unfertilized control, N, NP, NPK, 150% NPK, NPK+FYM, NPK+ Lime (in Inceptisol) and NPK+$ZnSO_4$ (in Vertisol). Our findings revealed that NPK+FYM, NPK+ Lime (in Inceptisol) and 150% NPK application improved P availability. Sequential fractionation of inorganic P indicated significant build-up of iron bound P (Fe-P) which accounted for 49.5 and 55.6% of total inorganic P (P_i) in Inceptisol in surface and sub-surface soil layers, respectively. Contrarily in Vertisol, calcium bound P (Ca-P) accounted for 65.7 and 69.9% of total P_i in 0-15 and 15-30 cm soil depths, respectively. The P adsorption study revealed that increase in phosphatic fertilizer dose and integrated application of FYM and lime (in Inceptisol) with NPK reduce P adsorption and improved its availability. In both the soils, the 'b' and 'k' values drastically reduced under NPK+FYM, 150% NPK and NPK+Lime (in Inceptisol) treatments implying better P availability than plots under NPK in surface soil. Highest P availability was observed in silt+clay fraction followed by small-macroaggregates, microaggregates and least in large-macro aggregates in Inceptisol. Whereas, in Vertisol, small- and large-macro aggregates were the dominant fractions governing P availability. Overall, it was observed that application of 150%P dose and integrating FYM or lime (in Inceptisol) with NPK increased P availability and reduced fixation. Hence, the integrated use of NPK and FYM (in Inceptisol and Vertisol) or lime (in Inceptisol) could be advocated over 150% NPK treatment for better utilization of resources by reducing soil P build-up and decrease cultivation cost.

Potassium stratification and supplying capacity of an Inceptisol in maize-wheat system under conservation agriculture

This study investigated depth-wise potassium (K) stratification and supplying capacity in a maize-wheat system under conservation agriculture (CA), focusing on soil K pools, quantity-intensity (Q/I) relationships, release-fixation thresholds, productivity, and K use efficiency. Soil and plant samples were collected during 2018-2020 from an ongoing CA experiment at ICAR-IARI, New Delhi. The split-plot design included four crop residue (CR) levels [CR_0 (0 t ha^{-1}), CR_2 (2 t ha^{-1}), CR_4 (4 t ha^{-1}), CR_6 (6 t ha^{-1})] in the main plots and five K fertilization levels [RDK_0 (0% RDK), RDK_{50} (50% RDK), RDK_{100} (100% RDK), RDK_{150} (150% RDK), and RDK_{50}+KSB (50% RDK + K solubilizing bacteria)] in the sub-plots, each replicated thrice. The CR_6 resulted in the highest organic carbon content (0.88%) and cation exchange capacity (13.3 cmol [p^+] kg^{-1}) at the 0–5 cm soil depth. Water-soluble K (66.3 mg kg^{-1}) and available K (310 mg kg^{-1}) peaked under CR_6-RDK_{150} at 0–5 cm and declined with depth. Non-exchangeable K increased with residue retention, reaching 1488 mg kg^{-1} under CR_6 at 60–90 cm soil, while total K remained unaffected. Under CR_6 at 0–5 cm soil, AR_e^K (10.5×10^{-4}), $-\Delta K_0$ (210 mg kg^{-1}), K_s (28.9 mg kg^{-1}), fixation threshold (253 mg kg^{-1}), and release threshold (121 mg kg^{-1}) were highest, while PBC^K (47.9 cmol kg^{-1}), $-\Delta G$ (-10.9 kJ mol^{-1}), and K fixation capacity (44.7%) significantly declined. CR_4 significantly improved maize (5.76 t ha^{-1}) and wheat (5.49 t ha^{-1}) yields. Under RDK_{50}+KSB, maize and wheat showed apparent recovery efficiencies (ARE_K) of 75.8% and 64.3%, and agronomic use efficiencies (AUE_K) of 33.1 and 30.2 kg grain kg^{-1} K, respectively. A positive K balance of 33.6 kg ha^{-1} under CR_6-RDK_{150} highlights the role of high residue retention and optimal K fertilization in enhancing productivity while mitigating K mining in the Indo-Gangetic Plain.

Acquisition of soil iron by iron deficiency tolerant and sensitive rice genotypes as influenced by organic acids and microbial intervention

Iron deficiency is a major challenge in aerobic rice and an important malnutrition concern worldwide. This study explored genetic variability in rice to improve Fe deficiency tolerance, especially under aerobic conditions. Fifty-seven genotypes were screened under Fe-deficient (1 µM) and Fe-sufficient (100 µM) hydroponic cultures, assessing growth, physiological traits, Fe uptake, accumulation, and phytosiderophore (PS) release. Iron Deficiency Tolerance Index (FeDTI) was calculated. A pot experiment validated responses of 10 genotypes under Fe-deficient (~2.1 ppm) and Fe-sufficient (~10 ppm) soils and their FeDTI was calculated. It showed PS release as a key determinant of shoot and grain Fe content under Fe deficiency. Based on FeDTI, five genotypes—Jaya, Pusa-205, Ananga, Danteshwari, and PAU-201—were Fe deficiency-tolerant (FeDTI> 0.66), while Jayati, Kalinga III, Sona Mahsuri, VI956394, and CO37 were sensitive (FeDTI< 0.33). Root traits and shoot Fe content correlated significantly with FeDTI, and PS release showed strong correlations with Fe accumulation ($r^2 = 0.67–0.70$). To investigate Fe release kinetics, an incubation study used low molecular weight organic acids (LWMOAs) and microbial cultures under Fe-deficient (FeDS) and Fe-sufficient (FeSS) soils. Another pot experiment evaluated tolerant (Danteshwari) and sensitive (SonaMahsuri) genotypes with LWMOAs (citric and oxalic acids) and microbial treatments (consortium of *Pseudomonas plecoglossida* and *Pante oagglomerans*, *Bacillus spp.*, *Trichoderma harzianum*, and *Aspergillus niger*)). Fe-tolerant genotypes outperformed sensitive ones under FeDS. Seed treatment with *Pseudomonas plecoglossida* and *Panteo agglomerans* was most effective, enhancing leaf greenness, active Fe, chlorophyll, and yield. Grain Fe content increased by 14.2% in tolerant and 13.8% in sensitive genotypes. These findings highlight strategies for Fe biofortification and sustainable rice production under aerobic conditions.

Long-term manuring and fertilization effect on soil fertility, phosphorus fractions and biological properties under soybean-based cropping systems in a Vertisol

The impact of organic and inorganic fertilization on soil propertieswas evaluate after 17 years under major soybean-based cropping systems in Vertisols of Central India. Soil samples were collected from soybean-wheat, soybean-mustard, and soybean-chickpea cropping systems using six fertilization treatments in a split-plot design. Analyses focused on soil pH, electrical conductivity (EC), organic carbon (SOC), nutrient availability, phosphorus (P) fractions, and biological properties. Results showed no significant impact of cropping systems on soil pH and EC. However, the soybean-chickpea system significantly increased SOC, available nitrogen (N), mineral N, available phosphorus (P) in surface soil, and available sulfur (S) in both soil layers compared to other systems. It also enhanced microbial biomass carbon (MBC), microbial biomass phosphorus (MBP), dehydrogenase activity (DHA), and phosphatase activities. Among fertilization strategies, combined organic and inorganic fertilization (e.g., 50% organic + 50% inorganic) enhanced SOC, nutrient availability (N, P, K, S), and biological properties in both soil layers compared to sole organic or inorganic treatments. Organic treatments (100% organic and 75% organic + 25% innovative approach) improved soluble and loosely bound P fractions and biological properties like MBC, acid and alkaline phosphatase activities. Inorganic treatments increased Al-P, Fe-P, and Ca-P fractions, while integrated fertilization balanced these effects. Phosphorus fractions followed the order: Ca-P > Res-P > Fe-P > Al-P > SL-P. Overall, the soybean-chickpea system outperformed other systems in nutrient availability and biological activity, emphasizing its potential in sustainable cropping. Integrated fertilization strategies were most effective in improving soil fertility and quality, suggesting their adoption for long-term productivity in soybean-based cropping systems.

Phosphorus dynamics and availability in soil amended with rock phosphate enriched compost under a maize-wheat cropping system

Phosphorus (P) is essential for crop growth, but managing its availability in agriculture is challenging due to its fixation, declining rock phosphate reserves, and environmental concerns. This study, initiated in 2017 at the ICAR-Indian Agricultural Research Institute (IARI), New Delhi, investigates the use of rock phosphate-enriched compost (RPEC) combined with inorganic P-fertilizers, such as diammonium phosphate (DAP), to improve soil fertility, optimize P availability, and enhance crop productivity. A field experiment in a maize-wheat cropping system examined six treatments: T1 (control), T2 (100% DAP), T3 (50% DAP + 50% RPEC), T4 (25% DAP + 75% RPEC), T5 (100% RPEC), and T6 (100% compost). Soil samples were collected during the 2021–2022 cropping season after maize and wheat harvests and analyzed for soil P fractions, adsorption-desorption behaviour, microbial activity, and crop yield. The study found that combined treatments, especially T3 (50% DAP + 50% RPEC), significantly increased bioavailable soluble and loosely bound Pover controlin surface soil, with ~142% and ~102% increases in wheat and maize, respectively. Organic P fractions, particularly labile organic P, were highest in T3, showing substantial improvements in both layers. The application of organic fertilizers reduced P adsorption, with the most significant effect seen at 50% and 75% P supplementation with RPEC. Both the desorption percentage and desorption index increased with RPEC application, indicating improved P availability. Microbial biomass Pand carbon were elevated in T3 and T6, respectively, highlighting the benefits of organic inputs. Enzymatic activitieswere enhanced with organic inputs, reflecting improved P mineralization. Crop yields and nutrient uptake were highest in T3, with significant increases in both maize and wheat. This study demonstrates that integrating RPEC with inorganic P-fertilizerscan improve P availability, reduce P fixation, and enhance crop productivity, while also promoting soil health and sustainability under maize-wheat cropping systems.

Theme 4: Remediation of Metal and Metalloids in Soil

Development of composite beads for the removal of chromium and crystal violet from simulated effluent and its impact on mung bean

The pollution of water bodies with dyes released from industrial effluents is a serious environmental problem. The discharge of heavy metals into drain water through industrial actions has become a big issue for humans and aquatic lives. Nowadays, disposal and utilization of agriculture waste has become an important concern. Agro-waste like sugarcane bagasse, rice husk and cornhusk etc. have traditionally been used as fuels but their burning adds to air pollution. The beads loaded with combined clay–biomass composite can help in better removal of dyes and heavy metal and easy recovery of the materials. But higher amount of composite material was found to be unstable and erupted during removal of dye from aqueous solutions. In order to meet these challenges, the work was directed towards the preparation and use of composite beads and assessment of their stability during crystal violet dye and chromium (VI) removal from simulated effluents. Based on their morphological and adsorption behaviour CACa7 beads were selected and used for bulk production of different treated simulated effluents to irrigate the mung bean crop grown in pots and assess the soil and crop growth parameters at 30 days after sowing (DAS) and 60 DAS. It was found that the soil properties were not influenced adversely by the application of treated simulated effluents. In addition, the biological properties showed positive results with the application of treated effluent at both 30 DAS and 60 DAS. Thus, it can be concluded that the composite beads can effectively remove Crystal violet and chromium from the simulated effluents with efficient recovery from the aqueous solutions and the effluents can be used effectively as an alternative source of irrigation after treatment by the beads without adverse effect on the soil properties and plant growth.

Solid-solution equilibria, fractions and availability of arsenic in soil as affected by amendments

Groundwater arsenic (As) contamination poses a severe global health risk. This study assessed the efficacy of organic (sugarcane bagasse, vermicompost) and inorganic (steel slag, fly ash) amendments in mitigating As contamination in soils from Nadia district, West Bengal, through adsorption-desorption experiments. Adsorption capacity increased at 30 ºC, with steel slag showing the highest adsorption (278 mg kg^{-1}), followed by sugarcane bagasse (264 mg kg^{-1}), vermicompost (246 mg kg^{-1}), and fly ash (242 mg kg^{-1}). A novel bentonite-supported nano zero-valent iron (nZVI-Bento) (at 0.5 g L^{-1}) exhibited significant As adsorption, reducing water As levels below permissible drinking water limits (10 µg L^{-1}). The adsorption maxima (q_{max}) predicted by the Langmuir adsorption isotherm were 354 and 198 mg g^{-1} for nZVI-Bare and nZVI-Bento, respectively. Pot culture experiments with rice grown on As-contaminated soils revealed that steel slag effectively reduced soil extractable As in three regions, while sugarcane bagasse performed better in Nonaghata and Uttarpara soils. Steel slag consistently reduced As accumulation in rice grains, except in Nonaghata and Uttarpara soils. Amendments altered As fractionation, increasing the amorphous Fe/Al oxide-bound fraction (F3) while reducing the weakly sorbed fraction (F1), limiting As availability for plant uptake. Bio-accessibility assays indicated that 66-71% of total As in rice grains was bio-accessible, correlating with total grain As levels. A multiple linear regression model accurately predicted grain As content, explaining 93% of its variability. Health risk assessments highlighted non-cancer risks (HQ) for adults and children exceeding permissible limits, with higher cancer risks (CR) in children. This study emphasizes the need for bioavailability-focused risk assessments and effective amendments, particularly steel slag and sugarcane bagasse, to mitigate As contamination and its associated health risks. It offers critical insights into addressing the global challenge of groundwater arsenic contamination.

Assessing stability of clay-humus-metal and metalloid complexes in different soil orders under paddy cultivation

Environmental contamination by heavy metals and metalloids poses a critical threat to ecosystems and human health due to their bioaccumulation and biomagnification. Paddy soils act as sinks for these toxic elements, with their mobility influenced by soil moisture, redox potential, and microbial activity. This study investigates the stability and spatial distribution of metals/metalloid fractions within clay-humus complexes of paddy soils across Vertisol, Alfisol, Entisol, and Inceptisol. Metals and metalloids analyzed include Zn, Fe, Mn, Cu, Ni, Pb, Cd, and As. Results reveal significant spatial variations, with Vertisol and Alfisol polluted by Ni and Pb, Entisol and Inceptisol 1 by As, and Inceptisol 2 by Ni. Other micronutrient cations remained within permissible limits. Clay mineral characterization (XRD, FTIR, SEM) showed Vertisol dominated by smectite, kaolinite, and illite. Alfisol by kaolinite and vermiculite and Entisol by kaolinite, mica, and quartz. Humic acid analysis indicated advanced humification and higher aromaticity in Vertisol and Inceptisols compared to Alfisol and Entisol. Stability constants of metals/metalloid-humic acid complexes were significantly higher in Vertisol and Inceptisols, attributed to functional group ionization at pH 7.5 and 35°C. EDTA mobilized metals effectively, achieving peak removal rates within 24 hours. These findings underscore the critical role of clay-humus complexes in metal retention and mobility, highlighting site-specific strategies for managing soil contamination and sustaining paddy cultivation.

Chemistry and availability of molybdenum in soils

The Green Revolution in India increased the use of nitrogen, phosphorus, and potassium fertilizers, boosting crop yields but depleting essential micronutrients like molybdenum (Mo), vital for nitrogen metabolism and fixation. The present study addresses knowledge gaps on Mo availability in Indian soils by analysing its sorption-desorption behaviour, testing extractants for plant-available Mo, and examining its distribution across different soil fractions. Twenty surface soil samples (0-15 cm) from seven states with diverse physical and chemical properties were collected. Laboratory experiments investigated Mo sorption-desorption and thermodynamic behaviour at 20 °C and 30 °C. A pot experiment with lentil (*Lens culinaris* L. var L4717) assessed plant responses to Mo at two levels (0, 0.05 mg kg^{-1}). Results showed that Mo sorption depended on soil pH, with acidic soils (pH 4-5) exhibiting maximum adsorption, while alkaline soils (pH >8) displayed negative adsorption. Sorption followed the Freundlich isotherm, characterized as spontaneous, endothermic, and irreversible. Desorption was hysteretic in acidic soils but reversible in alkaline soils. Plant Mo content increased with soil pH, ranging from 0.16–3.76 mg kg^{-1} in control pots to 0.25–6.39 mg kg^{-1} in treated pots. Among seven different extractants (AB-DTPA, ammonium acetate, ammonium oxalate, hot water, anion exchange resin, EDTA, and nitric acid) tested, anion exchange resin, ammonium oxalate, and hot water were found more suitable than rest with specific constrains, while resin correlating best with plant Mo levels. Oxalate extractable Mo showed a positive relationship with Bray % yield, with critical limits identified as 0.2 mg kg^{-1} (graphical) and 0.18 mg kg^{-1} (statistical). Mo was primarily found in residual soil fractions, limiting bioavailability, although organic-rich soils had up to 40% organic-bound Mo, enhancing bioavailability. These findings advance Mo management strategies to mitigate deficiencies and improve crop yields sustainably.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Thesis Title	Chairperson	Institute
1.	Abhishek Pratap Singh Chauhan (21797)	M.Sc.	Evaluation of urea loaded nano-clay biopolymer composites and biosolubilizers for enhancing nutrient availability and nitrogen use efficiency in rice and wheat	Dr. K.M. Manjaiah	ICAR-IARI, New Delhi
2.	Pradarshak Sen (21798)	M.Sc.	Carbon mineralization kinetics of different crop residues with pusa decomposer in soil	Dr. Abir Dey	ICAR-IARI, New Delhi
3.	Shalini Kumari (21799)	M.Sc.	Aggregate associated phosphorus fractions and enzyme activities in an inceptisol under conservation agriculture based maize-wheat system	Dr. Shrila Das	ICAR-IARI, New Delhi
4.	Debmalya Sarkar (21800)	M.Sc.	Determination of minimum silicon dose for enhancing phosphorus availabity in diverse soils	Dr. Debarup Das	ICAR-IARI, New Delhi
5.	Ankit Kumar (21801)	M.Sc.	Development of composite beads for removal-chromium and crystal violet from simulated effluent and its impact on mung bean	Dr. Indu Chopra	ICAR-IARI, New Delhi
6.	S. G. Sarowar (21802)	M.Sc.	Thermodynamic approach for assessing plant available potassium in soils	Dr. Debarup Das	ICAR-IARI, New Delhi
7.	Atul Meena (21803)	M.Sc.	Fungus inoculated rice straw biobed for enhancing phosphorus availability in soils	Dr. Indu Chopra	ICAR-IARI, New Delhi
8.	Chandra Saha (50087)	M.Sc.	Assessment of enhanced rock weathering for carbon sequestration and reclamation of an acid soil from Assam	Dr. Abir Dey	#ICAR-IARI, Assam
9.	Tripti Pal (50091)	M.Sc.	Identification of response-based nutrient deficiencies in Assam lemon grown on acid soil	Dr. A.K. Srivastava	#ICAR-IARI, Assam
10.	Sneha R (50093)	M.Sc.	Development of optimum soil fertility and leaf nutrient standards in relation to fruit yield of Assam lemon	Dr. A.K. Srivastava	#ICAR-IARI, Assam
11.	Arijit Chowdhuri (60123)	M.Sc.	Impact of natural farming on carbon fractions and properties in an Alfisol under rice-rabi maize system	Dr. Manoj Chaudhary	#ICAR-IARI, Jharkhand
12.	Purbasa Kole (60138)	M.Sc.	Soil carbon and nitrogen pools under different cropping systems of the eastern plateau and hills region	Dr. Sushanta Kumar Naik	#ICAR-IARI, Jharkhand
13.	Ravindra Kumar Rekwar (11127)	Ph.D.	Impact of conservation agriculture on dynamics of potassium in a Typic Haplustept under maize based cropping systems	Dr. V.K. Sharma	ICAR-IARI, New Delhi
14.	Anshuman Das (11335)	Ph.D.	Soil organic carbon sequestration in rice-wheat cropping system under conservation agriculture	Dr. Ranjan Bhattacharyya	ICAR-IARI, New Delhi

15.	Kingshuk Modak (11336)	Ph.D.	Impact of long-term fertilization on phosphorus dynamics in Inceptisol and Vertisol	Dr. D.R. Biswas	ICAR-IARI, New Delhi
16.	Md Basit Raza (11337)	Ph.D.	Solid-solution equilibria, fractions and availability of arsenic in soil as affected by amendments	Dr. S.P. Datta	ICAR-IARI, New Delhi
17.	Jyotirmaya Sahoo (11342)	Ph.D.	Impact of residue management on carbon dynamics in a Typic Haplustept under wheat based cropping systems	Dr. T.J. Purakayastha	ICAR-IARI, New Delhi
18.	Kavitha Pandu Jadhav (11343)	Ph.D.	Assessing stability of clay humus metal and metalloid complexes in different soil orders under paddy cultivation	Dr. Nayan Ahmed	ICAR-IARI, New Delhi
19.	Moumita Ash (11608)	Ph.D.	Potassium stratification and supplying capacity of an Inceptisol in maize-wheat system under conservation agriculture	Dr. M.C. Meena	ICAR-IARI, New Delhi
20.	Premlata Meena (11614)	Ph.D.	Effect of urea and nitrification inhibitors loaded nanoclay biopolymer composite on nitrogen use efficiency in maize-wheat cropping system	Dr. K.M. Manjaiah	ICAR-IARI, New Delhi
21.	Pooja Tamuk (11615)	Ph.D.	Acquisition of soil iron by iron deficiency tolerant and sensitive rice genotypes as influenced by organic acids and microbial intervention	Dr. T.J. Purakayastha	ICAR-IARI, New Delhi
22.	Protima Rani Sarkar (11659)	Ph.D.	Long-term manuring and fertilization effect on soil fertility, phosphorus fractions and biological properties under soybean-based cropping systems in a Vertisol	Dr. D.R. Biswas	ICAR-IARI, New Delhi
23.	Soura Shuvra Gupta (11869)	Ph.D.	Chemistry and availability of molybdenum in soils	Dr. M.C. Meena	ICAR-IARI, New Delhi
24.	Tirunagari Rupesh (11874)	Ph.D.	Phosphorus dynamics and availability in soil amended with rock phosphate enriched compost under a maize-wheat cropping system	Dr. D.R. Biswas	ICAR-IARI, New Delhi
25.	Dewali Roy (11878)	Ph.D.	Development of novel soil organic carbon-based protocols for soil quality assessment	Dr. T.J. Purakayastha	ICAR-IARI, New Delhi
26.	Sunita Yadav (11916)	Ph.D.	Soil carbon and nitrogen stock and quality under diverse land use systems in north eastern region of India	Dr. Mandira Barman	ICAR-IARI, New Delhi
27.	Riaj Rahaman (12179)	Ph.D.	Quality and stability of soil organic carbon in maintaining soil health and crop productivity under long-term experiments in different agro-ecological regions of India	Dr. Sunanda Biswas	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 inter-disciplinary 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 farm, large irrigation commands and watershed scales. It has mandate to conduct basic and applied research on all aspects of water management in agriculture and develop technologies for water conservation, improved water management; to participate in the post graduate teaching programmes of IARI for developing human resources and organize training programmes 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 programmes. The research findings of post graduate students have been grouped under the following themes:

Theme 1: Marginal Quality Water Use in Agriculture

Standardization of irrigation scheduling for soil moisture sensor-guided wastewater use in gladiolus (*Gladiolus grandiflora* L.)

The effect of wastewater irrigation scheduled at different Maximum Allowable Depletion (MAD) levels was assessed to determine its impact on soil health, flower export quality, and gladiolus production. The MAD of available soil moisture was used to standardize irrigation scheduling. Consequently, a randomized block design experiment was established, featuring three replications and eight treatments namely, T1: Groundwater irrigation scheduled at 25% MAD, T2: Groundwater irrigation scheduled at 50% MAD, T3: Groundwater irrigation scheduled at 75% MAD, T4: Groundwater irrigation scheduled according to farmers POP, T5: Wastewater irrigation scheduled at 25% MAD, T6: Wastewater irrigation scheduled at 50% MAD, T7: Wastewater irrigation scheduled at 75% MAD, T8: Wastewater irrigation scheduled according to farmers POP, Under open field conditions, the study found that wastewater irrigation at 50% MAD significantly improved soil health parameters (such as EC, pH, OC, NPK, and micronutrients) compared to groundwater irrigation. Additionally, flower quality and yield, including flower size, vase life (13.20 days), spike yield (1.30 lakhs/ha), water use efficiency (32.68 kg/ha-mm), and water productivity (3.26 kg/m3) were all enhanced with wastewater irrigation at 50% MAD. The highest economic benefit, reflected in the benefit-cost ratio (2.21), was also achieved at this MAD level. Therefore, 50% MAD was established as the standard for wastewater irrigation scheduling in gladiolus. The study suggests that using a 50% MAD irrigation schedule can improve the quality and production of gladiolus without adversely affecting soil health during short-term wastewater application.

Theme 2: Efficient Irrigation Technologies for Enhancing Water and Crop Productivity

Water dynamics under drip irrigation with application of hydrogels in red cabbage (*Brassica oleracea* var. *capitata* f. rubra)

Two year field study was conducted to study the effects of various hydrogel application techniques and assess the efficacy of recently developed cross–linked hydrogels (SPG 1118 and Pusa hydrogel) on growth and development of red cabbage using spilt plot design with three replications. The experiment consisted of two – irrigation regimes [full irrigation (100% ETC) and limited irrigation (75 %ETC)] assisted in main plots, with 5–methods of application [root dipping of Pusa Hydrogel, soil application of Pusa Hydrogel, root dipping of SPG 1118, soil application of SPG 1118 and Control – without application of hydrogel] assisted in sub plots. Results revealed that full irrigation recorded significantly higher head yield of ~16% compared to limited irrigation. Likewise, root application of SPG1118 exhibited ~12% over control. Whereas, the magnitude of increase in head yield under SPG1118 hydrogel was ~4% over Pusa hydrogel. Plant growth parameters viz; Plant height, number of leaves and plant height were significantly higher in root applied SPG 1118 hydrogel compared to soil applied Pusa hydrogel and control. However, higher root length (19–20.75 cm) and lower root volume (51.78–53.32 g) were observed in control compared to both hydrogels due to vertical development of root. Also, root application shows improved NPK uptake in head and leaf compared to soil application and control. Root applied SPG 1118 applied plots had 5-6% higher soil moisture content than no-hydrogel applied plots. Likewise, CWP, IWP and BC ratio were found higher in root applied SPG 1118 hydrogel. Therefore, combining root application of SPG 1118 with drip irrigation and fertigation further boosts the efficacy of hydrogel while reducing overall water and nutrient losses due to evaporation and deep percolation.

Crop evapotranspiration and soil moisture depletion based irrigation scheduling under drip fertigation in cabbage

The present study was conducted to investigate the impact of crop evapotranspiration (ETc) and soil moisture depletion (SMD)-based irrigation scheduling on yield, water productivity and profitability of cabbage crops under drip fertigation. The experiment was carried out in the research farm of Water Technology Centre, ICAR- Indian Agricultural Research Institute, New Delhi during the rabi season 2023–2024. The eight irrigation treatments were imposed for cabbage cultivation based on ETc (100%, 90%, 80%, 70%) and SMD (10%, 20%, 30%, 40%) to determine the optimum moisture regime for the cabbage crop under sandy loam soil. The CROPWAT model was used to compute reference evapotranspiration (ET0) using weather parameters such as temperature, humidity, wind speed, and sunshine hours. The Crop coefficient at different stages of the crop growth period was taken from FAO 56. The available water content of the soil at different depths was estimated using a pressure plate apparatus and accordingly, the irrigation water was applied at different levels of SMD. The analysis indicated that the minimum irrigation water applied in the 70% ETc treatment was 91 mm, while the maximum irrigation water applied in the treatment SMD 20% was 153 mm. The maximum yield was observed as 57.4 t/ ha in SMD 20% treatment. The maximum benefit-cost ratio was found in ETc 100% as 2.65 followed by 2.63 in SMD 20% treatment. Therefore, the study recommended that either 20% soil moisture depletion or 100 crop evapotranspiration treatment could be practised for cabbage cultivation under sandy loam soil in semi-arid regions.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Ankit Pratap Singh (21898)	M.Sc.	Standardization of irrigation scheduling for soil moisture sensor-guided wastewater use in Gladiolus (*Gladiolus grandiflora* L.)	Dr. D.S. Gurjar	ICAR-IARI, New Delhi
2.	Mohd Ekhlaq (21899)	M.Sc.	Crop evapotranspiration and soil moisture depletion based irrigation scheduling under drip fertigation in cabbage	Dr.V.K. Prajapati	ICAR-IARI, New Delhi
3.	Kishor N. (11639)	Ph.D.	Water dynamics under drip irrigation with application of hydrogels in red cabbage (*Brassica oleracea* var. *capitata* f. rubra)	Dr.Manoj Khanna	ICAR-IARI, New Delhi

Session IV: School of Basic Sciences

Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Biochemistry	09	02
Molecular Biology and Biotechnology	19	09
Plant Physiology	08	04
Total	**36**	**15**

SCHOOL OF BASIC SCIENCES

Chairperson: Dr. P. Ananda Kumar, Former Director, ICAR-NIPB, New Delhi

Dr. P. Ananda Kumar served as Director, National Institute of Plant Biotechnology (NIPB), New Delhi, India; Director, Institute of Biotechnology, Acharya N.G. Ranga Agricultural University, Hyderabad and Director, ICAR-Indian Institute of Rice Research, Hyderabad. Dr. P. Ananda Kumar is a botanist who specialized in Plant Physiology, Molecular Biology and Biotechnology. He obtained his M.Sc. degree in Botany from Sri Venkateswara University, Tirupati. He joined as a Scientist in the Agricultural Research Service of Indian Council of Agricultural Research in 1978. He obtained his Ph.D. degree in Plant Physiology from Indian Agricultural Research Institute (IARI), New Delhi. After working as Alexander von Humboldt Fellow in the University of Hannover, he moved to Biotechnology Centre, IARI in 1993. He specialized in the area of transgenic development for insect resistance utilizing the genes encoding insecticidal proteins of Bacillus thuringiensis. Dr Kumar developed fruit borer resistant brinjal and tomato, which were licensed to private companies. Pod borer resistant pigeonpea expressing two codon-modified Bt genesis is currently undergoing field tests. Dr. Kumar has published over 150 research articles, books and book chapters. He has three patents on codon-modified and chimeric Bt genes viz., Synthetic gene encoding a chimeric δ-endotoxin of Bacillus thuringiensis; Patent No. 237912; 14-1-2010; Synthetic gene encoding Cry1Fa1 δ-endotoxin of Bacillus thuringiensis, Patent No: No. 242768; 9-9-2010 and Promoter from Gossypium hirsutum L. for enhanced expression of foreign genes in late boll developmental stages of cotton, Patent No. 382816; 26-11-2021. His other research interests include functional genomics of rice. Dr. Ananda Kumar is recipient of many prestigious awards, notably, Mahindra Krishi Samriddhi Award - 2011 and Best Institution Award of ICAR - 2010 (both as Director, NRCPB), Recognition Award, National Academy of Agricultural Sciences - 2005, National Bioscience Award, Department of Biotechnology - 2001, VASVIK Award for Agriculture and Industry - 2000, Fellow, National Academy of Agricultural Sciences - 1997, Fellow, National Academy of Sciences, India -2011, Fellow, Alexander von Humboldt Stiftung, Germany - 1991, Fellow, A.P. Academy of Sciences - 2014, Young Scientist Award, Indian National Science Academy -1989, Prof Hiralal Chakravarty Award, Indian Science Congress Association - 1996. He is serving as the Editor, GM Crops and Food (USA) and Secretary, Society for Plant Biochemistry and Biotechnology, India.

BIOCHEMISTRY

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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 as well as to conduct teaching and training programmes to develop skilled human resource in the area of plant biochemistry and molecular biology. The research work carried out by the students of the Division during 2023-24 can broadly be classified into following two themes, for which the significant findings are presented below.

Theme 1: Development and Functional Capacity Evaluation of Nutritionally-rich Food Products

Development and validation of glucose nanosensor for predicting inherent glycemic response

The global prevalence of diabetes mellitus, a chronic metabolic disorder exacerbated by postprandial hyperglycemia, necessitates precise glycemic index (GI) quantification for effective management. Current methodologies for GI assessment are hindered by their labor-intensive nature and high costs, impeding widespread implementation in clinical and industrial settings. This study developed, validated and optimized a high-throughput *in vitro* digestion protocol for predicting glycemic response (GR), integrating an electrochemical glucose nanosensor and machine learning algorithms to enhance assessment efficiency. A comparative analysis of six *in vitro* methods (IVM-1 to IVM-6) was conducted, with optimization of the most efficacious model. The in-house optimized IVM-6 protocol demonstrated superior predictive accuracy (MAE-0.81, RMSE-0.89) and a 37-fold reduction in per-sample costs. The optimized protocol evaluated 53 diverse rice accessions, revealing a segregating predictive GI (pGI) range of 46.98 to 87.26, with corresponding Inherent Glycemic Potential (IGP) values of 21.12 to 77.5. Concurrently, a non-enzymatic electrochemical glucose nanosensor was developed, utilizing V_2O_5 nanomaterials further modified with Ti_3AlC_2 MAX phase. The sensor was characterized using SEM, HRTEM, SAED, EIS, and EDS. To assess its specificity and potential for interference mitigation, the sensor's response was evaluated against glucose and an array of potentially interfering food components, including monosaccharides, disaccharides, and other compounds. The sensor showed strong performance in complex food matrices, with glucose detection in *in-vitro* digesta closely matching colorimetric glucose measurements ($R^2 = 0.857$). Integrating machine learning models, including decision tree ($R^2 = 0.991$) and random forest regressors ($R^2 = 0.984$), yielded high predictive accuracy for glycemic responses. This study is the first to establish a correlation between pGI and IGP ($R^2 = 0.645$), using an innovative approach combining *in vitro* digestion, nanosensor technology, and machine learning. The approach offers rapid, cost-effective, and accurate GR assessments, revolutionizing nutritional labeling, crop breeding, and dietary management to combat the global diabetes epidemic.

Extraction and quantification of eritadenine towards the estimation of its anti-hyperlipidemic effect in Indian Shiitake (*Lentinula edodes*)

The Northeast region of India, a biodiversity hotspot, harbors medicinal mushrooms like Shiitake (*Lentinula edodes*), known for eritadenine, a bioactive compound with anti-hyperlipidemic properties. This study is the first to explore eritadenine in 26 Indian Shiitake accessions. Using Response Surface Methodology, optimal extraction conditions were established at 22 minutes, 36°C, and an 85x dilution factor. Eritadenine content ranged from 0.54 to 68.21 mg/g as screened by UV-Vis and validated through UPLC. *In vitro* assays confirmed eritadenine's anti-hyperlipidemic potential. Among 12 docking targets, HMG CoA reductase and pancreatic lipase exhibited the highest glide scores. Eritadenine inhibited HMG CoA reductase by 55.55% and pancreatic lipase by 69.52% at 100 µg, demonstrating its regulatory role in cholesterol biosynthesis and lipid digestion. Antioxidant activity was assessed using DPPH and β-carotene bleaching assays. Eritadenine showed dose-dependent free radical scavenging, achieving 43.47% activity at 120 mg in the DPPH assay and outperformed synthetic antioxidants like Butylated Hydroxy Toluene (BHT) in the β-carotene bleaching assay. It also mitigated oxidative stress and lipid peroxidation, targeting contributors to atherosclerosis and type 2 diabetes mellitus. This study highlights the nutritional and therapeutic potential of eritadenine and Indian Shiitake mushrooms, aligning with Sustainable Development Goal 3 (Good Health and Well-being). It advocates for their role in addressing non-communicable diseases through plant-based solutions. With support from initiatives like the National Medicinal Plants Board, this work promotes sustainable cultivation of bioactive-rich crops, providing a foundation for future dietary and therapeutic applications of Shiitake mushrooms.

Biochemical approaches for the production of plant derived iron, protein and provitamin A enriched nutrimix powder with improved shelf life

Vitamin A, iron, and protein deficiencies are widespread issues in developing countries such as India, leading to various health problems, including eye disorders, iron deficiency anemia, and impaired growth and maintenance of body tissues. To address these deficiencies, this research focuses on developing an enriched nutrimix powder that combines germinated soybean powder, hydrothermally-treated pearl millet powder, and processed carrot powder. The study utilized Response Surface Methodology (RSM) to determine the optimal combination of these ingredients based on solubility, dispersibility, and water absorption capacity. The best combination of soybean powder, pearl millet powder and carrot powder was found in the ratio of 3:1:4 respectively. Three samples of nutrimix powder were produced using three different methods. Among the various preparation methods evaluated, foam mat drying was identified as the most effective, as it demonstrated superior solubility (55.83%), dispersibility (53.67%), water absorption capacity (693.33%), and antioxidant activity. The foam mat dried sample also exhibited the highest protein content, iron content (6.99 mg/100g), and zinc content (1.51 mg/100g). Carotenoid profiling using UPLC revealed that all samples contained 90-96% provitamin A carotenoids, with the foam mat dried sample achieving a comparable carotenoid content (139.06 mg/100g) to other methods. Sensory evaluation by a panel of experts favored the foam mat dried sample for its color, texture, taste, flavor, and overall acceptability. This sample also showed higher anti-diabetic and antihypertensive properties. It demonstrated lower bulk density (0.39 g/mL), lower moisture content (0.54%), and better storage stability, especially when vacuum-sealed and stored at 2-4°C.The foam mat dried nutrimix powder exhibited higher bioaccessibility of iron, protein, and carotenoids compared to other methods, suggesting enhanced nutritional benefits. This research highlights the potential of different biochemical approaches in developing a plant derived iron, protein and provitamin A enriched, stable, and organoleptically acceptable nutrimix powder to combat nutrient deficiencies in vulnerable populations.

Enrichment of carotenoids in chickpea sprouts (*Cicer arietinum* L.) using plant growth regulators

Chickpea (*Cicer arietinum* L.) is in great demand in the agri-food sector due to its nutritional richness attributed to the presence of high levels of dietary fiber, high-quality proteins and a variety of health-promoting bioactive compounds. The chickpea sprouts are even more nutritious, compared to the seeds, because of higher levels of antioxidants, essential amino acids, and phenolic compounds. However, there are limited studies on carotenoids such as β-carotene (a precursor to vitamin A), lutein and zeaxanthin (crucial for maintaining eye health) in chickpea sprouts. In this study, the goal was to increase the carotenoid content and bioavailability in chickpea sprouts by treating germinating seeds with varying concentrations (100 to 500 μM) of different plant growth regulators viz. methyl jasmonate and methyl salicylate. Additionally, gibberellin A3 and cytokinin 6-benzylaminopurine were combined to mitigate any potential germination inhibition caused by these treatments. Several parameters were evaluated, including total carotenoid content, β-carotene, lutein, zeaxanthin, total phenolic content, apigenin, caffeic acid, ferulic acid, germinationrate, and sprout fresh weight in 4 days seed-old germinated seedlings. The findings revealed that sprouts treated with 250 μM methyl salicylate showed 4.1-fold and 4.4-fold increase in carotenoid and phenol content respectively without significantly affecting sprout fresh weight or germination rate. Furthermore, nutritional analysis indicated a 1.3-fold increase in amino acid content, a 2.1-fold enhancement in carotenoid antioxidant activity, and a 4.3-fold reduction in phytic acid (an anti-nutrient factor) with this treatment. Interestingly, there was no significant increase in mineral (iron and zinc) content. Functional analysis demonstrated a 2.1-fold increase in carotenoid bioaccessibility, a 2-fold improvement in inhibiting copper-induced oxidation of low-density lipoprotein (LDL), and a 1.8-fold increase in anti-diabetic activity as measured by α-amylase inhibition. The study suggests that methyl salicylate has considerable potential for enhancing carotenoid content and improving the nutritional profile of chickpea sprouts.

Characterization of protein digestive properties and functionality of millet protein isolates blends after processing treatments

Millet protein contains a higher amount of essential and non-essential amino acids including leucine, phenylalanine, proline, serine, tyrosine, aspartic and glutamic acid. Compared to rice, wheat, and maize, millets are better in terms of protein, minerals, and vitamins. Hence, it's vital to develop methods for isolating millet proteins along with optimized food processing for ensuring the protein quality. A modified iso-electric method was used to extract protein isolates from various millets, with crude protein content being highest in pearl millet (73. 52%), followed by foxtail millet (65. 62%), proso millet (60. 12%), and finger millet (57. 2%). Our study examined nitrogen and crude protein content in isolates after different treatments (infra-red, steam, microwave). Infra-red treatment for 5 minutes resulted in the least protein loss and highest in-vitro protein digestibility (IVPD) compared to control, steam and microwave treatments for all the millets; therefore infra-red treatment for 5 minutes was utilized for making treated millet protein blend (MB) in the ratio (pearl: proso: foxtail: finger :: 3:3:2:2). A control millet protein blend (MB) of the isolates was also made in the same ratio for comparisons. Infra-red treated MB had improved digestibility and solubility. Analysis also showed better functional properties, indicating the effectiveness of Infra-red processing in enhancing the quality of MB for vegan meat analogues. Further SEM results showed treated MB had more fragmentation and higher surface area, leading to increased solubility and digestibility. SDS-PAGE results showed differences in band intensity of protein subunits between treated and control samples which may have affected the difference in functional properties. Thus, the present study clearly indicates the efficiency of infra-red processing method in increasing the quality of MB and its utilization in developing meat analogue for vegan population.

Influence of processing treatments on protein digestive properties and functionality of pulse protein isolate blends

Pulses are valued for their excellent nutritional content and are promoted in health programs to combat malnutrition. Lentils, chickpeas, mung beans, and soybeans are increasingly recognized for their nutritional value (essential amino acids, fiber, vitamins, and minerals). To improve their protein availability and digestibility, protein isolation and thermal treatments are crucial. This study focused on extracting protein isolates (PIs) from soybean (Sb), chickpea (Cp), green gram (Gg), garden pea (Gp), and lentil (Ln) using a modified ultrasonication alkali-assisted isoelectric precipitation method. Thermal treatments, including hydrothermal (HT), autoclave (AC), and infrared (IR) heating, were applied for 5 and 10-minute intervals. HT (10 minutes) resulted in the highest *in vitro* protein digestibility. AC treatment negatively affected digestibility. HT-treated PIs (PB-T) were then blended in ratio (SbPI: CpPI: GgPI: GpPI: LnPI = 15:10:30:25:20) to meet the FAO/WHO recommended EAA requirements. PB-T exhibited superior digestibility (90.75%), solubility (62.77%) compared to the control PB-C (86.49% and 56.90%, respectively). Scanning electron microscopy (SEM) revealed increased surface area, leading to increased digestibility in blend, which was further corroborated by the presence of higher free sulfhydryl group content and fragmentation in PB-T, enhancing digestibility and solubility. In emulsion stability, higher stability was observed in PB-T, then further characterized by SDS-PAGE analysis and the results showed differences in band intensity of protein subunits [Lectins (170 kDa), Legumin (20-40 kDa) and Convicillin (290 kDa)] was observed in PB-T compared to PB-C, suggesting that these proteins might imparted emulsion stability to the proteins. Viscosity, foaming capacity, and water/oil holding capacity, were also improved in PB-T. Shelf-life analysis showed PB-T had higher antioxidant activity (34.82% DPPH scavenging) and a reduced comprehensive peroxide value (4.85%), indicating a 50% longer shelf life. These findings suggest that HT treatment (10 minutes) significantly enhances protein quality and shelf life, making HT-treated isolate a viable alternative to animal protein for “smart food” formulations.

Development of processing methods to improve pigeon pea protein quality: by characterizing its effect on polyphenol protein interaction, techno functionality and cytotoxic properties of protein isolates

Pigeon pea (*Cajanus cajan* L.), an important legume crop presents a valuable source of plant-based protein, particularly in regions facing protein malnutrition. However, antinutritional factors like polyphenols hinder its utilization by affecting protein digestibility. This study evaluated the effects of processing treatments (cooking, hydrothermal, autoclaving, infrared heating and germination) on polyphenol composition, protein quality of two pigeon pea genotypes, Pusa Arhar 2018-4 and ICP 1452, characterized by high and low polyphenol contents, respectively as well as functional properties, and biological activities of pigeon pea protein isolates (PpPIs) from them. Total polyphenol levels in 30 genotypes ranged from 215.33 to 1250.22 mg GAE/100 g, with darker seed coats correlating with higher concentrations. LC-MS identified 16 polyphenols in Pusa Arhar 2018-4 and 14 in ICP 1452, with biochanin A as a predominant compound. Processing treatments reduced antinutritional factors, increased essential amino acids (0.78–6.95%) and *in vitro* protein digestibility (IVPD), reaching 84.32% in Pusa Arhar 2018-4 and 90.4% in ICP 1452. Autoclaving was most effective, reducing total polyphenols (36.49%) and trypsin inhibitor activity (68.58% in Pusa Arhar 2018-4, 64.97% in ICP 1452) and enhancing degree of hydrolysis. Structural analysis (SDS-PAGE, FTIR, SEM and CLSM) showed reduced protein-starch interactions, increased enzyme accessibility and changes in protein structure. Autoclaving significantly altered functional properties, including reduced protein solubility and water-holding capacity, while improving oil-holding capacity, foaming capacity (22.9–34.31%) and emulsifying stability. Cytotoxicity assays confirmed no adverse effects and autoclaved hydrolysates exhibited improved amino acid bioavailability and upregulated PepT1 gene expression in Caco-2 cells, suggesting enhanced protein absorption and potential cholesterol regulation. Molecular docking revealed strong biochanin A interactions with globulins, with autoclaving reducing binding affinity. These findings demonstrate the potential of thermal processing to enhance pigeon pea protein quality, digestibility and functional properties, paving the way for its broader food and health applications.

Theme 2: Understanding Nutritional Quality and Abiotic Stress Tolerance of Crop Plants

Unravelling the trans-generational efficacy of seed priming towards morpho-physiological and biochemical imprints to mitigate drought stress in rice (*Oryza sativa* L.)

This study represents the first exploration of seed priming effects on transgenerational drought resilience in rice (*Oryza sativa* L.), a staple food for over half the global population. Climate change, particularly drought, poses significant threats to rice yield and production stability, necessitating innovative strategies. This research investigates a novel approach combining seed priming with stress memory assessment across generations to enhance drought tolerance. Second-generation rice plants were derived from seeds of the first generation primed with the cocktail of methyl jasmonate, iron sulfate, and zinc sulfate (MJIZ). This priming induced beneficial morpho-physiological and biochemical imprints, transferable across generations. Significant improvements were observed in traits such as relative water content (RWC), endogenous ABA, chlorophyll a/b, carotenoid content, soluble protein (SP), total phenolic content (TPC), proline, lipid peroxidation (LP), protein oxidation (PO), antioxidant activity, and enzyme activities (SOD, POX, CAT) in drought-tolerant (N-22) and drought-sensitive (PS-5) genotypes. Under drought, PS-5 outperformed N-22 in yield traits like tillers per plant (TNP), panicles per plant (PN), and test grain weight (TGW). Both genotypes exhibited a modest 3-4% reduction in chlorophyll content, while N-22 showed a 65% increase in TPC. PS-5 displayed a 70% increase in DPPH scavenging activity, while N-22 exhibited superior antioxidant enzyme activity, underscoring its inherent drought tolerance. Proline content increased 5-fold in N-22 and 4.5-fold in PS-5. Double-stressed second-generation samples retained robust stress memory, with higher morpho-physiological and biochemical performance compared to unprimed controls. Correlation analysis revealed strong positive associations among yield traits and stress-responsive parameters. This study establishes a cost-effective, user-friendly seed priming technique for enhancing drought resilience across generations. Future research should explore molecular mechanisms, including epigenetic modifications, to sustain long-term drought tolerance and improve crop productivity under changing climatic conditions.

Effect of melatonin on rice rhizosphere microbiota and associated soil enzymes

This study evaluated the effects of melatonin concentrations (0, 50, 100, and 150 ppm) on soil properties and microbial activity. Key parameters analyzed included soil pH, electrical conductivity (EC), nutrient availability, and microbial populations. The results indicated that melatonin application reduced soil pH and increased EC, with these effects becoming more pronounced at higher doses. The availability of essential nutrients, including organic carbon, nitrogen, phosphorus, and potassium, improved significantly, with maximum levels observed at 150 ppm. Secondary nutrients such as calcium and magnesium also increased with melatonin application, further enhancing soil quality. Microbial populations, including bacteria, fungi, and actinomycetes, responded positively to melatonin treatment. The highest microbial counts were recorded at 150 ppm, though populations gradually declined over time. Additional analyses of the optimized 150 ppm dose revealed notable increases in enzyme activity and the growth of beneficial microorganisms, such as nitrogen-fixing and phosphate-solubilizing microbes. These findings suggest that melatonin not only boosts soil fertility but also fosters an environment conducive to microbial activity, crucial for sustainable agricultural practices. The study highlights melatonin's potential as an effective soil amendment, particularly at 150 ppm, for enhancing soil health and nutrient availability. By improving soil properties and promoting beneficial microbial activity, melatonin could reduce the reliance on chemical fertilizers and contribute to more sustainable farming practices. This research broadens our understanding of melatonin's role in soil ecosystems and offers a promising strategy for improving agricultural productivity while supporting environmental sustainability. Further studies could explore long-term impacts and applications of melatonin in various soil and crop systems, paving the way for its practical use in agriculture.

Study on differential accumulation pattern of L-DOPA in faba bean (*Vicia faba* L.) leaves: Biochemical and molecular perspectives

Bean (*Vicia faba* L.), a winter legume, is a natural source of L-3,4-dihydroxyphenylalanine (L-DOPA), a potential therapeutic agent for Parkinson's disease. Profiling of L-DOPA and other catecholamines indicated that very young leaves (VYL) exhibit higher metabolite accumulation compared to mature leaves (ML). The study demonstrated a genotypic and developmental stage-specific dependence in L-DOPA accumulation within leaf tissues. Elevated levels of L-DOPA and its precursor molecule, i.e. L-tyrosine in young leaves suggest a precursor-induced metabolite content, whereas the reduced availability of L-tyrosine in mature leaves likely accounts for their lower L-DOPA accumulation. Additionally, the study observed preferential accumulation of phenolics in young leaves, while flavonoids and tannins were more prevalent in mature leaves, indicating a possible shift in metabolic flux towards complex phenolic synthesis during leaf maturation. Gene expression analysis of polyphenol oxidases (PPOs) in VYL and ML revealed selective and differential expression of PPO genes in leaves. Among the induced genes, such as*Vf*1g760, *Vf*1g240, *Vf*1g640, and *Vf*1g440, the induction of *Vf*1g440 was found to be significantly higher. The redirection of metabolic flux associated with the developmental processes may be further studied using multiomics approaches to understand regulatory network controlling the L-DOPA accumulation in Faba bean.

Comparative analysis of seed quality among tolerant and sensitive rice cultivars (*Oryza sativa* L.) in response to drought stress

This study explored the effects of drought stress on the metabolome, proteome, and nutritional indices in the grain and bran of Nagina 22 (N22; drought-tolerant) and Indica rice 64 (IR64; drought-sensitive). Metabolomic profiling revealed that N22 grain and bran had a greater number of significantly upregulated metabolites than IR64 under drought. There was enhanced upregulation of phenols, flavonoids, and anthocyaninsin the bran of N22 and IR64 as compared to their grain fractions. Protein profiling revealed upregulated proteins associated with glycolysis, starch, sucrose metabolism, and defence in N22. Genes associated with grain filling and sucrose transport (e.g., SUS, SUT, INV, SWEET, Snrk2) were significantly upregulated in N22 under drought. Except for carbohydrate and amylose content, bran had higher concentrations of proximate nutrients, minerals, and amino acids than grains in both genotypes. Protein content ranged from 9-11% in grain to 13-15% in bran, whereas amylose was higher in N22 grain (20.44%) compared to bran (4.84%) under drought. N22 accumulated significantly higher levels of amino acids and carbohydrates in bran and grain than IR64. Proline accumulated at a higher concentration (2.732 g/100g) than other amino acids in N22 under drought. Fatty acids, such as palmitic, linoleic, and oleic acids dominated, whereas myristic and linolenic acids had the lowest content in grain and bran of both genotypes. IR64 grain under drought exhibited the maximum concentration of micronutrients (Fe, Mn, Zn, and Cu). Macronutrients (Na, Ca, K, Mg, P) increased under drought in both genotypes. Phytohormones (ABA, IAA, Zeatin) increased under drought and the increase was more in N22 grain and bran than IR64. A strong interaction between starch-lipid-protein was observed under control, which loosened under drought in both grain and bran. Bran showed stronger starch-lipid interactions due to higher lipid content than grains. This study unveiled potential molecular targets for breeding drought-tolerant and nutritionally-enhanced rice varieties.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Mohammed Salman C K (21754)	M.Sc.	Development and validation of glucose nanosensor for predicting inherent glycemic response	Dr. Veda Krishnan	ICAR-IARI, New Delhi
2.	Bidyutprava Nayak (21755)	M.Sc.	Extraction and quantification of eritadenine towards the estimation of its anti-hyperlipidemic effect in Indian Shiitake (*Lentinula edodes*)	Dr. Archana Singh	ICAR-IARI, New Delhi
3.	Prathwinraj A (21756)	M.Sc.	Biochemical approaches for the production of plant derived iron, protein and provitamin A enriched nutrimix powder with improved shelf life	Dr. Sweta Kumari	ICAR-IARI, New Delhi
4.	Madhunisha Chandrashekar (21757)	M.Sc.	Enrichment of carotenoids in chickpea sprouts (*Cicer arietinum* L.) using plant growth regulators	Dr. Sweta Kumari	ICAR-IARI, New Delhi
5.	Soumili Nayak (21901)	M.Sc.	Characterization of protein digestive properties and functionality of millet protein isolates blends after processing treatments	Dr. Suneha Goswami	ICAR-IARI, New Delhi
6.	N. Mansoor Shaji (21936)	M.Sc.	Influence of processing treatments on protein digestive properties and functionality of pulse protein isolate blends	Dr. Vinutha T	ICAR-IARI, New Delhi
7.	Shakthi Thangavel E. (21937)	M.Sc.	Unravelling the trans-generational efficacy of seed priming towards morpho-physiological and biochemical imprints to mitigate drought stress in rice (*Oryza sativa* L.)	Dr. Archana Singh	ICAR-IARI, New Delhi
8.	P. Arunkumar (21938)	M.Sc.	Effect of melatonin on rice rhizosphere microbiota and associated soil enzymes	Dr. Aruna Tyagi	ICAR-IARI, New Delhi
9.	Ayush Singhania (90027)	M.Sc.	Study on differential accumulation pattern of L-DOPA in faba bean (*Vicia faba* L.) leaves: Biochemical and molecular perspectives	Dr. Sujit Bishi	**IARI-IIAB, Ranchi
10.	Minakshi Dutta (11734)	Ph.D.	Development of processing methods to improve pigeon pea protein quality: by characterizing its effect on polyphenol protein interaction, techno functionality and cytotoxic properties of protein isolates	Dr. Vinutha T	ICAR-IARI, New Delhi
11.	Nand Lal Meena (11907)	Ph.D.	Comparative analysis of seed quality among tolerant and sensitive rice cultivars (*Oryza sativa* L.) in response to drought stress	Dr. Aruna Tyagi	ICAR-IARI, New Delhi

***Outreach institute*

MOLECULAR BIOLOGY AND BIOTECHNOLOGY

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Prof. Jasdeep C. Padaria

ICAR-National Institute for Plant Biotechnology (ICAR-NIPB) is the premier research institution of the Indian Council of Agricultural research (ICAR), engaged in plant molecular biology and biotechnology research. Established in 1985, it was initially known as Biotechnology Centre, as the division of Molecular Biology & Biotechnology under the aegis of the Indian Agricultural Research Institute (IARI). In 1993 it was upgraded to a National Research Centre on Plant Biotechnology (NRCPB) with a vision to impart the cutting edge technologies and skills in agricultural biotechnology to the National Agricultural Research System (NARS). NRCPB was later upgraded to full-fledged institute as NIPB in 2019 to provide effective leadership and biotechnology oriented products along with highly trained manpower. Since its inception in 1985, the centre has been contributing significantly to develop a pool of competent human resource by offering regular M.Sc. and Ph.D. programmes in partnership with PG School, IARI as the Discipline of Molecular Biology & Biotechnology (MBB). So far, 196 students have received M. Sc. degree and 145 students have received Ph. D. degree in MBB. Additionally, NIPB agreed to initiate and take full responsibility for conducting the UG programme, B. Tech. Biotech., from AY 2022-23. Currently 68 Ph.D. and 15 M. Sc. are registered in the Discipline of Molecular Biology and Biotechnology. A total of 53 students are registered under B. Tech. Biotech. program. The research work carried out by the students of the Division during 2023-24 can broadly be classified into following six themes, for which the significant findings are presented below.

Theme 1: Search and Deployment of Genes for Stress Tolerance and Yield Traits in Rice (*Oryza sativa* L.)

Molecular characterization of genes governing heat tolerance in rice

In the current climate change scenario, rice grain yield is estimated to decrease by 41% by the end of 21st century, due to high temperature stress (HTS). Though several QTLs for HTS are reported in rice, only a few candidate genes (CGs) underlying these QTLs have been delineated. This research was undertaken with the twin objectives of (i) identification of the CGs underlying three major QTLs for HTS, *qspf4.1*, *qSTIY5.1* and *qSTIPSS9.1*, from a recombinant inbred (RI) population of, IR64 and Nagina22, contrasting for HTS and (ii) functionally validate one of the CGs for HTS tolerance. There were 18, 54 and 65 genes in the three QTL regions *qspf 4.1*, *qSTIY5.1* and *qSTIPSS9.1,* respectively. Thirty-two genes, amongst them showed SNPs in genic regions. Network analysis of the CGs identified 57 interacting partners. The ratio of unique to common amino acid substitutions between IR64 and N22, with reference to Nipponbare, was higher in QTL-genes, 2.93-fold (2.58:0.88), compared to the network genes, at 1.313-fold (0.88:0.67). Expression analysis of these 89 (=32+57) genes under heat stress identified 43 DEGs, i.e., 16 from QTL and 27 from network genes. *OsHSFB4C* (LOC_Os09g28200), a HSF from *qSTIPSS9.1*, was selected for functional validation. Time course expression analysis of *OsHSFB4C* in panicles and flag leaves confirmed its differential HTS response in the parents and extreme RI lines. Both the allelic variants of this gene were cloned into pCAMBIA1300, transformed into GV3101 *Agrobacterium*, and used for *Arabidopsis* transformation. The overexpression (OE) transgenic lines were validated with vector-specific primers. T_2OE lines of N22 allele showed enhanced HTS tolerance while that of IR64 didn't. Expression analysis of *OsHSFB4C* in the transgenic line validated the findings. Thus, the current research provided an insight about heat responsive genes which could be promising players in HTS and functionally characterized one of them.

Identification, characterization and functional validation of drought-responsive microRNA(s) in rice (*Oryza sativa* L.)

Rice, a staple food crop, faces frequent drought stress incidences, due to climate change, thus endangering food security. In this context, identification of genes and regulons that impart drought tolerance assumes greater significance for deployment in crop production. MicroRNAs are one such important regulon with a major role in abiotic stress management. This study was undertaken with the objectives of (i) in-silico identification of drought-responsive (DR) miRNA-mRNA modules in rice and their integration with drought-tolerant QTLs (ii) validation of the modules identified by expression profiling and (iii) functional validation of one of the DR miRNAs. From two pairs of rice genotypes with high and low drought tolerance, DR miRNA-mRNA modules were identified by integrating sRNA and degradome-sequencing data. These modules were then overlaid on drought tolerant QTLs which narrowed them to 61 target genes and 18 miRNAs. Major DR miRNAs identified were Osa-miR2919, Osa-miR3979, Osa-miR169a, Osa-miR397a and Osa-miR530-3p in which Osa-miR2919 was found to be involved in regulation of cytokine and brassinosteroid synthesis whereas rest were involved in grain filling and seed sterility under drought stress. Meta-analysis of sRNA data from all the publically available 28 datasets resulted in the identification of 216 known DEMs and 759 putative novel miRNAs. The DEMs that were represented by more than three genotypes/tissue included members from the Osa-miR166, Osa-miR156, Osa-miR160, Osa-miR408, Osa-miR530 and Osa-miR396 families. To make the results of the meta-analysis easily accessible, a database named 'RiceMetaSys: Drought_miR' (http://14.139.229.201/RiceMetaSys_miRNA/), was developed. Expression analysis validated 18 DEMS and 33 target genes in eight rice genotypes under drought stress. Canopy temperature measurements using IR cameras clearly distinguished the genotypes based on their degree of drought tolerance. *Arabidopsis* transgenic developed for Osa-miR3979 showed enhanced root growth and osmotic stress tolerance. Further analysis led to identification of Osa-miR3979 as a regulon of AT2G37940, AT1G6381 and AT3G18400.

Exploiting OsmiR167-OsARF12 module for improved root system architecture in rice through CRISPR/Cas9-based genome editing technology

Rice sustains over half the global population, especially in Asia, but its production faces declining yields and high water demands. With a growing population, enhancing rice productivity is urgent need. Root system architecture (RSA) plays a vital role in stress tolerance, as it facilitates water and nutrient uptake, hormone regulation, and overall productivity. Auxin, particularly Indole-3-acetic acid (IAA), is key in RSA regulation via auxin response factors (ARFs). Among these, OsARF12 is critical for root development. However, OsARF gene expression is tightly regulated by factors like microRNAs (miRNAs), notably miR167, which binds to OsARF12 coding sequences, suppressing its expression and limiting RSA robustness. This study analyzed miR167 and OsARF expression, revealing that miR167 post-transcriptionally regulates OsARF12 and OsARF25 in roots and OsARF12 and OsARF17 in shoots. 5'RLM-RACE confirmed miR167-mediated cleavage of OsARF6, OsARF12, OsARF17, and OsARF25. To overcome this regulation, a prime editing guide RNA (pegRNA) was designed and integrated into a CRISPR prime editing vector to disrupt the miR167 binding site in OsARF12 without altering its protein sequence. Restriction digestion analysis confirmed successful pegRNA integration. This strategy aims to enhance root elongation and iron accumulation in rice by modifying OsARF12 regulation. The proposed approach could lead to development of rice varieties with improved RSA, drought tolerance, and grain yields, addressing global food security challenges.

Screening and characterization of T DNA-free multigenic genome edited rice mutants of *Pi21*, *MPK5* and *Spl11* for blast resistance

The rice blast, caused by *Magnaporthe oryzae*, is a significant threat to global rice production, leading to severe yield losses. To combat this, breeding programs have focused on incorporating resistance (R) genes. An alternative approach involves targeting negative regulators of blast disease resistance using CRISPR/Cas9-mediated genome editing. In a previous study in our laboratory, multiplexed CRISPR/Cas9-mediated genome editing was employed to knock out three well-known negative regulators of blast resistance (*MPK*5, *Spl*11 and *Pi*21). This study analysed the genome-edited Taipei 309 rice plants of the T_1 generation to assess transgene segregation, mutation inheritance, and disease resistance. T-DNA region-specific PCR confirmed the presence of the CRISPR/Cas9 transgene in 11 of the 13T_1 generation plants, while two plants were identified as transgene-free. Gene-specific PCR and Sanger sequencing revealed that the *Pi21* gene was knocked out via a 1 bp insertion in all mutant lines, leading to both frameshift mutations and premature termination codons producing non-functional proteins. Similarly, *MPK5* and *Spl11* knockouts were achieved through insertions, deletions, and substitutions, resulting in truncated proteins. Approximately 53% of the mutations in *MPK5* and 61% in *Spl11* were heterozygous, while the rest were homozygous. Phenotypic characterization of the Cas9-negative, multigenic genome-edited plants using a detached leaf assay demonstrated enhanced resistance to rice blast compared to the wild type, with significantly smaller lesion sizes. Two T_1 plants were identified as transgene-free based on *Cas9* PCR assay and carried mutations in all three targeted genes, although some mutations were heterozygous. Further generations are expected to yield homozygous mutations, providing a stable line for use in breeding programs aimed at enhancing blast disease resistance. This study highlights the potential of multiplex genome editing using known negative regulators to develop rice varieties with durable resistance to rice blast, thereby contributing to global food security.

Targeted alterations in conserved structural motif in central repeat domain of a *Xanthomonas oryzae* pv. *oryzae* TAL effectors to study effect on virulence in rice

Xanthomonas oryzae pv *oryzae*, causal for rice bacterial blight disease, deploys DNA binding protein, Transcription activator like effectors (TALE) to hijack host genes. Its central repeat domain is composed of 34 amino acids long tandem repeats. The sequence and number of 12th and 13th residues of each repeat, Repeat Variable Di residue (RVD)in a TALE decides its specificity for the host target. *SWEET13*, major rice bacterial blight susceptibility gene, is targeted by TALE PthXo2 to cause disease on *indica* rice. The *japonica* allele of SWEET13 evades binding of PthXo2 and is resistant. PhoX2B, an ortholog of PthXo2 harbors aberrant 36 as in two of its repeats causing frame shift in binding to *japonica* allele. A PthXo2B cloned from an Indian *Xoo* strain IX-221 (named as Tal7) in our lab causes disease in both *indica* and *japonica* rice. But, its RVD identical designer TALE (dTALE) with custom repeat backbone does not. Sequence comparison identified differences in repeat backbone indicating its possible role in impacting TALE targeting profile. Current work was designed to test this hypothesis, by generating dTALEs with the motifs as in the native Tal7 and also to generate variants of Tal7 to test if either or both motifs and if its location matters. PCR directed site directed mutagenesis for desired amino acids in 4th and 6th repeat sequence carrying plasmids, was carried out. All 21.5 repeats constituting the Tal7 including the modified repeats were sequentially assembled using Golden gate cloning and cloned into expression vectors through Gateway cloning followed by transformation of *Xoo* strain PXO99A-ME2 with the expression constructs. Thus, the work has generated five constructs ready for artificial infections on *indica* rice, to test if the motifs in backbone are responsible for virulence on *indica* rice. It would help in identifying the novel S gene in *indica* and pave the way for a new perspective on target recognition by TALE.

Molecular dissection of the *qGN4.1* QTL underlying high grain number phenotype in rice

Yield in rice is primarily determined by grain number per panicle (GNPP), grain weight, and tiller number and numerous genes and QTLs controlling the trait have been identified. Here, we investigate the previously identified QTL *qGN4.1*, located on chromosome 4 responsible for phenotype high grain number per panicle (comment: can be replaced with GNPP) in rice. The objective of this study was to refine and narrow down *qGN4.1* for which a fine mapping population was developed by crossing the rice mega variety, Samba Masuri (SM), with its high-yield variant, *qGN4.1*, QTL introgressed NIL Annapurna (SM-*qGN4.1*). Homozygous recombinants generated in F2:3 population were comprehensively analysed and upon comparing the genotypic and phenotypic data, the QTL region was further narrowed down to a 70 kb region delimited by two KASP markers LOC_Os04g52479_KASP-1 and LOC_Os04g52590_KASP-2. This 70 kb region includes the gene *LOC_Os04g52590*, which has previously been identified as highly overexpressed in high GNPP QTL introgressed lines compared to low GNPP lines, indicating its role in regulating the high GNPP phenotype in *qGN4.1* QTL introgression lines. Analysis of the promoter region, 2 kb upstream of the *LOC_Os04g52590* gene, in both SM and SM-qGN4.1 revealed a higher abundance of certain cis-regulatory elements, along with a unique element involved in endosperm expression in SM-qGN4.1[U1] . These structural differences in the promoter region of SM-qGN4.1 QTL NILs [U2] may contribute to the observed consistent differential expression of the gene and the higher yield phenotype. To investigate further, we cloned the promoter region into a reporter series binary vector for expression analysis and also generated a vector construct to knock out LOC_Os04g52590 in high GNPP QTL NILs. The constructs have been mobilized in rice plants, and the results are pending. Overall, the study aimed to delimit the *qGN4.1* locus to gain a deeper understanding of the molecular network underlying the contribution of *LOC_Os04g52590* to the high grain number per panicle phenotype in rice.

Theme 2: Molecular Mechanism for Stress Tolerance and Nitrogen Uptake in Wheat (*Triticum aestivum* L.)

Elucidating the molecular processes underlying acquired and transgenerational thermotolerance in wheat

Wheat (*Triticum aestivum* L.) is a critical global staple crop, but its productivity faces threats from increasing heat stress exacerbated by climate change. High temperatures during key growth stages, such as anthesis and grain-filling, negatively impact growth, physiology, and yield by reducing photosynthetic efficiency, increasing respiration rates, and impairing metabolic processes. This study investigates the potential role of melatonin seed priming to mitigate heat stress effects at the terminal growth stage in wheat. Melatonin, an indole compound, enhances oxidative stress tolerance by scavenging reactive oxygen species (ROS), activating antioxidant mechanisms, and improving physiological functions. A two-year experiment was conducted using two diverse wheat genotypes: heat-tolerant (HD 3271) and heat-sensitive (HD 2967). The treatments included control, heat priming, melatonin priming, and combined melatonin-heat priming under ambient and high temperatures. Physiological, morphological, biochemical, and molecular parameters were analyzed to evaluate performance. Melatonin priming improved germination, chlorophyll content, membrane stability, and stress-related gene expression. Enhanced accumulation of sugars (raffinose, sucrose, glucose, and fructose) and modulated hormone levels (ABA, GA3) under stress suggested melatonin's role in maintaining metabolic balance. Transcriptome analysis identified differentially expressed genes linked to photosynthesis, antioxidant systems, and hormonal pathways, highlighting melatonin's regulatory role. Melatonin priming demonstrated transgenerational benefits, improving stress tolerance in subsequent generations. Diverse heat responsive genes showed regulation under heat stress, confirming the protective effects of melatonin in imparting heat tolerance. These findings reveal the potential of melatonin seed priming as a sustainable strategy to enhance wheat thermo tolerance and ensure stable yields in a warming climate.

Identification of Quantitative Trait Loci (QTLs) associated with tolerance to salt stress in wheat

The present study aimed to map QTLs associated with salt tolerance at the vegetative and reproductive stages using a recombinant inbred line population derived from a cross between HD2851 and Kharchia 65 (KH65). Mapping population of 195 recombinant inbred lines (RILs) of wheat was evaluated at vegetative and reproductive stages under control and salt stress conditions during the 2022-23 and 2023-24 growing seasons. Correlation analysis showed a significant positive correlation ($p<0.01$) between grain yield and chlorophyll content, K^+/Na^+ ratio, plant height, spike length (SL), flag leaf length, flag leaf area and thousand-grain weight. Na^+ content showed a significant negative correlation ($p<0.01$) with grain yield. Genotyping of 195 RIL and two parents was conducted using 35K Axiom Wheat Genotyping Array.1,308 polymorphic SNP markers were used to construct a linkage map covering 8,274.66 cM. A total of 76 QTLs associated with 20 morphological, physiological and yield component traits were identified; 41 were identified under control and 35 under salt stress conditions. These QTLs were distributed across 20 wheat chromosomes, excluding chromosome 2D. The positive alleles for 24 QTLs were derived from KH65, while the alleles from HD2851 had negative effects on 52 QTLs. Twelve major QTLs were identified for shoot length (*QSl.Ctrl-5A*), root length (*QRl.Ctrl-7D* and *QRl.Ctrl-3B*), shoot fresh weight (*QSfw.S-4B*), shoot dry weight (*QSdw.S-4B*), total dry weight (*QTdw.S-7A* and *QTdw.S-7D*), Na^+ content (*QNa⁺.S-2A*), days to heading (*QDth.S-6B.1*) and salt tolerance index (*QSti.S-5B*, *QSti.S-4B* and *QSti.S-7A*), explaining 10.02% to 14.36% of the phenotypic variance. *In silico* analysis of genomic regions identified candidate genes *TraesCS6B03G1189600* (Glutathione transferase) and *TraesCS7A03G1088600* (Cytochrome P450 monooxygenase). These genes significantly upregulated under salt stress. Thirty SNP markers were closely linked to QTLs associated with salt tolerance traits. These identified markers can be used in marker-assisted selection (MAS) to improve salt tolerance in bread wheat genotypes. The candidate genes can be isolated and functionally characterized to better understand their role in salt tolerance.

Molecular characterization of a high-affinity nitrate transporter gene (*TaNRT2.5*) of bread wheat (*Triticum aestivum* L.)

Nitrate is one of the primary forms of nitrogen available in soil taken up by plants majorly through two types of nitrate transport systems, i.e., LATS (Low-Affinity nitrate Transport System) and HATS (High-Affinity nitrate Transport System). One of the genes encoding HATS, i.e., *TaNRT2.5*, has been shown to be expressed specifically in shoot than other 46 *TaNRT2* genes identified genome-wide in the bread wheat reference genome. Interestingly, this is the most ancient gene, and the homeologs of this gene contain an intron of different lengths, often absent in monocot, contrary to other *NRT2s* genes, indicating different layers of its regulatory control. The present study aimed at cloning and characterizing the *TaNRT2.5* gene and corresponding promoter sequence from a high nitrate uptake efficient wheat genotype, K9107. The cDNA sequence of A homeolog showed a high degree of sequence homology with Chinese Spring (CS), except for substituting two amino acids in the cytosolic loop. However, among promoter sequences cloned, *TaNRT2.5-D* upstream sequence showed insertion of 62 bp than that of CS along with three extra Cis-Regulatory Elements (CREs), one of them indicating drought inducibility. Three reporter constructs, including a deleted *TaNRT2.5D* promoter, were generated for further investigation. Later, Arabidopsis transgenic stable lines were also generated using these reporter (GUS) constructs. The *TaNRT2.5A* promoter activity is confirmed by transient GUS expression. Further, to gain an insight into the differential homeolog expression of *TaNRT2.5*, qPCR analysis was conducted in root, leaf, and shoot tissues of the 14-day-old K9107 wheat seedlings under drought and nitrogen stress conditions. The fold change expression pattern showed differential expression of homeologs, indicating control of different CREs in gene expression under different stress conditions and in different tissues. The present study lays the foundation for further studies to unravel the underlying mechanism of TaNRT2.5 in nitrate transport under different N regimes and drought conditions.

Identification of genes that are potential negative regulators of heat stress tolerance in wheat

The study aimed at identifying potential negative regulators of heat stress tolerance in wheat. Based on the negative log2 fold values, 12 candidate genes were selected from the transcriptome data of heat stress tolerant wheat genotype Raj 3765 (SRR16347581 and SRR16347579; Azameti et al., 2022). *In silico* analysis, revealed that the selected 12 candidate genes have 100% identity with genes of *T. aestivum* cv. Chinese spring. The proteins coded by these genes, especially those on genome D have a role in stress response. The 12 genes selected were analysed for differential expression under heat stress (42^{o}C for 6 hours) at 30-day old seedling stage in a panel of 19 wheat genotypes. qRT-PCR studies revealed that the homolog of gene Id *TraesCS403G0519100* from *T. aestivum* cv. Chinese spring was up-regulated in heat sensitive genotype HD-2967 and DWR-1006. Up-regulation of the candidate gene, in the heat sensitive genotypes, suggests that the said gene may play a role in heat stress tolerance. The homolog of *TraesCS403G0519100* from wheat genotype HD 2967 was cloned and sequenced. The candidate gene isolated from genotype HD2967 was found to be of 377 bp and had 95% identity with *TraesCS4D03G0519100* of wheat cv. Chinese spring. Protein of the candidate gene from genotype HD2967 showed 89.17% homology with a 17.9kDa class I heat shock protein. Our study forms the basis of employing genome editing tools to mutate the identified negative regulator of heat stress tolerance for increasing resilience in wheat against rising temperatures towards ensuring global food security amidst climate change.

Studies on the effect of silicon amendment on pink stem borer *Sesamia inferens* Walker in wheat under climate change scenario

Silicon (Si) plays a vital role in mitigating biotic and a biotic stresses in crops, yet its impact under climate change scenarios remains understudied. This study investigates the impact of silicon amendment on wheat plants infested with the pink stem borer (PSB) (*Sesamia inferens* Walker) under climate change conditions using an open-top chamber (OTC) setup. The experiment included four scenarios: elevated CO2 (600 ± 25 PPM), elevated temperature (+3°C), their combination, and ambient conditions. Results revealed that Si application significantly reduced PSB damage, with dead heart percentages ranging from 12.93% to 19.71% in Si-treated plants, compared to 21.18% to 28.68% in untreated plants. Elevated CO_2 increased dead hearts, while Si application under ambient conditions showed the best outcomes. Larval recovery indicated that Si-supplemented plants produced smaller larvae, demonstrating enhanced plant defense. Morphological assessments showed Si improved shoot and root growth and biomass under climate change conditions. Moreover, Si supplementation altered pest morphology, resulting in smaller mandibles in PSB larvae. Silicon supplementation significantly enhanced defense enzyme activities in wheat plants under stress conditions. Under elevated CO_2, peroxides (22.16 µmol/min/mg protein) and polyphenol oxidase (3.62 absorbance change/min/g) activities were higher in Si-treated plants, Similarly, elevated temperature conditions with Si supplementation increased superoxide dismutase (93.75 units/mg protein), catalase (12.78 nmol/min/mg protein), and phenylalanine ammonia-lyase (17.18 µM Trans-cinnamic acid/min/mg protein) activities. Si also improved TSS, phenols, and protein contents under elevated CO_2, temperature, though these levels were highest in Si-treated plants under ambient conditions. This study underscores the potential of Si in enhancing wheat resistance to PSB, offering a sustainable pest management strategy to address climate change-induced challenges in agriculture.

Theme 3: Developing Aphid-resistance in Mustard (*Brassica juncea*)

Study of aphid effector(s) for developing aphid-resistance in Indian mustard

Mustard aphid (*Lipaphis erysimi* Kaltenbach, Hemiptera: Aphididae) significantly impacts rapeseed-mustard productivity, including Indian mustard (*Brassica juncea* L.). Due to the lack of genetic resistance in cultivated varieties, systemic insecticides are widely used for control. However, aphid populations grow rapidly under favorable conditions, making chemical control ineffective. Additionally, continuous insecticide use has led to resistance development among aphids and raised environmental concerns. Developing sustainable alternatives, such as aphid-resistant mustard varieties, is critical. Traditional breeding methods face limitations due to the absence of resistance sources within crossable germplasms. Thus, molecular understanding on host-aphid interaction is essential to address these challenges. Indian mustard relies on intrinsic defense mechanisms involving jasmonic acid (JA), salicylic acid (SA) signaling pathways, and the Brassicaceae-specific glucosinolate-myrosinase system. The myrosinase enzyme degrades the glucosinolate compounds into toxic derivatives upon herbivore attack. However, mustard aphid's ability to overcome glucosinolate- myrosinase system, rendering host plants susceptible, is not fully understood. In susceptible host-aphid interactions, aphids secrete effector molecules in their saliva that suppress host defenses. Identifying these effectors is vital to understanding how host defenses are compromised. This study examined the differential expression of the glucosinolate-myrosinase pathway in *B. juncea* exposed to two aphid species: mustard aphid, which causes host susceptibility, and cowpea aphid (*Aphis craccivora*) which trigger host resistance. Using gene expression and UPLC-QToF-ESL-MS, the study revealed that mustard aphids down regulated the transcription of the key glucosinolate biosynthetic and myrosinase genes in mustard plants, while these genes were upregulated in manifesting resistance against cowpea aphid. Further, bioinformatics analysis of mustard aphid head transcriptomes identified two effector molecules. Comprehensive gene expression studies in both Indian mustard and *L. erysimi* demonstrated that these effectors play a role in modulating host-defense mechanisms, leading to plant susceptibility. The study generated two potential leads which can be further utilized for devising strategies of developing aphid resistant plants in Indian mustard.

Identification and cloning of a candidate susceptible(s) gene for *Sclerotinia* stem rot disease in Indian mustard (*Brassica juncea*)

Stem rot disease, caused by the fungus *Sclerotinia sclerotiorum*, affects over 600 plant species and significantly impacts oilseed *Brassica* crops, particularly Indian mustard (*B. juncea*). The disease primarily infects the stem, reducing oil quality and yield by up to 90% in severe cases. This study analyzed transcriptomic datasets from susceptible and tolerant cultivars, identifying polygalacturonase (PG) and pectin methylesterase (PME) as key genes. The candidate susceptibility-responsive gene, *BjPME3*, was found to have seven homologs in *B. juncea* cv. Varuna, with structural analysis revealing conserved domains and regulatory elements. Spatiotemporal expression studies pinpointed *BjPME3B5* and *BjPME3A5* as potential susceptibility genes. Gene-specific gRNAs were designed and constructs were developed for CRISPR/Cas9 genome editing. Among 16 effectors tested, SsEC7541 was identified as a strong interacting partner with BjPME3B5. The CRISPR constructs for *BjPME3A5* and *BjPME3B5* aim to enhance resistance in *B. juncea*, while SsEC7541 may be used for Host-Induced Gene Silencing in susceptible plants.

Theme 4: Stress Tolerance and Quality Trait Improvement in Pulses

Identification of key genes associated with seed protein content in chickpea by RNA-seq and small RNA analysis

Chickpea is an important legume crop which provides a source of livelihood to the poor and marginal farmers. The present study explores the genes, microRNAs and circular RNAs affecting seed storage protein accumulation in six chickpea genotypes, with contrasting seed protein content. Using RNA-seq and small RNA-seq analysis, we identified 2,810 differentially expressed genes (DEGs) and several microRNAs. A total of 42 conserved miRNAs belonging to 17 families were identified. miR166 was the most abundant miRNA while miR398, miR399, and miR164 were least abundant in both the genotypes. In addition to known miRNAs, 691 novel and distinct miRNAs were identified. The target genes were predicted using psRNA Target server, and it was found that ATP-binding cassette transporter gene (ABC) and ABA-Insensitive 5 (ABI) gene targeted by miR156 and miR319, respectively showed negative correlation and are involved in seed protein accumulation in chickpea. A comprehensive analysis of AAT gene family was carried out in chickpea leading to identification of109 AAT genes, representing 10 subfamilies with random distribution across the chickpea genome. Tissues specific expression pattern of many CaAAT genes was observed. Mature seed transcriptome data revealed that genotypes having high protein content showed low expression of CaAATs compared to the genotypes having low protein content. To have a better insight into complex traits and identify more regulatory players, we worked on identification of circular RNAs, relatively new players which play an important role in gene regulation. Seven circRNAs, including three common to both algorithms were prioritized for validation. Integration and better understanding of differentially expressed genes, circRNAs and miRNAs data holds promise for chickpea crop improvement, offering avenues for targeted manipulation to enhance quality traits.

Functional characterization of homologs of tomato SELF-PRUNING 5G (*SP5G*) Gene for role in flowering in pigeon pea

Pigeon pea is a climate-smart, protein-rich pulse, but breeding efforts are hampered by challenges such as indeterminacy and non-synchronous flowering. To address these issues, we conducted a genome-wide analysis to identify and characterize floral orthologs in pigeon pea using comparative genomics and expression profiling. A total of 412 floral orthologs were identified, including 148 genes associated with floral meristem identity, photoperiod, and circadian pathways. Phylogenetic and synteny analyses revealed purifying selection pressures and restricted gene duplication. In the course of floral induction, dynamic expression profiling is observed in key floral orthologs, particularly florigen (*FT*) and anti-florigen (*TFL1*) genes. Functional studies of the *CcCEN-like 2* gene, a floral repressor, demonstrated its critical role in delaying flowering and regulating plant architecture. Transgenic tobacco expressing *CcCEN-like 2* exhibited delayed flowering, reduced fruit set, and altered morphology. Silencing this gene in pigeon pea led to compact branching with early flowering. These findings offer insights into improving pigeon pea breeding for early flowering and determinacy traits.

Molecular characterization of m6A methylation/demethylation dynamics in pigeon pea

The methylation- demethylation dynamics of RNA plays major roles in different biological functions, including stress responses, in plants. m^6A methylation in RNA is orchestrated by the coordinated function of methyltransferases (writers) and demethylases (Erasers). Genome-wide analysis of genes involved in methylation and demethylation was performed in pigeonpea. Blast search, using Arabidopsis gene sequences, resulted in identification of two methylation genes (CcMTA70, CcMTB70), two genes encoding adaptor proteins for methylation (CcFIPA and CcFIPB) and 10 demethylase (ALKBH) genes (CcALKBH1A, CcALKBH1B, CcALKBH1C, CcALKBH2, CcALKBH8, CcALKBH8A, CcALKBH8B, CcALKBH9, CcALKBH10A andCcALKBH10B) in the pigeonpea genome. Relative expression analysis of the identified genes in various tissues at different developmental stages revealed the highest level of expression in leaf and the least in root. CcALKBH10B demonstrated the highest and CcALKBH2 the lowest level of expression in all the tissues analysed. CcALKBH8 showed the highest induction in expression upon exposure to heat stress, and CcALKBH10B demonstrated the highest level of induction in expression during drought, salt and biotic (*Helicoverpa armigera* infestation) stresses. FTO was a major demethylase involved in demethylation in humans and few reports suggest growth and development and yield enhancement in plants. So, human gene FTO was codon modified and synthetic FTO gene was used to develop pigeon pea and potato transgenic plants. It was found that potato transformed callus was growing at faster rate as compared to pigeon pea but there was less difference seen in case of pigeon pea. In the later stage of growth in the field there was a difference between control and transformed plants for both pigeon pea and potato but that effect is not pronounced. Overall, the present study would pave the way for better understanding of m^{6}A methylation demethylation dynamics in pigeonpea, its involvement in stress regulation and impact on growth and development of the pigeonpea plant.

Molecular response of bacterial endophytes mediated defence against the Fusarium wilt in chickpea

Chickpea (*Cicer arietinum* L.) is an important legume crop, among the biotic stress Fusarium wilt by *Fusarium oxysporum* f. sp. *ciceris* poses a major economic threat. Chemical pesticides used for its management are less effective and have environmental concern. Bacterial endophytes live inside the plant tissues offering an eco-friendly alternative for mitigation of diseases. In this study, a total 94 bacterial endophytes were isolated chickpea plant tissues namely, root (29), stem (37), leaf (22) and flower (6). Morpho-biochemical characterization of 94 isolates showed 62.7 % Gram-positive, 85.1% catalase positive, 26.6% oxidase positive. *In-vitro* evaluation of PGP traits showed 23, 20, 8 and 11 isolates were positive for production of IAA, siderophore, phosphate solubilization and DNase assay, respectively. Dual culture assay showed 14 isolates were antagonistic against *FoC* . Among these 14 isolates, 5, 5, 3, 10, 6, 11, 10 were positive for citrate utilization, nitrate reduction, zinc solubilization, urease, amylase, protease and cellulase production, respectively. 16S-rDNA sequencing of 24 potential isolates having antagonistic and PGP traits showed that they belong to 7 different genera and nucleotide sequence of these isolates were submitted to NCBI. Gene specific PCR based detection showed presence of lipopeptides surfactin and fengycin genes indicating their role in antagonism. Surfactin *sfp* gene was cloned from NIBSM_CR-14 and NIBSM_CF-1 isolates and characterized. Based on PGP and antagonistic potential, three isolates NIBSM_CR-12, CR-14 and CF-1 were selected for *in-planta* validation. Bio-primed chickpea plants showed enhanced PGP parameters and 39-60% protection over control against *FoC* infection. Molecular response in tri-partite interaction study showed elevated defence related enzymes and up-regulation of NAC-TF, ABP-19a, 14-3-3 and LOX genes by RT-PCR analysis in bio-primed plants indicating induction of endophytes mediated resistance against pathogen. This study suggests role of these endophytes in EMR and their potential as bio-stimulant and bio-control agents.

Molecular insights into the fungicidal action of green silver nanoparticles against the chickpea wilt caused by *Fusarium oxysporum* f. sp. *ciceris*

Silver nanoparticles (AgNPs) are potential antimicrobial and can emerge as an ideal nanofungicide in sustainable agriculture. The current evaluation aimed to elucidate the molecular basis along with morpho-physiological responses of chickpea upon exposure to greenly synthesized AgNPs against *Fusarium oxysporum*. To this end, AgNPs were synthesized by reductional method and were characterized by obtaining 427 nm, 42 – 53.93 nm, and -17.4 to -38.7 mV as SPR, size, and zeta potential respectively. *In-vitro* trials (25 ppm to 300 ppm) were conducted through PFT and *in-vivo* field trials were conducted comparing AgNPs concentrations (75 ppm, 150 ppm, and 300 ppm) against an infected and healthy sample, and positive control (1000 ppm, Bavistin). 300 ppm AgNPs exhibited higher plant height, branching, and chlorophyll content. Moreover, lower infection percentage, histological profiling as well as revival of soil microbes at 300 pm doses validated the protective role of AgNPs. At the molecular level, 300 ppm AgNPs led upregulation of stress and defense-related genes, including Chalcone Synthase (*CHS*), Phenylalanine Ammonia Lyase-2 (*PAL*-2), laccase, non-specific Lipid Transfer Proteins (*nsLTP*s), and Natriuretic Peptide Receptors (*NPR*-1) in leaves, and CHS, nsLTPs, glutaredoxin (GRX), GEBD and chitinase in roots and the potential basis were validated applying molecular docking. Current findings pave the way for using AgNPs in controlling wilt disease in chickpea.

Understanding the nano-silica induced molecular regulations in chickpea, *Cicer arietinum* L.

The current evaluation explores the molecular role of silica nanoparticles (SiNPs) as a potential growth promoter and fertilizer for chickpea cultivation. To this end, SiNPs were synthesized by co-precipitation method and recorded 201.9 nm size, -45.8Mv zeta potential value & 200nm image size as evaluated by DLS, and FESEM. CMC capped nanosilica was coated around chickpea seed, Birsa channa 3 variety with 50ppm, 150ppm, 250ppm SiNPs as treatments and positive control (TEOS @1000ppm) for conducting an in vivo pot experiment. Under morphological evaluations, highest plant height was recorded as 14.33±0.47 cm, number of branches was 21.67±1.70 cm, root length was 23.17±0.24 cm at 150ppm delivered nanosilica dose on 30th DAS in comparison to PC. The highest chlorophyll content was 59.15±0.64 spad units and higher phenolic content by HPLC estimation was recorded at 250ppm dose in comparison to PC. There was an increased colony count in microbial profiling under nano-silica treated plants. Upregulation in silica responsive genes like Low silica rice (*Lsi*3), Protochlorophyllide oxidoreductase (PCO), Dehydration-Responsive Element-Binding protein (*DREB*), Phenylalanine Ammonia-lyase 2 (*Pal*-2) etc. were noted in 150ppm which is well supported by molecular docking profiling. Hence, application of seed coated SiNPs of 150 ppm followed by 250 ppm can be effectively delivered as alternative fertilizer for chickpea cultivation.

Molecular characterization of key host factors involving in pathogenesis of mungbean yellow mosaic India virus in mungbean

Mungbean (*Vigna radiata* (L.) R. Wilczek), a short-duration, warm-season pulse crop extensively cultivated in tropical and subtropical regions. Its productivity is critically threatened by Yellow Mosaic Disease (YMD), caused by begomo viruses such as mungbean yellow mosaic India virus (MYMIV) and mungbean yellow mosaic virus (MYMV), leading yield losses of up to 100% depending on the infection. They possess a bipartite DNA-A and DNA-B genome, exploiting host machinery for replication and infection. However, the molecular interactions of host factors involved in the MYMIV pathogenesis remain unclear. This study elucidates the molecular mechanisms underlying MYMIV pathogenesis in mungbean by characterizing key host transcription factors. Through transcriptomic analysis, transcriptional factors (TFs) as WRKY, NAC, ERF, LHY, LYS, NIM1, CHUP1 and LRR—were identified as potential contributors to the MYMIV pathogenesis. Real-time qPCR was used to validate temporal expression of these TFs in mungbean following MYMIV inoculation by whitefly. This revealed a peak expression of WRKY (4.3-fold) and NIM1 (2.1-fold), at 3 hours post-inoculation, while ERF showed (6.5-fold) and LRR (2-fold), at 6 hours. CHUP1 (7.6-fold) and LHY (4.5-fold) at 2 hours and within 1 hour respectively. NAC exhibited 2.8-fold at 24 hours, while LYS reached 2-fold within 0.5 hours and 3.1-fold at 6 hours. Following the designing of the full-length primers, the ERF and LHY were PCR amplified, cloned and sequenced. A three-tiered confirmation process involving nucleotide and protein BLAST, ORF identification, and protein modeling verified the identity and structural similarity of the ERF and LHY TF to NAD(P)H-quinone oxidoreductase chloroplastic proteins and REVEILLE 1-like respectively. Phylogenetic analysis, revealed ERF's close homology with non-leguminous species, while the LHY clustered with leguminous crops, highlighting their evolutionary divergence. This study presents novel findings in *V. radiata*, identifying critical TFs involved in the MYMIV pathogenesis in mungbean, offering a foundation for further functional validation of these genes to enhance resistance against YMD.

Identification and expression analysis of gene(s) responsible for nodulation in winged bean {*Psophocarpus tetragonolobus* (L.) DC.}

Winged bean {*Psophocarpus tetragonolobus* (L.) DC.}, a high-protein legume from the Fabaceae family, cultivated in tropical and subtropical regions, including India. The plant excels in nodulation and nitrogen fixation across various tropical soils, with the capacity to produce nodules up to 5 cm in diameter and up to 21 grams per plant. To explore the genetic basis of winged bean's exceptional nodulation and broad rhizobial associations, we performed IsoSeq sequencing on root nodules, yielding 2,854 full-length transcripts. These were annotated with BLAST against the NCBI NR database. From this dataset, we selected 14 key nodulation-related genes for expression analysis in winged bean, faba bean, and chickpea: NORK, GRDP1, PLDα1, Nodulin 35, ARGlu1, NRG2, CBP60B, CBTA2, INR2, NPF, DELLA-GAI, DELLA-GAI-1, NDX1, and PICBP. RT-qPCR-based analysis revealed significant gene expression variations correlating with nodule size and nodulation efficiency. Winged bean exhibited high expression levels of DELLA-GAI, PLDα1, NODULIN 35, ARGlu1, NRG2, CBP60B, and PICBP. Uniquely, the elevated expression of DELLA-GAI, NODULIN 35 and PLDα1 in winged bean underscores their crucial roles in nodule development and function. This study provides insights into the genetic mechanisms driving effective nodulation in winged bean and informs potential improvements in legume breeding for enhanced nodulation traits.

Identification and characterization of genes responsible for anthocyanin content in winged bean {*Psophocarpus tetragonolobus* (L.) DC.}

Winged bean (*Psophocarpus tetragonolobus*) is a high-protein legume known for its nutritional versatility, with all edible plant parts. This study dissects anthocyanin QTLs to pinpoint the gene involved in anthocyanin production in winged bean. We analyzed anthocyanin QTLs qAntho1.1a, qAntho5.1, and qAntho1.1b using the flanking marker and a chromosome-level reference genome sequence. Gene prediction from these QTL regions identified 20 genes for qAntho1.1a, 18 for qAntho5.1, and 6 for qAntho1.1b. In-silico annotation of these genes using the NCBI database highlighted seven key anthocyanin pathway genes: qAntho1.1a-10 (Phosphoglycolate phosphatase), qAntho1.1a-14 (AP2-like ethylene-responsive TF), qAntho1.1a-18 (Dehydrogenase/reductase SDR family member-7), qAntho5.1-5 (Hypersensitive-induced response protein), qAntho5.1-6 (Hypersensitive induced response protein-1), qAntho5.1-7 (Hypersensitive-induced response protein-1), and qAntho1.1b-6 (Gibberellin 20-oxidase-like protein). Expression analysis of these genes, performed using RNA isolated from Purple-3 and CR-2 genotypes with leaf and pod tissues revealed differential expression patterns. Notably, qAntho1.1a-10 and qAntho1.1b-6 showed upregulated expression in the Purple-3, whereas these genes were not expressed in the CR-2. This differential expression pattern indicates the involvement of these genes in anthocyanin production in the winged bean. The study enhances our understanding of anthocyanin QTLs and identifies key genes that could be targeted for breeding winged bean varieties with enhanced anthocyanin content.

Theme 5: Stress Tolerance, Genetic Diversity and Post Harvest Quality in Vegetables and Fruits

Amelioration of cold induced sweetening in potato (*Solanum tuberosum L.*) by simultaneous silencing of genes encoding UDP-glucose pyrophosphorylase and vacuolar acid invertase

This study presents a multifaceted approach to improve postharvest quality and stress tolerance in cold-stored potatoes using RNA interference (RNAi) and CRISPR/Cas9 genome-editing techniques. CISCOM RNAi transgenic potato lines were developed by silencing two key genes, *vacuolar acid invertase* (*StvaINV*) and *UDP-glucose pyrophosphorylase* (*StUGPase*), involved in sugar metabolism during cold storage in two cold-induced sweetening (CIS)-sensitive Indian potato varieties, Kufri Chipsona 1 (KC1) and Kufri Chipsona 3 (KC3). By co-silencing these genes, transgenic lines showed a 95% reduction in reducing sugars and improved chips colour post-cold storage. Simultaneous silencing of *StvaINV* and *StUGPase* prevented unwanted sucrose build up, addressing the increased sweetness associated with *StvaINV*-only silencing in prior studies. Tuber yield, dry matter content, and growth remained unaffected in most transgenic lines, demonstrating that CISCOM RNAi successfully improves cold chipping quality without impacting agronomic traits. Further, m6A epi-transcriptomic analysis using Nanopore direct RNA sequencing revealed m6A methylation dynamics in the potato tubers during cold storage. Cold-stored wild-type KC1 tubers exhibited increased m6A levels, associated with elevated expression of metabolic and stress-related genes, while transgenic lines maintained stable m6A methylation, likely contributing to reduced sweetening. Additionally, a novel pCR vector system for CRISPR/Cas9-mediated gene editing in plants was developed, targeting the phytoene desaturase (PDS) gene in tobacco and potato. The vector achieved mutation efficiencies up to 61.11% in potato and 12.73% in tobacco, validating its efficacy across plant species. Overall, CISCOM RNAi and pCR CRISPR/Cas9 approaches demonstrate significant promise for mitigating cold-induced sweetening and enhancing quality in stored potatoes, potentially addressing major quality issues in the potato processing industry.

Screening and characterisation of okra germplasm against okra yellow vein mosaic disease transmitted by whitefly (*Bemisia tabaci* Gennadius)

The study evaluated 16 okra germplasm entries, including wild accessions, cultivated lines, and advanced breeding lines, for resistance to okra yellow vein mosaic disease (OYVMD) and its vector, whitefly (*Bemisia tabaci*), under artificial conditions at ICAR-NIBSM, Summer 2024. Disease incidence and whitefly population correlated positively with total sugars, reducing sugars, and protein content and negatively with trichome density, trichome angle, phenolic compounds, and defensive enzyme activity. Wild germplasm *A. moschatus sub. sp. moschatus* (IC 629859) and *A. tuberosus* (IC 470750) exhibited high resistance (0% disease incidence), low whitefly population (intrinsic rate: 0.026–0.027; finite rate: 3.60–3.85), and high population doubling time (25.71–27.08 days). Resistance was linked to high trichome density (891.88–12228.10/cm^2), trichome length (605.07–1370.93 µm), high phenolic content (2.27–3.04 mg/g), tannins (5.23–5.73 mg/g), and high enzyme activity: peroxidase (53.85–57.87 µmol/min/mg), catalase (181.99–199.52 nmol/min/mg), and SOD (95.78–97.42 units/mg). Four other resistant accessions (disease incidence: 8.85–21.81%) included *A. moschatus sub. sp. moschatus* (IC 624232), *A. tetraphyllus var. pungens* (IC 618015), *A. moschatus* (IC 598240), and *A. enbeepeegeearensis* (IC 582757), with lower intrinsic rates (0.029–0.033), finite rates (4.10–5.30), and survival ratios (2.10–2.45). One germplasm *A. esculentus* (IC 117262-1) showed moderate resistance. Seven germplasm were categorized as moderately susceptible germplasm including *A. caillei* (IC 506060 and IC 506198) and advanced breeding lines like IC 523737 × IC 599703-1, showing higher disease incidences (56.28%–74.59%), higher whitefly populations, and shorter doubling times. Susceptible entries IC 117288 and IC 117299 (>75% incidence) had low trichome density (33.80–141.89/cm²), reduced enzyme activity, and high sugar (3.36–4.61%) and protein (14.87–15.15 mg/g) levels. Resistance traits were multifactorial, offering insights for breeding OYVMD-resistant lines.

Studies on genetic diversity and population dynamics of *Amrasca biguttula* (Ishida) in okra in Chhattisgarh

Okra {*Abelmoschus esculentus* L. (Moench)}, is an important vegetable crop in Chhattisgarh which faces various biotic and abiotic stresses, including infestation by the okra leafhopper (*Amrasca biguttula*). This study examined the genetic diversity, and population dynamics of the leafhopper under different sowing dates.A total of seven haplotypes of *A. biguttula*belonging to two clades on okra were found. The most widespread and dominant haplotype was CLHH 7, found throughout the state, suggesting its greater adaptability. Other haplotypes were localized: CLHH 1 (Balod district), CLHH 2 (Kondagaon), CLHH 3 (Dhamtari), CLHH 4 (Kanker), CLHH 5 (Surguja), and CLHH 6 (Durg). The divergence between the north and central populations of Chhattisgarh was 0.00191, between the north and south populations was 0.00186, and between the central and south populations was 0.00215.Late-sown okra (06.12.2023) had the lowest leafhopper population with 1.53 leafhoppers/3 leaves whilesignificantly higher populations (3.083 and 6.36 respectively) were observed in mid-sown (20.12.2023) and early sown (06.12.2023). The peak population occurred during 9th and 10th standard weeks (9.411 and 9.944 respectively). Besides, leafhopper populations were positively correlated with both maximum temperature (0.775, 0.774, and 0.689) and minimum temperature (0.737, 0.736, and 0.564), while relative humidity had a negative correlation (-0.684, -0.696, and -0.606). Warmer temperatures led to higher population densities, accelerating leafhopper development and feeding activities. This study reports 7 haplotypes of which CLHH 7 as dominant with overall low genetic diversity. Sowing okra in early December, significantly reduces leafhopper infestation and damage. Additionally, leafhoppers preferentially congregated more on the middle leaves of okra compared others.

Development of in-vitro regeneration protocol for strawberry (*Fragaria × ananassa*)

Strawberries (*Fragaria × ananassa*) are mainly propagated by runners. However, current propagation methods using runners can lead to disease issues, and transporting seedlings from these regions incurs additional costs. To address these problems, this study developed an effective micropropagation protocol for the 'Winter Dawn' variety of strawberry. The protocol optimized key stages of tissue culture, including explant sterilization, shoot induction, shoot multiplication, root induction, and seedling hardening. Sterilization was most effective with 4% NaClO and 8% $HgCl_2$, achieving complete contamination control. Runners showed the best response in shoot induction when cultured in SM3 medium (MS medium with 1.0 mg/L BAP and 0.1 mg/L kinetin), resulted 94% shoot regeneration rate. This medium also excelled in shoot-multiplication, producing 6-10 shoots per sub-cultured tissue. For root induction, RM2 medium (1 mg/L IBA) achieved a 94% rooting rate with an average root-length of 12.2 cm in 45 days. During hardening, plants were acclimatized under polyhouse conditions, bypassing the primary hardening phase. Three hardening media were tested, all achieving a 100% survival rate. Notably, a simpler soil and vermicompost (HM2) medium was as effective as those with cocopeat. This protocol provides a cost-effective approach to large-scale strawberry propagation, improving commercial strawberry cultivation in India.

Theme 6: Exploration of Microbial Genes for Crop Protection and Productivity Enhancement

Exploring biocontrol potential by unraveling presence of chitinase genes and antifungal activity in *Bacillus thuringiensis* isolates representing diverse agroclimatic zones of India

Fusarium oxysporum and *F. graminearum*, two of the top five fungal plant diseases, are plant pathogenic fungi that pose a danger to agricultural productivity and call for long-term biocontrol measures. This study explores the biocontrol potential of genetically diverse *Bacillus thuringiensis* (Bt) isolates collected from various agro climatic zones in India. Thirty-four Bt isolates were selected based on their insecticidal genes profiles studied previously in our laboratory. Genetic diversity of selected isolates identified through Amplified Ribosomal DNA Restriction Analysis (ARDRA) method, which produced 22 distinct band patterns and further helped us to include most diverse isolates for performing bioassays. Out of total 34 selected isolates, PCR screening revealed presence of exo-chitinase (*chi36*) and endo-chitinase (*chi74*) genes in 24 and 21 isolates, respectively. Dual culture bioassays demonstrated significant antifungal activity by isolates SK-957 against *F. oxysporum* and SK-966 against *F. graminearum*, with inhibition rates of 57.95% and 64.1%, respectively. Interestingly, isolate SK-783, despite being negative for chitinase genes, exhibited moderate antifungal activity (46.67%), suggesting involvement of other bioactive factors. Chitinolytic activity, confirmed using Chitinase-Detection Agar in isolates SK-957, and SK-966, correlated with bioassay findings of fungal mycelial degradation and cell wall thinning, indicating chitin breakdown. In view of the importance of chitinases, cloning and sequencing of *chi36* and *chi74* genes from best performing isolates SK-957 and SK-966 revealed over 96% similarity to known chitinase genes, with unique sequence variations. Phylogenetic analysis highlighted evolutionary conservation with other *Bacillus* species, and protein structural analysis confirmed high stability and quality. This study underscores the significant biocontrol potential of Bt isolates SK-957 and SK-966 due to their high chitinolytic activity and antifungal effectiveness. The findings establish a foundation for utilizing genetically diverse Bt isolates as sustainable biocontrol agents in integrated pest management (IPM) systems, offering an environmentally friendly alternative to chemical fungicides for improved crop protection.

Occurrence broad-spectrum entomotoxic and plant growth promoting genes in native *Bacillus thuringiensis* isolates recovered from diverse habitats of India for biological pest control

Screening of 35 *Bacillus thuringiensis* (Bt) isolates recovered from different agro-ecological regions of India was carried out for occurrence of *cry*and plant growth-promoting genes. Presence of lepidopteran-toxic *cry1* and *cry2* and coleopteran-toxic *cry7/8* genes in nine and three isolates respectively, was confirmed by PCR. Aphidicidal *cry11* was present in ten isolates. Nematicidal Genes (*cry5, cry6, cry12, cry14* and *cry21)* were identified in 6,12, 2 and 10 isolates respectively. Bt isolates from Trans-Gangetic Plain Region exhibited diversity of *cry* genes across different insect orders. Bt isolates also contained genes for plant growth promotion, such as phytase and acid phosphatase, aiding in phosphorus solubilization, and siderophores biosynthetic pathway genes. The *cry11* gene from isolates SK-768 and SK-793 and *phyC* gene from isolates SK-768, SK-783, and SK-793 were amplified, cloned and confirmed by plasmid profiling, restriction analysis and PCR. Laboratory bioassays with *Spodoptera frugiperda* and acetone-precipitated toxins from three Bt isolates *viz*. SK-223, SK-793, and SK-935and BGSCBt strain HD1, used as reference, were carried out at 1,10,100 and 1000 ppm concentrations.HD1 treatment showed highest 7th day larval mortality (80%) and lowest LC50(54.83 ppm), followed by SK-793 (65%). Sub-lethal effects such as reduced larval and pupal weights, extended generation periods and pupal and adult malformations were also observed. In bioassays with spore-crystal mixtures from *cry1* and *cry2*-positive Bt isolates and *Chilo partellus* larvae, Bt isolate SK-793 was significantly more toxic, followed by HD1, as compared with control larvae. Bt isolate SK-793 exhibited toxicity against both *S. frugiperda* and *C. partellus* and contained aphidicidal *cry11* gene and plant growth-promoting genes and is a potential candidate for developing biopesticide and enhancing crop protection and growth. Our study has identified promising isolates with predicted broad-spectrum toxicity and plant growth- promoting potential, underscoring their potential in integrated pest management and sustainable agriculture.

List of the students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Pooja Ludhani (21758)	M.Sc	Screening and characterization of T DNA-free multigenic genome edited rice mutants of Pi21, MPK5 and Spl11 for blast resistance	Dr. Amol K. Solanke	ICAR-IARI, New Delhi
2.	R Hari Chandana (21759)	M.Sc.	Molecular characterization of a high-affinity nitrate transporter gene (TaNRT2.5) of bread wheat (*Triticum aestivum* L.)	Dr. Subodh K. Sinha	ICAR-IARI, New Delhi
3.	Durgam Revanth (21760)	M.Sc.	Exploiting OsmiR167-OsARF12 module for improved root system architecture in rice through CRISPR/Cas9-based genome editing technology	Dr. Anil Kumar Singh	ICAR-IARI, New Delhi
4.	Akshay Kumar Ghodake (21761)	M.Sc.	Exploring biocontrol potential by unraveling presence of chitinase genes and antifungal activity in *Bacillus thuringiensis* isolates representing diverse agroclimatic zones of India	Dr. Sarvjeet Kaur	ICAR-IARI, New Delhi
5.	Arpita Dash (21762)	M.Sc.	Molecular dissection of the qGN4.1 QTL underlying high grain number phenotype in rice	Dr. Deepak Singh Bisht	ICAR-IARI, New Delhi
6.	Anurag Kumar (21763)	M.Sc	Targeted alterations in conserved structural motif in central repeat domain of a *Xanthomonas oryzae* pv. *oryzae* TAL effectors to study effect on virulence in rice	Dr. Rhitu Rai	ICAR-IARI, New Delhi
7.	Shreyas D. (21764)	M.Sc.	Identification and cloning of a candidate susceptible(s) gene for *Sclerotinia* stem rot disease in Indian mustard (*Brassica juncea*)	Dr. Navin C. Gupta	ICAR-IARI, New Delhi
8.	Jagbandhu Pan (21765)	M.Sc.	Occurrence broad-spectrumentomotoxic and plant growth promoting genes in native *Bacillus thuringiensis* isolates recovered from diverse habitats of India for biological pest control	Dr. Sarvjeet Kaur	ICAR-IARI, New Delhi
9.	Akash Nigam (21768)	M.Sc.	Identification of genes that are potential negative regulators wheat of heat stress tolerance in wheat	Dr. Jasdeep C. Padaria	ICAR-IARI, New Delhi

10.	Debanjan Basu Roy (80028)	M.Sc	Screening and characterization of okra germplasm against okra yellow vein mosaic disease transmitted by whitefly (*Bemisia tabaci* Gennadius)	Dr. Mallikarjuna Jeer	**ICAR-NIBSM, Raipur
11.	Rashmi Kumari (80029)	M.Sc.	Molecular characterization of key host factors involving in pathogenesis of mungbean yellow mosaic India virus in mungbean	Dr. P.N. Sivalingam	**ICAR-NIBSM, Raipur
12	Subramanian K (80030)	M.Sc.	Molecular response of bacterial endophytes mediated defense against the Fusarium wilt in chickpea	Dr. Vinay Kumar	**ICAR-NIBSM, Rai
13.	Chethankumar M (80031)	M.Sc.	Studies on the effect of silicon amendment on pink stem borer *Sesamia inferens* Walker in wheat under climate change scenario	Dr. K C Sharma	**ICAR-NIBSM, Raipur
14.	Sneha Sharma (80032)	M.Sc.	Studies on genetic diversity and population dynamics of *Amrasca biguttula* (Ishida) in okra in Chhattisgarh	Dr. J. Sridhar	**ICAR-NIBSM, Raipur
15.	Palli Tarun Kumar (90025)	M.Sc.	Understanding the nano-silica induced molecular regulations in chickpea, *Cicer arietinum* L.	Dr. Biplab Sarkar	**ICAR-NIBSM, Ranch
16.	Anusha T (90028)	M.Sc.	Molecular insights into the fungicidal action of green silver nanoparticles against the chickpea wilt caused by *Fusarium oxysporum* f.sp. *ciceris*	Dr. Biplab Sarkar	**ICAR-NIBSM, Ranchi
17.	Jamshida D (90029)	M.Sc.	Identification and characterization of genes responsible for anthocyanin content in winged bean (*Psophocarpus tetragonolobus* L.)	Dr. Kishor U. Tribhuvan	**ICAR-NIBSM, Ranchi
18.	Divakar Singh (90030)	M.Sc.	Identification and expression analysis of gene(s) responsible for nodulation in winged bean (*Psophocarpus tetragonolobus* (L.))	Dr. Kishor U. Tribhuvan	**ICAR-NIBSM, Ranchi
19.	Ankit Patel (90032)	M.Sc.	Development of *in-vitro* regeneration protocol for strawberry (*Fragaria* × *ananassa*)	Dr. Kishor U. Tribhuvan	**ICAR-NIBSM, Ranchi
20.	Sougata Bhattacharjee (11069)	Ph.D.	Functional characterization of homologs of tomato SELF-PRUNING 5G (SP5G) gene for role in flowering in pigeon pea	Dr. Debasis Pattanayak	ICAR-IARI, New Delhi
21.	L. Ashakiran Devi (11070)	Ph.D.	Study of aphid effector(s) for developing aphid-resistance in Indian mustard	Dr. R. C. Bhattacharya	ICAR-IARI, New Delhi
22	Bablee Kumari Singh (11071)	Ph.D.	Molecular characterization of genes governing heat tolerance in rice	Dr. S. V. Amitha Mithra	ICAR-IARI, New Delhi

23.	Shaziya Sultana (11367)	Ph.D.	Elucidating the molecular processes underlying acquired and transgenerational thermotolerance in wheat	Dr. Sharmistha Barthakur	ICAR-IARI, New Delhi
24.	Krishnayan Paul (11546)	Ph.D.	Amelioration of cold induced sweetening in potato (*Solanum tuberosum* L.) by simultaneous silencing of genes encoding UDP-glucose pyrophosphorylase and vacuolar acid invertase	Dr. Debasis Pattanayak	ICAR-IARI, New Delhi
25.	Deepesh Kumar (11550)	Ph.D.	Identification, characterization and functional validation of drought-responsive microRNA(s) in rice (*Oryza sativa* L.)	Dr. S. V. Amitha Mithra	ICAR-IARI, New Delhi
26.	Gopal (11552)	Ph.D.	Identification of key genes associated with seed protein content in chickpea by RNA-seq and small RNA analysis	Dr. P. K. Jain	ICAR-IARI, New Delhi
27.	Priyanka Kumari (11928)	Ph.D.	Molecular characterization of m6A methylation/demethylation dynamics in pigeon pea	Dr. Debasis Pattanayak	ICAR-IARI, New Delhi
28.	Ahmed Mohammed Ismail (11934)	Ph.D.	Identification of quantitative trait loci (QTLs) associated with tolerance to salt stress in wheat	Dr. Kanika	ICAR-IARI, New Delhi

*** 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. The salient findings of the research work carried out by the students is classified into two theme areas as below.

Theme 1: Nutrient Stress in Crop Plants

Physiological basis of tolerance to low phosphorus and iron toxicity stress in rice germplasm from north east India

In the north-eastern regions of India, >80% of agricultural land is predominantly acidic in nature, resulting in iron (Fe) toxicity and phosphorus (P) deficiency, major bottleneck for rice production. Screening of 82 indigenous rice genotypes in hydroponics with treatment combinations as: low P + Fe toxicity (LP+FeT), sufficient P + Fe toxicity (FeT), and control was carried out to understand the physiological basis of tolerance to combined stresses. In leaves, the chlorophyll content reduced by 11.5% under LP+FeT as compared to control. Reduction in shoot biomass and increased root biomass under LP+FeT was observed as compared to control. A significant increase in primary root length (PRL), total root length (TRL), total root surface area (TRSA), root average diameter (RAD), and total root volume (TRV) under low P + Fe toxicity stress indicated the dominance of low P stress response rather than Fe toxicity. The acid phosphatase activity and organic acid exudation from roots increased significantly under FeT. The PCA identified 14 traits governing genotypic variability in response to Fe toxicity under low P stress which were used to identify the efficient and inefficient genotypes through multi-trait genotype-ideotype distance index analysis. The efficient genotype (RCPL-1-432) revealed an increase in biomass, chlorophyll content, PRL, TRSA, TRV, RAD, root tips and forks numbers with reduced total iron content, whereas reverse trend was observed in the inefficient genotype (Maimine). The expression of candidate genes like high-affinity phosphate transporter (*OsPHT1;1* and *OsPHT1;4*) increased while reduced expression of Fe uptake genes (*OsIRT1*, *OsYSL15*, and *OsYSL9*) in roots under both stress conditions were observed in RCPL-1-432. Ferritin gene (*OsFER2*) was highly expressed in the efficient than inefficient genotype. In conclusion, the identified genotypes can thrive in acidic soils and may serve as donor in rice breeding program.

Identification and characterization of amino acid permease family genes in response to nitrogen stress in rice (*Oryza sativa* L.)

The study investigated amino acid permeases (AAPs) in rice, focusing on their role in nitrogen use efficiency (NUE). AAPs mediate amino acid transport and uptake, affecting plant development and NUE. The research had four main objectives: bioinformatics analysis of AAP genes, evaluation of specific AAP haplotypes, expression profiling, and development of genome editing constructs. Bioinformatics analysis identified 19 AAP genes in MTU1010. Protein localization, co-expression net-work, prediction of protein motifs, membrane motifs and phosphorylation site were also conducted. *In silico* expression profiling revealed that nitrogen supply and deficiency influenced their expression, with AAP1 and AAP16 exhibiting the highest expression in leaves. AAP3, AAP5, and AAP11, are previously reported as negative regulators of NUE, yield, and quality. Physiological evaluation such as plant biomass, leaf area, root system architecture, CCI, Tissue N, Total N content, enzyme assays of N assimilation enzymes such as NR, GS, GOGAT, GDH and estimation of soluble protein content in shoot and root tissues were performed in selected haplotypes. Genotypes with non-synonymous mutations in these genes demonstrated improved growth and nitrogen content than MTU1010. Rice accessions like "Local," "NCS901," and "Bhainsa Mundariya," showed superior biomass accumulation relative to MTU1010. The observed variation in plant growth among AAP haplotypes underscores their potential for improving NUE in Indica rice. Guide RNAs (gRNAs) for *AAP3, AAP5* and *AAP11* were designed and were successfully cloned into the p2XSgR-SpCas9-Os vector, and integrated into the binary vector pCAMBIA1300. Genome editing of AAPs, using the constructs developed in this study can enhance NUE and contribute to sustainable rice production systems.

Genome wide association studies for phosphorus use efficiency in diverse bread wheat germplasm

Understanding the changes in root system architecture of bread wheat under phosphorus (P) limited conditions is critical for identifying specific traits contributing to improved P uptake and utilization. Experiments were conducted under optimum P (OP) and low P (LP) conditions in hydroponics (334 genotypes) to study the root traits, while in soil (304 genotypes) for P utilization efficiency (PUtE). Results revealed a strong genotypic and phenotypic association of PUtE with root volume, shoot dry weight, root dry weight, and total biomass was observed under OP conditions. Under LP condition, a strong positive correlation of P utilization efficiency with root volume, root surface area, shoot dry weight, root dry weight, and total biomass, and a negative correlation with average diameter was observed. Cluster analysis grouped the 334 genotypes into four clusters based on the relative values of nine root traits. Higher fold increase of total root length, total biomass, total root tips, and P utilization efficiency in best performing genotype in Cluster I indicated a strong relation to P use efficiency and genotypes identified were IC 539601, LUAN, IC 536317, IC 111943, IC 335700, EC 577628, KRL-1-4, and IC 111918. The 35 K Wheat Breeder's SNP-array was used for GWAS and found 33 reliable MTAs and 12 potential candidate genes associated with root, biomass and P indices. Further, to study the genetic basis of photosynthetic response to low P stress, 159 genotypes were grown in soil for two growing seasons. GWAS resulted in identification of 76 candidate genes from 25 reliable marker-trait associations (MTAs). Among them, 16 were identified as potential candidate genes with functional relevance to enhanced photosynthetic efficiency. Thus, this study provides insight into genetic basis of low P stress tolerance. Further functional analysis will provide valuable information for understanding the underlying genetic mechanism to facilitate marker-assisted breeding in wheat.

Theme 2: Abiotic Stress Tolerance of Crop Plants

Identifying the genomic regions associated with root characteristics under moisture deficit stress in wheat (*Triticum aestivum* L.)

Wheat (*Triticum aestivum* L.) is a crucial global food crop, but climate change, particularly drought stress, has increasingly affected its productivity. This study aimed to identify genomic regions associated with early vigor and drought tolerance in 198 wheat recombinant inbred lines (RILs) derived from HD3086 and HI1500 with the parents. Conducted at Nanaji Deshmukh Plant Phenomics Centre, ICAR-IARI, New Delhi, the experiment used germination paper, pot, and pipe culture setups to assess root traits and drought response at various stages. Observations were taken at multiple developmental stages, including 15, 21, 45, 75, and 80 days after sowing (DAS) and at harvest. The study focused on phenotyping key root traits such as root length, root fresh weight, root dry weight, and root-to-shoot ratios, alongside yield-related traits including seed weight and harvest index. Quantitative Trait Loci (QTL) mapping revealed significant genomic regions linked to early vigor traits, such as coleoptile length and shoot length, drought tolerance traits, including root fresh weight, root dry weight, and specific root length. Additionally, important agronomic traits like seed weight per ear and harvest index were associated with specific QTLs under drought conditions. The in-silico analysis identified several candidate genes linked to the QTLs, including Auxin repressed protein, RHT1, and Stress Responsive Protein 2, providing insights into the genetic mechanisms driving early vigor and drought tolerance. Two standout RILs, RIL 13 and RIL 67, were identified for their superior early vigor and drought tolerance, respectively, making them promising candidates for future wheat breeding programs aimed at improving drought resilience. The findings from this study contribute valuable knowledge toward the development of wheat varieties with enhanced drought tolerance and robust early growth, essential for ensuring crop performance under climate stress conditions.

Marker trait association analysis for seedling stage drought tolerance in lentil (*Lens culinaris*)

Lentil (*Lens culinaris*) is the third most important cold-season legume. Drought stress leads to poor yield and quality in lentil. Present study was conducted to identify significant marker trait associations (MTAs) with drought tolerance trait using association mapping approach. A diverse lentil panel (243 genotypes) was evaluated under irrigated and drought conditions. Drought stress was imposed by restricting the pre-sowing irrigation. Traits like (germination%, NDVI, root length, total root length, root surface area, root volume, root length density, forks, tips, number of branches, shoot and root fresh weight and dry weight, shoot and root length, vigor indices-I and II had significant reduction on exposure to stress. PCA revealed two principal components explaining 56.3% variation in control and 60.7% variation in drought condition. Seedling vigor is strongly correlated with Root and growth traits. IC560032, FLIP-96-51, IC560246, P3227, IC560051, IG134349 was selected as drought tolerant genotypes based on stress susceptibility index < 0.5. A total of 44,870 SNPs were identified after quality processing of sequencing data. STRUCTURE software revealed that five sub-populations in panel. MTA analysis determined 64 SNPs in control and 72 SNPs in drought. The putative candidate genes controlling drought tolerance in lentil genotypes at seedling stage were Chr2:206859313, Chr1:126169278, Chr7:246065957, Chr1:327906249 and Chr4:476664664 encoding for legumain like *cysteine endopeptidase*, *Ribulose bisphosphate carboxylase large chain/ Clp protease*, *ascorbate oxidase*, *isopropylmalate dehydratase*, *fructokinase* and auxin responsive protein. Further studies are required to validate the candidate genes before their introgression in high yielding cultivars for the development of drought tolerant lentil varieties.

Physiological characterization of mustard (*Brassica juncea* L.) genotypes for drought tolerance

Drought stress severely restricts crop growth and yield, especially in rain-fed areas. Indian mustard (*Brassica juncea*) suffering significant productivity losses due to moisture stress during critical developmental stages. This research aimed to physiologically characterize mustard genotypes for drought tolerance through a series of controlled experiments. Study involved the screening of 160 mustard genotypes in nutrient medium containing 8% PEG-6000 (-1.25 bar) to mimic osmotic stress using root and shoot traits, including length, surface area, volume, and other traits. Superior genotypes were identified through Multi-Trait Genotype Ideotypes Distance Index (MGIDI), Factor Analysis Index-Based Best Linear Unbiased Prediction (FAI-BLUP) and Smith-Hazel Index (SH). Kranti, Pusa Jaikisan, RH-1566, DJ-26 and Varuna were identified as best performing genotypes under the given stress. On the basis of performance under stress, the least and top affected lines selected and grown in pots and subjected to drought at 50% flowering. Various physiological traits were measured, including relative water content, chlorophyll content, photosynthesis rate, stomatal conductance, transpiration rate, antioxidant enzymes and proline accumulation, at multiple intervals to evaluate drought tolerance mechanisms. Overall, these results revealed Brassica lines including Kranti, Pusa Jaikisan, RH-1566, DJ-26 and Varuna exhibited enhanced root characteristics and better performance in terms of physiological attributes, indicating effective osmotic adjustment. The findings from this research provides critical insights into the physiological responses of *Brassica juncea* under drought stress, emphasizing the importance of selecting resilient genotypes for breeding programs and pave the way for developing drought-resilient mustard varieties, essential for enhancing productivity and ensuring food security in water-limited environments.

Physiological and biochemical basis of amelioration of heat stress through nitrogen management in wheat

Wheat (*Triticum aestivum L.*) is the world's most important grain crop, and is ranked third in global production by weight, after maize and rice. Climate change, particularly the rising disparity between daytime and nighttime temperatures, negatively impacts wheat productivity. This study examined the effects of post-anthesis high night (3°C and 6°C; HNT1 and HNT2) and high day (5°C; HDT) temperatures, alongside rescheduled N doses, on gas exchange, stem reserve mobilization, yield components, C:N ratio, and flour quality in N-efficient and inefficient wheat genotypes under late-sown conditions under the Heat and Drought Wheat Improvement Consortium (HeDWIC) project of CIMMYT, Mexico. Results showed that high temperatures reduced pre-anthesis photosynthesis (Pn) and respiration (Rn), with low N doses exacerbating these effects, especially under HDT. Under HNT2, low N doses exhibited less reduction in pre-anthesis Pn compared to full N doses due to compensatory mechanisms like increased stomatal conductance (Cs). However, increased respiration demand under HNT2 limited overall carbon fixation. At maturity, higher water-soluble carbohydrate (WSC) content under HNT1 suggested inefficient translocation to developing grain. The reduction in yield under high temperature stress was positively correlated to grain number and hundred seed weight. Foliar N application in later stages did not mitigate yield loss under HDT, though it increased grain protein content. Under high night temperatures, it maintained yields comparable to full N doses. Notably, higher grain N content did not improve yield under HDT, indicating a shift in the carbon-nitrogen balance. Flour quality, measured by sedimentation values, increased under HDT, reflecting altered protein structure at the expense of yield. This study emphasizes the need for nitrogen management strategies tailored to address the challenges posed by daytime heat stress.

Physiological and biochemical characterization of common bean genotypes in reproductive stage under drought and heat stress

Common bean (*Phaseolus vulgaris* L.) is a key legume crop worldwide, but its productivity is threatened by water deficit stress (WDS) and high-temperature stress (HTS), both exacerbated by climate change. WDS affects physiological and biochemical processes, seed nutrient quality, and yield, while HTS disrupts metabolism and seed set. Morphological, physiological, and yield-contributing traits were studied, identified four genotypes with superior performance under both non-stressed and WDS conditions. The identified WDS-tolerant genotypes were further tested for HTS tolerance with and without exogenous melatonin (300 µM). HTS was induced at two levels: HTS-I (29–32°C) and HTS-II (32–35°C), with staggered sowing to intensify stress. Melatonin was applied during vegetative and flowering stages, significantly improving performance under HTS, particularly in yield-contributing traits. Additionally, a spectroradiometric approach was explored to develop non-destructive methods for estimating relative water content (RWC). Spectral reflectance (350-2500 nm) and RWC were measured in five genotypes under varying water stress levels. Key wavelengths (756 and 1309 nm) and spectral indices were identified, resulting in a strong univariate model ($R^2 \approx 0.83$). Multivariate models, especially SVR ($R^2 = 0.97$, RPD = 3.38), outperformed PLSR, RF, and MLR. These findings highlight the potential for developing precise tools to assess crop stress tolerance. This research provides a foundation for breeding robust common bean varieties capable of withstanding WDS and HTS, addressing critical challenges posed by climate variability

Physio-biochemical and molecular basis of photo-thermo insensitivity in chickpea genotypes (*Cicer arietinum* L.)

Chickpea growth is significantly influenced by temperature and photoperiod, both of which are increasingly impacted by climate change, putting the traditional growth cycle at risk. This study evaluates the performance of chickpea genotypes across different seasonal conditions, focusing on photo-thermo-insensitivity (PTI) and adaptation to non-conventional growing seasons. Days to flowering (DF) were longest in the *rabi* season (75 days), intermediate in *kharif* (70 days), and shortest in *summer* (60 days). Pod plant^{-1} followed a similar trend, with genotypes like Vijay, Phule-G-1424-4-2, and Phule-G-08108 failing to set pods in *summer*. Seed yield and 100-seed weight were highest in *rabi* (1445 kg ha^{-1}, 19 g), followed by *kharif* (1120 kg ha^{-1}, 15.24 g) and *summer* (303 kg ha^{-1}, 14.84 g). Genotypes IPC-06-11 and ICE-15654-A ranked highest in photo-insensitivity. Canopy temperature and proline accumulation were key indicators of heat tolerance, with IPC-06-11 and JG-14 performing best under heat stress. PCA revealed canopy temperature, pod number, and test weight as the main contributors to genotype variation. Molecular analysis confirmed the role of PHY A, CRY1, and smHSP in regulating PTI, with contrasting expression patterns observed between tolerant and susceptible genotypes. IPC-06-11 and ICE-15654-A emerged as strong candidates for further development due to their superior performance across seasons. These findings highlight the need for climate-smart PTI traits, emphasizing targeted breeding strategies to enhance chickpea resilience to extreme temperatures and photoperiod variations in the face of climate change.

Deciphering the interactive effect of nitrogen and high night temperature on yield and starch quality in rice

This study investigated the effect of high night temperature and varying dose of nitrogen at heading and their interactive effect on rice nitrogen use characteristics, grain yield, and quality parameters. The response of NUE efficient genotypes to split topdressing with N at heading showed that short-duration genotypes were resilient at low and medium N doses, maintaining or increasing biomass and grain yield, whereas long-duration genotypes showed reductions. High N doses led to decreased yield in short-duration genotypes but sustained yield in long-duration ones. Genotype-specific strategies were observed, with some genotypes maintaining or increasing grain N content under higher N applications. Trends in starch content, gel consistency, and alkali spreading values revealed dose- and genotype-specific variations in grain quality. A pot study with two short-duration genotypes, Vandana and Nagina 22 (N22), differing in HNT sensitivity, examined physiological and molecular responses to N doses and growing temperatures related to (ambient and high night temperature) on physiological and molecular responses, related to starch and N metabolism, yield and quality. N22 showed minimal reduction in grain weight (1–2%) and increased yield under HNT, while Vandana exhibited yield reduction but improved grain protein content at low and medium N doses. Vandana experienced significant losses in starch and amylose content, whereas N22 exhibited variable responses. Both genotypes showed decreased gel consistency with increased N doses, although some treatments improved head rice yield. Vandana showed higher activities of *ADP-glucopyrophosphorylase*, *granule-bound starch synthase*, and *soluble starch synthase* under HNT with varying N doses, while N22 exhibited distinct enzymatic patterns. Gene expression analyses highlighted significant diurnal variations and responses in starch and N metabolism genes under HNT and different N levels. This study underscores the intricate interactions between N levels and HNT, offering insights into genotype-specific resilience and adaptation strategies for improving rice productivity and quality under climate change.

Phenotyping and identification of superior donors for high temperature tolerance in rice

Rising global air temperature will be one of the major limitations for the world's food production in the future. High-temperature causes harmful effects on the quality, growth, and yield of rice (*Oryza sativa* L.), affecting their overall production. Higher spikelet fertility is the most desirable trait for mitigating the effects of climate change and may be the focus for developing rice varieties with climate resilience under future climate change scenarios for sustainable rice production. In this context, identification of efficient genotypes and genes, introgression of candidate genes in the cultivated varieties are necessary to enhance yield and quality. In our study, spikelet fertility (SF) and panicle weight (PW) were investigated in a set of 241 Indian rice accessions, under natural and controlled environmental conditions for two years. All the plants grown in pots were exposed to high temperature (38°C) stress from booting till philological maturity to evaluate them for reproductive stage high-temperature stress tolerance. High temperature (HT) significantly reduced the spikelet fertility and panicle weight under HT stress. A genome-wide association (GWA) mapping on spikelet fertility and panicle weight was carried out using 1 million SNPs and a robust mixed model. A total of 20 QTLs were found associated with spikelet fertility, 55 for panicle weight, 12 for grain number per panicle and 20 QTLs for chlorophyll fluorescence under HT stress. Six promising QTLs (one each on chromosome 2, chromosome 3, chromosome 11, chromosome 9 and two on chromosome 5) and haplotype variants of seven putative candidate genes (*LOC_Os05g15160*, *LOC_Os05g16420*, *LOC_Os09g15670, LOC_Os09g15700, LOC_Os11g29790, LOC_Os02g41560 and LOC_Os03g14090*) were discussed. Furthermore, our study identified accessions with high SF, PW, F_v/F_m and GNPP under high temperatures, suggesting their potential as donors. The significant QTLs identified in this study may be further investigated for fine-mapping and map-based cloning in the future

Stem reserve mobilization and staygreen traits for yield stability in wheat under combined heat and drought stress

Stay-green (SG) and stem reserve mobilisation (SRM) are two important traits, which can contribute to grain filling during abiotic stress conditions. However, these two traits are mutually exclusive traits *i.e*. both the traits cannot contribute to grain filling at the same time. In addition, water soluble carbohydrates (WSCs) serve as potential buffer for grain filling, when current leaf photosynthesis is inhibited by abiotic stress. At this juncture, a field experiment was undertaken during rabi season 2021-22 under control, drought, heat and, combined heat and drought stress conditions to unveil the genetic basis of SG and SRM using 220 RILs population developed by crossing two contrasting wheat genotypes, HD3086 (SG) and HI1500 (SRM). Genotyping of 21 days wheat seedling was carried out with 35K Axiom Wheat Breeder Array followed by QTL mapping by ICIM (Inclusive Composite Interval Mapping) software. From this study, total 11, 2 and 1 QTLs were mapped for SPAD value, leaf senescence rate (LSR) and stem reserve mobilisation efficiency (SRE) respectively. From the candidate gene mining, genes like chlorophyll synthase, 7-hydroxymethyl chlorophyll a reductase (7-HCAR), rubisco small subunit, pyrroline-5-carboxylate synthase (P5CS), L-ascorbate peroxidase-2 were found to be linked to leaf greenness (SPAD value). For LSR genes like K^+ transporter-9, glycine decarboxylase-1-like (GDC), aspartyl protease family protein-2-like were found to be associated with mapped QTLs on chromosome 2D and 4B. For SRE of the main culm, genes like endoglucanase-8-like, 9-cis epoxycarotenoid dioxygenase (NCED1), serine-threonine (ST) protein kinase

OSR1-like and pentatricopeptide repeat containing protein (PPR5) were found be linked with mapped QTL for SRE. The mapped QTLs were also validated by employing physiological and gene expression approach. By using multi-trait genotype-ideotype distance index (MGIDI), HDHI113 and HDHI87 were selected as superior lines for SG and SRM traits. In addition, from the QTLs analysis of SRM from different components of main culm, total 84 QTLs were mapped, out of which 44 were major QTLs. These QTLs can be transferred to elite wheat cultivars after validations

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Baiarilang Chyne (21517)	M.Sc.	Physiological basis of tolerance to low phosphorus and iron toxicity stress in rice germplasm from north east India	Dr. Renu Pandey	ICAR-IARI, New Delhi
2.	Haritha SI (21769)	M.Sc.	Identification and characterization of amino acid permease family genes in response to nitrogen stress in rice (*Oryza sativa* L.)	Dr. Lekshmy Sathee	ICAR-IARI, New Delhi
3.	Sreehari V. Santhosh (21770)	M.Sc.	Identifying the genomic regions associated with root characteristics under moisture deficit stress in wheat (*Triticum aestivum* L.)	Dr. Sudhir Kumar	ICAR-IARI, New Delhi
4.	Neteti Siddartha Kumar (21923)	M.Sc.	Marker trait association analysis for seedling stage drought tolerance in lentil (*Lens culinaris*)	Dr. Ruchi Bansal	ICAR-IARI, New Delhi
5.	Unti Miiri Ezing (21773)	M.Sc.	Physiological characterization of mustard (*Brassica juncea* L.) genotypes for drought tolerance	Dr. Mahesh Kumar	ICAR-IARI, New Delhi
6.	Thokchom Malemnganbi Devi (21772)	M.Sc.	Physiological and biochemical basis of amelioration of heat stress through nitrogen management in wheat	Dr. Anjali Anand	ICAR-IARI, New Delhi
7.	Kruthika S (70018)	M.Sc.	Physiological and biochemical characterization of common bean genotypes in reproductive stage under drought and heat stress	Dr. Gurumurthy S.	**ICAR-NIASM, Baramati
8.	Apoorva Ashu (70022)	M.Sc.	Physio-biochemical and molecular basis of photo-thermo-insensitivity in chickpea genotypes (*Cicer arietinum* L.)	Dr. Gurumurthy S.	**ICAR-NIASM, Baramati
9.	Adhip Das (11099)	Ph.D	Phenotyping and identification of superior donors for high temperature tolerance in rice	Dr. Viswanathan C.	ICAR-IARI, New Delhi
10.	Devika S. (11100)	Ph.D	Deciphering the interactive effect of nitrogen and high night temperature on yield and starch quality in rice	Dr. Anjali Anand	ICAR-IARI, New Delhi
11.	Vijay Rajamanickam (11324)	Ph.D	Genome wide association studies for phosphorus use efficiency in diverse bread wheat germplasm	Dr. Renu Pandey	ICAR-IARI, New Delhi
12.	Sukumar Taria (11851)	Ph.D.	Stem reserve mobilization and staygreen traits for yield stability in wheat under combined heat and drought stress	Dr. Ajay Arora	ICAR-IARI, New Delhi

***Outreach institute*

Session V: School of Horticultural Science

Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Floriculture and Landscaping	09	08
Fruit Science	09	11
Post Harvest Management	06	05
Vegetable Science	13	07
Total	**37**	**31**

SCHOOL OF HORTICULTURAL SCIENCE

Chairperson: Dr. S. Uma, Former Director, ICAR-NRC for Banana, Tiruchirapalli, Tamil Nadu

Dr. S. Uma served as the Director of ICAR-National Research Centre for Banana (NRCB) in Tiruchirapalli, Tamil Nadu. She is known for her work in banana research and development, including banana germplasm conservation and developing technologies for banana processing. She received her B.Sc. (Horticulture), M.Sc. (Floriculture and Landscaping), and Ph.D. (Horticulture) degrees from University of Agricultural Science, Bengaluru and Post Doctoral Fellowship (2003-04) from KUL, Leuven, Belgium. She served as a Scientist at ICAR-Indian Instiutte of Horticultural Research (IIHR), Bengaluru (1990-95); Senior Scientist and Principal Scientist at ICAR-NRCB (1995-2007 and 2007-19, respectively). She is the recipient of Life Time Achievement Award for Germplasm Conservation in Musa by Bioversity International, France, 2004; Pisang Rajah Award, by Bioversity International, France & BAPNET, Philippines, 2009; Punjabrao Deshmukh Best Woman Agricultural Scientist Award by ICAR, New Delhi, 2009; Shri Girdhari Lal Chadha Memorial Gold Medal in Fruit Science by Horticulture Society of India, 2011; Dr. MH. Marigowda National Endowment Award for Best Horticultural Research - 2018 by University of Agricultural Sciences, Bangalore, 2018; Dr. Kalayya Krishnamurhty National Award for Best Agricultural Research - 2019-20 by University of Agricultural Sciences, Bangalore in 2020; as Director, ICAR award - Sardar Patel award for the outstanding institute award (small Category); CII_ Cold Chain Award for the year 2022; Best Woman Researcher Award by Dinamalar Tamil Daily group of Publications, 2011; Kadali Puraskar Award by AIPUB, 2003; Biodiversity Conservation Award - 2019 by Dr. B. Vasantharaj David Foundation, Chennai, 2019; Sir J.C. Bose Memorial Award for the contribution in the field of Horticulture and Plant Biotechnology by the Indian Science Monitor, Chennai, 2019. She is the Fellow of National Academy of Agricultural Sciences, Horticulture Society of India (HSI), Indian Society of Plant Genetic Resources (ISPGR), Association for the Improvement, Utilization and production of Banana (AIPUB) and Confederation of Horticultural Associations of India (CHAI). She was the Chair - The Banana Asia Pacific Network (BAPNET) - 2020-23 & BAPNET Representative, Bioversity International, France; Steering Committee Member - World Banana Forum, FAO - 2018; Member of the External Advisory Board (EAB) for the Banana - University of Wagenhein, Netherlands, 2020; National Consultant (Tissue culture) FAO, Rome -2001-04; Member of Editorial Board - Indian Journal of Horticultural Sciences, 2012-15; Member of Editorial Board - Current Horticulture, 2017; Member - Executive Council - AIPUB since 1997; General Secretary - AIPUB, 2005-2007; zzTreasurer - AIPUB, 1997-2005.

FLORICULTURE AND LANDSCAPING

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Prof. Kanwar Pal Singh

Division of Floriculture and Landscaping has comprehensive research programmes in important ornamental crops on various aspects such as crop improvement using conventional and biotechnological approaches, standardization of production technology for open field and protected environments, micropropagation, landscaping etc. Division is also contributing towards Under Graduate and Post Graduate teaching as well as human resource development and involved in dissemination of information/technology through outreach programmes for the benefit of farming community. The post-graduate research findings are being presented under various themes.

Theme1: Breeding for Biotic/Abiotic Stress Tolerance and Assessment of Quality Traits

Phenotypic expression of qualitative and quantitative traits in French marigold (*Tagetes patula* L.) under different growing conditions

Marigold is one of the important ornamental crops in the family Asteraceae. French marigold (*Tagetes patula* L.) is widely valued for its ornamental beauty in gardens and landscapes. Seasons play a crucial role in plant growth. In the present research, 20 genotypes of French marigold were selected and seeds were sown during July and September for rainy and winter season crop respectively, which are then transplanted in open field. The objective was to study the morphological and biochemical behaviours during both seasons. Higher plant height, plant spread, internodal length, stem diameter, leaf length, leaf width, number of primary and secondary branches, number of flowers per plant, flower yield per square meter was observed in the genotypes grown during rainy season when compared to that of winter season. Greater length and width of ray floret, flower diameter, flower weight was observed in winter season. Also, early flower bud initiation, early flowering and longer duration of flowers with increased flower longevity was recorded during winter season when compared to rainy season. Chlorophyll and carotenoid pigments decreased while chlorophyll a/b ratio increased during winter season due to decrease in temperature and low light intensity. Total phenolic content, proteins, soluble sugars and the activity of antioxidant enzymes like superoxide dismutase, catalase and peroxidase was also increased during winter season due to chilling temperature. Considering the yield performances of genotypes and their biochemical activity, 'Pusa Arpita' followed by 'Fr/R-14-6' during rainy season, genotypes 'Fr/R-14-6' and 'Fr/R-2' during winter season were found suitable for loose flower production. Reduced plant height in 'Orange Winner', 'Valencia Yellow', 'Dainty Marietta' during rainy season and 'Dainty Marietta', 'Fr/R-6', 'Fr/R-7' during winter season was found more suitable for flower beds, pot plants and other landscape purposes. As the seasonal cycle controls plant growth and development, this study will help the growers/consumers in selecting appropriate genotypes for a given season.

Screening of marigold genotypes (*Tagetes* spp.) against *Alternaria* leaf spot under *in vitro* and *in vivo* conditions

Marigold (*Tagetes* spp.), a member of the Asteraceae family native to Mexico, is widely cultivated for its ornamental and commercial value. Despite its beneficial insecticidal, bactericidal and fungicidal properties, marigold is highly susceptible to various plant-pathogenic fungi, especially *Alternaria* spp., which causes significant damage, particularly in form of black leaf spot sand inflorescence blight. Given the lack of effective chemical control and growing concerns about environmental impact, identifying marigold genotypes resistant to *Alternaria* is crucial for reducing fungicide dependence, promoting organic farming and fostering sustainable agriculture. Thus, our study was aimed to identify the most virulent *Alternaria* isolate responsible for leaf spot disease in marigold and evaluate marigold genotypes for resistance. Phenotypic evaluation revealed considerable variation in growth (plant height, spread) and floral traits (flower size, weight, colour) among the genotypes. Pathogen isolation from infected marigold plants revealed that 7 out of 10 isolates belonged to *Alternaria*, confirming its role as the primary pathogen. Pathogenicity assays identified isolate 'I-3' as most virulent, which was identified as *Alternaria alternata* through morphological, molecular and phylogenetic analyses. and used for both *in vitro* and *in vivo* screening. Cultural variation was observed when the pathogen was cultured on six different media, with PDA and host-extract media supporting optimal growth and abundant sporulation. *In vitro* and *in vivo* screening of the sixty genotypes revealed five, namely AMS-48, AMS-123, Pusa Parv, Pusa Utsav, and MGO-3, to be moderately resistant to *Alternaria* infection. These genotypes showed consistent resistance across both screening methods and can be valuable sources for breeding disease-resistant marigold varieties. This research contributes to the development of improved marigold cultivars and supports sustainable agricultural practices by reducing reliance on chemical fungicides.

Nematicidal efficacy of *Chrysanthemum coronarium* against *Meloidogyne incognita*

Chrysanthemum coronarium is an annual species, belongs to family Asteraceae producing loose flowers with white, cream and yellow colors. Organic amendments and green manure present viable alternatives to the harmful chemical, currently employed for controlling plant-parasitic nematodes. These are sources of nematicidal compounds, extracted from various plant as naturally occurring pesticides (Pyrethrum). The aqueous extract of three genotypes with six concentrations was tested *in-vitro* condition. It was concluded that genotype Pusa 15-16 White found significantly superior and showed highest J_2 mortality. At 24 hrs., the plant part fresh leaf was more toxic with (55.69%) mortality at 80% conc. However, even with increasing time duration, the fresh leaf and more concentrated aqueous extracts were found best in respect of nematicidal efficacy. The interaction effects at higher time duration, fresh leaf of genotype Pusa 15-16 White showed maximum mortality (81.67%) and at 72 hrs of 60% concentration, 0% survivability seen. The maximum nematostatic potential with revival rate of (50%) observed in genotype Pusa 15-16 White, while *T. erecta* found 100% effective. The chemical profiling of extracts (using LC-MS & GC-MS), various pyrethrins and other bioactive compounds found in genotype Pusa 15-16 White in significant quantities. Overall, from the present study it is evident that Pusa 15-16 White was the most promising genotype followed by Pusa 15-16 Cream and Pusa 15-16 Yellow for RKN control as a biocontrol.

Screening of tuberose (*Polianthes tuberosa* Linn.) genotypes for salinity and heavy metals stress tolerance

The present was undertaken to evaluate eighteen genotypes of tuberose for salinity stress tolerance at five salinity levels (control, 2, 4, 6, and 8 dS/m). It was observed that salinity stress negatively affected all morphological, physiological and biochemical parameters across genotypes compared to control. 'Pearl Double' was found as the most tolerant genotype, showing the lowest percentage reduction in key parameters, while 'Arka Shringar' was the most sensitive, with the highest percentage reduction. At 8 dS/m, 'Pearl Double' recorded a higher membrane stability index (54.21%) and proline content (11.46 µmol/g) compared to 'Arka Shringar' (43.11% and 5.62 µmol/g, respectively). Superior ion regulation in 'Pearl Double' was indicated by lower sodium (9.61 mg/g) and chloride (3.82 mg/g) levels, whereas 'Arka Shringar' showed higher sodium (14.07 mg/g) and chloride (6.90 mg/g) levels. Eighteen tuberose genotypes were evaluated under seven heavy metal toxicity levels (Control, cadmium-RMC (0.01 ppm), cadmium-10X RMC (0.10 ppm), cadmium-25X RMC (0.25 ppm), chromium-RMC (0.10 ppm), chromium-10X RMC (1.0 ppm), chromium-25X RMC (2.5 ppm)). Heavy metal toxicity negatively impacted all morphological, physiological, and biochemical traits. 'Prajwal' was identified as the most tolerant genotype, with minimum percentage reductions, while 'Hyderabad Single' was the most sensitive. 'Prajwal' recorded higher superoxide dismutase activity (22.85 mmol/mg protein/min), peroxidase activity (4.86 mmol/mg protein/min) and proline content (6.12 µmol/g) whereas, 'Hyderabad Single' recorded the lower superoxide dismutase activity (17.67 mmol/mg protein/min) and proline content (3.20 µmol/g). These findings hold significant implications for the future of tuberose cultivation and breeding programs. By utilizing 'Pearl Double' and 'Prajwal' in breeding programs, it is possible to develop improved tuberose varieties that combine high ornamental value with enhanced stress tolerance. The cultivation of these tolerant genotypes can provide farmers with a viable alternative for growing tuberose in regions affected by salinity and heavy metal contamination, where traditional genotypes often fail to produce good yield.

Assessment of genetic diversity for carotenoid content and screening for resistance to *Alternaria* spp. in marigold (*Tagetes* spp.)

Marigold (*Tagetes* spp.) is an important commercial crop, valued for its flower and carotenoid content. Alternaria leaf spot and flower blight is the major problem in its commercial cultivation. Present investigation was conducted for assessing genetic diversity for carotenoid content and screening for resistance to *Alternaria* spp. in marigold. Maximum variability was observed among fertile lines compared to that in sterile lines, suggesting potential for further improvement in pollen parents. Genetic diversity among marigold pre-breeding lines was assessed using 122 markers, of which 46 SSRs were found to be highly polymorphic. Weighted Neighbor-Joining dendrogram grouped pre-breeding lines into three major clusters, thus, genetically distinct lines can be selected for hybrid development. *Tagetes erecta* pre-breeding lines were evaluated for carotenoid content, which ranged between 0.76 - 2.57 g/100g dry petal meal. Selection index was constructed and superior sterile and fertile pre-breeding lines for four breeding targets *i.e.*, total number of flowers/plant, flower yield/plant, number of seeds/capitulum and carotenoid content were identified. Carotenoid content in flowers varied significantly across seasons, with highest recorded during rainy season. Thus, demanding need for identifying stable carotenoid-rich pre-breeding lines. Based on mean performance and genotype stability index, stable sterile and fertile lines were identified that could serve as seed and pollen parents for developing stable carotenoid-rich hybrids. The rainy seasons, ideal for carotenoid extraction and high flower demand, coincides with peak disease outbreaks of Alternaria leaf spot and flower blight. Marigold genotypes screened under natural epiphytotic field conditions revealed differential response towards pathogen *Alternaria tagetica*, with five moderately resistant genotypes identified and resistance was confirmed by artificial inoculation using detached leaf assay. Distinct pre-breeding lines identified for resistance and carotenoid content in the study along with morpho-molecular diversity analysis possess the potential for development of commercially viable marigold hybrids.

Studies on polyploidy induction and assessment of induced variation sin *Bougainvillea* species

Bougainvillea is a popular ornamental plant known for its vibrant bracts and lush foliage. Understanding the genetic basis of traits in bougainvillea is essential for breeding programs aimed at enhancing its ornamental value. Polyploidy, the condition of having multiple sets of chromosomes, is common in plants and can lead to variations in morphological, physiological, and reproductive traits. It has been explored as a strategy to introduce genetic variability and improve desirable traits in ornamental plants. Flow cytometry, a technique for measuring DNA content and ploidy level, was utilized to determine the genome size and ploidy level of Bougainvillea genotypes. Flow cytometry analysis revealed the ploidy status of bougainvillea genotypes, among the samples analyzed, the majority were diploid, while a few exhibited tetraploid and triploid characteristics, and the 2C content of variety Mary palmer Special was 8.262 pg whereas 2C content of variety Chitra was measured as11.701pg. To induce variation, four diploid varieties (Shubhra, Vishakha, Lady Hudson, and Lady Mary Baring) were treated with colchicine (0.1% to 0.5%) and oryzalin (50 µM to 200 µM) at different durations (48, 72, and 96 hours). Flow cytometry confirmed the ploidy levels of the induced polyploids, which included diploids, tetraploids, triploids, and mixoploids. Polyploidy induction led to variations in vegetative traits such as growth habit, intermodal length, thorn characteristics, blade morphology, leaf coloration and petiole attributes across different varieties and treatments. Leaf coloration of variety Vishakha showed slightly pink colour border as secondary colour of the leaf blade. Floral traits including inflorescence length, peduncle length, bract characteristics, and floral tube color exhibited diverse responses to polyploidy induction. The young bract and main bracts of Vishakha variety had pink colour but they showed orange colour when treated with 0.2% colchicine for 72 hrs. Other than this there were very few variations in floral characters of the treated varieties of bougainvillea. This study provides valuable insights into the induction of polyploidy and the resulting variations in vegetative and floral traits in Bougainvillea species.

Theme 2: Standardization of Technologies for Sustainable Floriculture

Influence of cyanobacterial inoculation on root traits, growth and flower quality in chrysanthemum (*Chrysanthemum morifolium* Ramat.)

An experiment was conducted in a semi-climate-controlled greenhouse to evaluate the impact of cyanobacterial inoculants on Chrysanthemum var. *Zembla*. Cyanobacterial cultures- *Anabaena torulosa* (BF1), *Anabaena-Trichoderma* (An-Tr), and *Anabaena doliolum* (BF4)- were applied at the nursery stage as media amendments and through drenching at 0, 15, and 30 days after transplanting (DAT).It was observed among the various treatments of cyanobacterial inoculants, plants subjected to BF1 under both media amended and drenching had better growth parameters: plant height (92.8 cm), stem girth (0.7 cm), 33 leaves/plant, plant fresh (91.5 g), dry (12.9 g) weight, root fresh (10.56 g) and dry (1.73 g) weight, were observed at 120 DAT, early in flower bud appearance (82 days), number of buds per plants (12.7 buds/plant), early in flower opening (90.9 days) and exhibited significant values of plant pigments (leaf chlorophyll *a* of 1.8 mg/g fwt, chlorophyll *b* of 0.59 mg/g fwt, leaf carotenoid of 0.78 mg/g fwt and total leaf chlorophyll of 2.39 mg/g fwt were recorded at 120 days after transplanting). In contrast, treatment An-Tr showed better flower parameters (flower fresh (7.33 g) and dry (1.27 g) weight, flower longevity (11.8 days) and vase life (14.37 days)), as well as soil dehydrogenase activity (50.3 µg TPF/g soil/d) among all treatments. Additionally, treatments with cyanobacterial strain: BF1 had showed good amount of total soil chlorophyll at both 40 DAT (1.6 mg/g soil) & 120 DAT (1.1 mg/g soil).

Phytoextraction of heavy metals using marigold (*Tagetes erecta* Linn.) from waste water irrigated and inherently polluted soil

Soil and water contamination by heavy metals is a significant environmental challenge. Phytoextraction, a sustainable remediation strategy, enables plants to accumulate and remove heavy metals from contaminated soils. This study evaluates marigold (*Tagetes erecta* Linn.) for its potential in phytoextraction, focusing on growth, physiological, and antioxidant responses in contaminated soils. In the first experiment, marigold was grown in inherently polluted soil amended with Farm Yard Manure (FYM), Green Manure (GM), and Metal Solubilizing Bacteria (MSB). FYM resulted in the tallest plants, broadest canopy spread, and highest flower production. The combination of FYM, GM, and MSB enhanced chlorophyll, protein, phenol content, and antioxidant enzyme activities. The control treatment recorded the lowest growth and physiological parameters but exhibited the highest photosynthetic rate and transpiration. Soil analysis showed that FYM and GM improved organic carbon, reduced pH, and increased electrical conductivity, while GM + FYM + MSB treatment facilitated maximum heavy metal accumulation in plant shoots and flowers. The second experiment assessed marigold performance in wastewater-irrigated soil with varying concentrations of nickel (Ni) and zinc (Zn). Low Zn (2 mg/L) and Ni (0.2 mg/L) levels improved plant height, biomass, and seed yield, while high metal concentrations reduced growth and triggered oxidative stress. Antioxidant enzymes like catalase and superoxide dismutase increased under stress conditions. Post-harvest soil analysis revealed higher DTPA-extractable Ni and Zn with increased metal treatments and marigold accumulated the highest metal content under combined high-dose treatments. This study underscores marigold's potential as a phytoextractor, with low metal levels enhancing growth and high doses driving metal accumulation and oxidative stress responses. These findings highlight the plant's dual role in remediation and sustainable biomass production.

Effect of growth elicitors on vegetative, flowering and corm traits of gladiolus

This research was carried out to study the effect of growth elicitors on vegetative, flowering and corm traits of gladiolus taking two varieties i.e. Pusa Shanti and Pusa Rajat. The experiment was conducted under two factor- split plot design.Among both the varieties Pusa Shanti gives the better-quality crop, in contrast spike and corm yield of Pusa Rajat was highest. By considering various treatments, application of BA@150 ppm was found the best, followed by NAA@450 ppm and Si 3%. Less number of days taken for spike emergence (92.93 days), minimum number of days required for first floret opening (110.4 days), least number of days taken for 50% flowering (120.00 days), maximum spike length (94.9 cm), spike weight, spike girth (1.43cm), more number of florets/spike (21.21), maximum rachis length, floret diameter, floret length, maximum spike yield/hectare (2,55,297.2), maximum number of corms/plant (1.93) and cormels/plant (81.06), maximum weight of corms/plant (170.94 g), highest number of corms/hectare, whereas nutrient content in plants like highest total P (0.20%) and total K (3.26%) was recorded with BA @150 ppm. The NAA@450 ppm resulted in maximum floret longevity (5.67 days), maximum single corm weight (88.07), soil nutrient content like highest organic carbon (0.53%) and plant nutrient contents like highest total Ca (1.75%), Na (0.098%) and maximum Ca/Na ratio (18.09 ppm). Whereas, Si 3% recorded maximum leaf area (556.57 cm^2), fresh weight (147.54 g) and dry weight of plant (109.24 g), highest available P in soil (34.21 kg/ha), highest N and K uptake and also maximum B:C ratio (1:3.0). In addition to improving the crop's ability to absorb nutrients, the current study showed that growth elicitors greatly raised the nutrient content, flowering, and corm yield of the Pusa Shanti and Pusa Rajat cultivars, respectively.

Photomorphogenetic studies in *Chrysanthemum morifolium* cv. Zembla

A set of experiments was conducted to assess the impact of LED lights on morphological and physiological attributes in chrysanthemum cv. Zembla, also their effect on gibberellic acid levels and FT/TFL1 genes in *Chrysanthemum morifolium*. Self-rooted cuttings were raised in the plug trays under semi automated greenhouse conditions. Different photoperiods were provided for 15 h/day exposure under the growth chamber. Different LED treatments, i.e. red (100% R), blue (100% B), red+blue (80% R: 20% B), white (100% W), and ambient natural light source (under greenhouse) and fluorescent light (FL) as control were used. The flower buds were subjected to HPLC to analyze GA_3 hormone. Plant leaves were also subjected to qRT-PCR and the regulation of FT and TFL1 genes was also assessed. Plant height, internode length, stem diameter, number of leaves, leaf area, leaf area index, fresh and dry weight of leaf and stem were observed highest in the plants raised under greenhouse and remained at par with 80% R 20% B. Chlorophyll content, NPR, stomatal conductance, NRR, NAR, RGR were observed elevated under greenhouse, showing a close proximity to the plants exposed under 80% R 20% B LEDs. Bud diameter, flower diameter, flower weight were observed highest in 80% R 20% B LEDs, which was at par with the values from the greenhouse grown plants, while these parameters were recorded minimum in the plants raised under blue (100% B) LEDs. Earliest bud induction (66.6 days) was observed in plants exposed with a mixture of 80% R 20% B LEDs lights, while it got delayed (102.6 days) in Blue (100% B) LEDs. Gibberellic acid levels were recorded to be highest in plants under 80% R 20% B LEDs and minimum in Blue (100%) LEDs. Flowering promoter gene CsFTL3 was expressed highest in 80% R 20% B LEDs while the repressor gene CsTFL was expressed highest in Blue LEDs.

Effect of silicon on growth, flowering and corm traits of gladiolus under different soil conditions

The present study focuses on assessing the influence of silicon additives on the growth, flowering, and corm characteristics of Gladiolus cv. Pusa Shanthi in various soil and climatic conditions. The study aimed to identify optimal silicon levels, combined with fertilizers and vermicompost, to improve plant morphological, physiological, and biochemical traits. The trials included diverse pot and field configurations, assessing silicon treatments across a range of soil salinity levels. Silicon significantly improved vegetative growth, including plant height (121.83 cm), leaf area (1587.38 cm^2), and early flowering (4 days earlier). It also enhanced flowering quality, corm yields, and ornamental characteristics, increasing economic profitability. The best-performing field treatment (T11) combined soil-applied silicon (60 kg/ha), foliar silicon (1%), vermicompost (10 tons/ha), and RDF (200:100:100 kg/ha NPK), resulting in improved spike length (103.96 cm), corm weight (78.34 g), and cormels per plant (41.48) with a benefit-cost ratio (BCR) of 2.5:1. In pots, silicon at 150 mg/kg soil achieved superior growth, while soils with an electrical conductivity (EC) of 0.12 mS were most favourable for flowering. Silicon-treated plants in saline conditions exhibited resilience, with higher corm weights (57.36 g), prolonged vase life (13.41 days), and reduced oxidative stress. Biochemical analysis showed increased chlorophyll content (2.28 mg/g), Membrane Stability Index (82.40%), and Relative Water Content (10%). The findings demonstrate silicon's vital role in enhancing plant growth, flowering quality, and stress tolerance, offering a sustainable strategy for improving gladiolus productivity and economic returns in challenging environments.

Studies on seed production in China aster (*Callistephus chinensis* (L.) Nees.)

An investigation was carried out on seed production in China aster [*Callistephus chinensis* (L.) Nees] to enhance seed yield. Floral biology studies revealed that anthesis and anther dehiscence was observed in forenoon to afternoon with stigma receptivity in fully expended rays, number of ray and disc florets were observed maximum in Arka Poornima. Pollen germination was found highest in media 15% sucrose + 30% PEG +BK medium. Seed set was recorded maximum in Arka Kamini (54.13%).Studies on effects of open pollination and self-pollination seed setting highest number of seeds from primary and secondary branches in Arka Kamini (139.68 and 141.80) and

(93.21 and 142.07), also maximum seed weight per flower head (0.76) and (0.26), seed germination (80.95) and (85.42). Maximum seed vigour was recorded in Arka Poornima (491.04) and (489.56). Artificial self-pollination seeds obtained from primary branches was recorded maximum in Arka Poornima (86.50). Maximum seed weight (g) per flower head was in control (0.476). Seed weight per plant was maximum in Arka Kamini (2.71). Studies with micronutrients, Arka Kamini recorded number of seeds from primary (145.40) and secondary branches (154.82), per plant seed weight (3.90) and seed germination (84.33). Arka Poornima recorded maximum seed weight from primary (0.611) and secondary branches (0.651), seed weight per flower head (0.597) and seedling vigour index (538.62). In GA_3 studies, Arka Kamini recorded maximum number and weight of seeds from primary (138.33) and secondary branches (141.29), seed weight per flower head (0.442) and per plant (3.91), 1000 seed weight (2.60) and vigour index (523.71).

Theme 3: Tissue Culture and Value Addition in Floriculture

Extraction of natural dye from rose petals and its application on fabric

Roses, ornamental shrubs, are used for various purposes, including landscaping and cut flowers. Their petals contain anthocyanin, a natural pigment that can be used to create dyes. Natural dyes are environmentally friendly alternatives to synthetic dyes. However, the use of rose petal dye in the textile industry is limited due to challenges in standardization, understanding dye interactions, and assessing colour fastness. This study aimed to address these limitations by optimizing the extraction process, screening mordants and mordanting techniques, and evaluating the overall stability of the natural dye on fabrics. Rose petals from *Rosa chinensis* were used to extract the natural dye. The study found that the optimal conditions for extraction were a temperature of 25°C, a solid-to-solvent ratio of 1:5, and 0.015% HCl as the solvent with maximum anthocyanin content of 19.653 mg/L and a redness index of 240.314. Stability studies showed that anthocyanin degradation was influenced by temperature, exposure time, and pH. There was more degradation in natural conditions compared to continuous light or dark conditions. The colour of the dye became brighter at lower pH levels and blue at higher pH levels. The study also evaluated the use of alum and potassium dichromate as mordants with different mordanting techniques on various fabrics. The results indicated that the premordanting technique with alum was most effective in preserving the original color of the rose natural dye on all fabrics. Colour fastness tests were conducted on the dyed fabrics, and the results showed that cotton fabric had the best overall fastness using the postmordanting technique, while silk fabric had the highest color strength with potassium dichromate.

Development of *in-vitro* protocol for efficient regeneration of rose (*Rosa x hybrida* L.) genotypes using axillary and non-axillary explants

Roses (*Rosa* spp.) have significant global economic importance. These are propagated sexually and asexually, but sexual methods cause high heterozygosity, while asexual methods are slow and season-dependent. *In-vitro* propagation ensures rapid, reliable multiplication and disease-free plants. This study aimed to develop a protocol for efficient regeneration and mass multiplication of rose genotypes Pink Parfait Seedling, BRRS-1 and Pusa Alpana using axillary buds, leaves and petal explants. Pre-treating axillary buds of Pink Parfait Seedling (RS-03-2017) and BRRS-1 (RH-1-2018) genotypes and petals of PPS (RS-03-2017) and Pusa Alpana with Carbendazim (0.2%) + Metalaxyl-45 (0.2%) and 8-HQC (200 mg/l) for 3 and 1.5 hours, respectively, gave minimal contamination and maximum survival followed by surface sterilization with 0.1% $HgCl_2$ for 5 minutes whereas for 3 minutes showed least contamination, high survival rates. Leaf explants of *in-vitro* plantlets, required no pre-treatment. Best culture establishment found in MS with BAP (4.0 mg/L) + NAA (0.2 mg/L) + GA_3 (0.5 mg/L), shoot proliferation in MS +

BAP (3.0 mg/L) + NAA (0.2 mg/L) + GA_3 (0.5 mg/L) and longest shoots in MS + GA_3 (0.5 mg/L) in Pink Parfait Seedling (RS-03-2017) and BRRS-1 (RH-1-2018). For rooting, ½ MS + NAA (0.5 mg/L) found to be superior. Hardening with plastic cups having Cocopeat + Vermiculite + perlite mixture with ½ strength MS medium gave maximum survival rates. In leaves, MS+NAA (0.1mg/L) +BAP (3.0mg/L) +TDZ (1.0mg/L) +$AgNO_3$ (3mg/L) promoted rapid and efficient callus formation in Pink Parfait Seedling (RS-03-2017) and BRRS-1 (RH-1-2018). Concerning petals, MS + NAA (0.2 mg/L) + BAP (2 mg/L) + 2,4-D (1 mg/L) + TDZ (2 mg/L) gave efficient callus formation in shorter period in Pink Parfait Seedling (RS-03-2017) and Pusa Alpana. No regeneration noted in leaf and petal explants. This study confirms that *in-vitro* regeneration via axillary buds is a rapid and efficient method for rose breeding.

Theme 4: Soilless Culture and Vertical Gardening in Flower Crops

Optimization of pot mums and growth media for vertical gardening and bibliometric renaissance

This study conducted for optimization of pot mums and growth media for vertical gardening and bibliometric renaissance exploring two main areas i.e. improving chrysanthemum cultivation for vertical gardening and analyzing research trends in this field. Six chrysanthemum varieties and twelve different growth media combinations were assessed under this experiment. The study revealed significant differences in the performance of the varieties: Yellow Charm excelled in plant spread, leaf development, and root growth. Sadbhawana and Pusa Sona showed superior branching and overall plant mass. Pusa Sona was notable for its early flowering, abundant bud production, and enhanced flower weight. Regarding growth media, two combinations were particularly effective: T2 (soil, sand, and FYM in a 2:1:1 ratio): This combination promoted plant height, spread, and nutrient content. T3 (soil, sand, and vermicompost in a 2:1:1 ratio): It enhanced branching, leaf surface area, and flowering metrics. Additionally, T12 (perlite, FYM, and soil in a 2:1:1 ratio) showed promise, particularly for fresh and dry weight, root diameter, and root volume. These results suggest that T2 and T3 are ideal for pot mum cultivation in vertical gardening systems. The bibliometric analysis revealed interesting trends in chrysanthemum research. Publication rates surged from 4 articles per year before 2010 to 29 articles per year after 2010. Chen F. was the most prolific researcher, with 63 publications, and China led in contributions with 194 publications. The 2001 study by Ahloowalia and Maluszynski on induced mutations in plant breeding was the most cited, with 315 citations. *BioMed Central Genomics* published the most articles, while *IEEE Transactions on Image Processing* had the highest impact factor (10.6).In conclusion, this research offers valuable insights into both chrysanthemum cultivation in vertical gardening and the evolving trends in chrysanthemum research.

Studies on soilless culture of pot gerbera (*Gerbera jamesonii* Bolus ex Hooker f.)

An experiment was carried out in factorial completely randomized design to study the effect of three growing media on performance of ten pot gerbera varieties. The study revealed that the media (M_2) composed of cocopeat + perlite + vermiculite (3:1:1) showed better physico-chemical properties such as bulk density (0.34, 0.40 and 0.46 g/cm^3), water holding capacity (49.91, 44.01 and 39.80 %) and pH (5.78, 5.99 and 6.05) measured at monthly intervals on 30,60 and 90 DAP, respectively. Among the varieties, Glorious White had maximum plant height (22.8 cm), leaf length (20.1 cm) and leaf breadth (10.4 cm) while minimum days for first flower bud appearance (29.8), opening (35) and their harvest (41). Highest number of flowers per plant (17.5) was recorded in var. Glorious Orange. The biochemical parameters varied significantly among the varieties due to differences in growing media and found that maximum chlorophyll a (9.14 mg/g fwt), chlorophyll b (3.65 mg/g fwt) and total chlorophyll (12.79 mg/g fwt) were recorded in var. Glorious Orange grown on media (M_2) composed of cocopeat + perlite + vermiculite (3:1:1). Glorious Orange grown on media (M_2) recorded maximum leaf relative water content (91.20 %), transpiration rate (13.86 mmol H_2O m^{-2} s^{-1}), photosynthetic rate (14.03 µmol CO_2 m^{-2} s^{-1}) and water use efficiency (0.55 mmol CO_2 mol^{-1} H_2O) at 90 DAP. Glorious Orange grown in media having coco-peat + perlite + vermiculite (3:1:1) recorded non-significant but maximum crop water productivity (6.17 kg/kL) as compared to other interactions among the treatments. The economic analysis was made and found that the variety, Glorious Orange grown on media composed of coco-peat + perlite + vermiculite (3:1:1) received the highest monetary returns along with the highest BC ratio.

Standardization of *Dendrobium* orchid production under vertical farming structures and post-harvest handling protocols

With increasing population and shrinking arable land, transitioning to vertical farming systems is crucial for sustainable agriculture. *Dendrobium* orchids, a high-value cut flower crop hold significant potential for vertical farming, enhancing domestic availability, reducing import dependency and boosting floriculture exports. This study developed protocols for cultivating *Dendrobium* cv. *Emma White* in vertical systems, optimizing potting medium, pot type, growing structures, spacing and planting geometry to maximize productivity and profitability. Standardization of value-addition techniques was also attempted. Plants grown on vertical frames using a mixed potting medium (coconut husk chips, charcoal and terracotta tile bits in 1:1:1 v/v) in netted pots showed superior vegetative traits, including higher pseudo bulb count, length and internodal length. Charcoal medium in netted pots enhanced vegetative traits like leaf number, width, length and area. These plants registered earlier spike initiation (175.33 days), maximum spikes plant^{-1} (8.88), florets spike^{-1} (7.67), longest spikes (49.38 cm), increased spike longevity (62.33 days) and extended vase life (42 days) along with superior physiological parameters. Spacing plants at 30 × 30 cm in a quincunx planting system on vertical frames resulted in superior vegetative, physiological and flowering traits, including earlier spike initiation (171.50 days) and maximum spikes plant^{-1} (8.92). Value addition protocols were standardized, with hot air oven drying using silica gel producing high-quality dried florets and resin encapsulation (2:1 resin-to-hardener ratio) extending storability to 178.67 days. In conclusion, cultivating *Dendrobium* using charcoal in netted pots spaced at 30 × 30 cm on vertical frames in a quincunx system is sustainable and profitable, boosting yield and plant density by 142.8% over conventional system with a 3.77 benefit-cost ratio. Value added products can contribute to further in enhancing the income and generate employment opportunities. Aligning with UN Sustainable Development Goals (SDG 8, 11 and 15), promoting economic growth, sustainability and environmental conservation.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Amulya Kalahal (21880)	M.Sc.	Influence of cyanobacterial inoculation on root traits, growth and flower quality in chrysanthemum (*Chrysanthemum morifolium* Ramat.)	Dr. M. C. Singh	ICAR-IARI, New Delhi
2.	Tejaswini P. (21881)	M.Sc.	Effect of growth elicitors on vegetative, flowering and corm traits of gladiolus	Dr. Kishan Swaroop	ICAR-IARI, New Delhi
3.	Vidya Maruti Nargudkar (21882)	M.Sc.	Optimization of pot mums and growth media for vertical gardening and bibliometric renaissance	Dr. Ajai Kumar Tiwari	ICAR-IARI, New Delhi

4.	Swati (21883)	M.Sc.	Development of in-vitro protocol for efficient regeneration of rose (*Rosa* x *hybrida* L.) genotypes using axillary and non-axillary explants	Dr. Namita	ICAR-IARI, New Delhi
5.	Deepika (21884)	M.Sc.	Phenotypic expression of qualitative and quantitative traits in French marigold (*Tagetes patula* L.) under different growing conditions	Dr. M. R. Dhiman	ICAR-IARI, New Delhi
6.	Aashna Kumari (21885)	M.Sc.	Nematicidal efficacy of *Chrysanthemum coronarium* against *Meloidogyne incognita*	Dr. Gunjeet Kumar	ICAR-IARI, New Delhi
7.	Sanapala Keerthana (21886)	M.Sc.	Extraction of natural dye from rose petals and its application on fabric	Dr. Babita Singh	ICAR-IARI, New Delhi
8.	Athira N (21918)	M.Sc.	Phytoextraction of heavy metals using marigold (*Tagetes erecta* Linn.) from wastewater irrigated and inherently polluted soil	Dr. Prativa Anand	ICAR-IARI, New Delhi
9.	Shorya Sharma (21963)	M.Sc.	Screening of marigold genotypes (*Tagetes* spp.) against *Alternaria* leaf spot under in vitro and in vivo conditions	Dr. Reeta Bhatia Dey	ICAR-IARI, New Delhi
10.	PriyaYadav (11256)	Ph.D.	Studies on polyploidy induction and assessment of induced variations in *Bougainvillea* species	Dr. S. S. Sindhu	ICAR-IARI, New Delhi
11.	Neeraj Singh Negi (11257)	Ph.D.	Photomorphogenetic studies in *Chrysanthemum morifolium* cv. Zembla	Dr. M. C. Singh	ICAR-IARI, New Delhi
12.	Chander Prakash (11258)	Ph.D.	Screening of tuberose (*Polianthes tuberosa* Linn.) genotypes for salinity and heavy metals stress tolerance	Dr. Sapna Panwar	ICAR-IARI, New Delhi
13.	Chetna Jyoti (11504)	Ph.D.	Studies on seed production in China aster (*Callistephus chinensis* (L.) Nees.)	Dr. Rajiv Kumar	**ICAR-IIHR, Bengaluru
14.	Vidyashree (11769)	Ph.D.	Studies on soilless culture of pot gerbera (*Gerbera jamesonii* Bolus ex Hooker f.)	Dr. M. C. Singh	ICAR-IARI, New Delhi
15.	Sindhu K (11773)	Ph.D.	Effect of silicon on growth, flowering and corm traits of gladiolus under different soil conditions	Dr. Kishan Swaroop	ICAR-IARI, New Delhi
16.	Labdhi Dedhia (11777)	Ph.D.	Assessment of genetic diversity for carotenoid content and screening for resistance to Alternaria spp. in marigold (*Tagetes* spp.)	Dr. Tejeswini	**ICAR-IIHR, Bengaluru
17.	Chandana S (11778)	Ph.D.	Standardization of *Dendrobium* orchid production under vertical farming structures and post-harvest handling protocols	Dr. Sujatha Nair	**ICAR-IIHR, Bengaluru

***Outreach institute*

FRUIT SCIENCE

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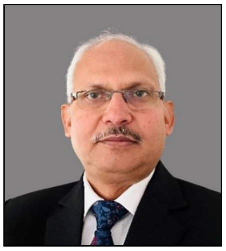

Prof. R. M. Sharma

The Division of Fruits & Horticultural Technology is a premier centre of research and post-graduate education. The division has excelled in the development of quality Human Resource for strengthening Horticultural research through post-graduate teaching and organizing training programmes in frontline areas in perennial fruit crop improvement, hi-tech production, plant propagation and nursery management, stress resilient fruit production techniques and application of new molecular tools on mandated fruit crops. During the last five decades, the Division has significantly contributed through research for the advancement of Horticulture, by ushering in the frontiers of knowledge in fruit crops, and providing practical solutions to the problems, being confronted by fruit industry and stakeholders.The post-graduate research findings are being presented under various themes.

Theme 1: Genetical Studies and Molecular Characterization

Validation of new hyper-variable mango SSRs and diversity analysis of heirloom mango varieties

The present investigation was undertaken at the Division of Fruits and Horticultural Technology, ICAR-IARI, New Delhi during 2023-24 to characterize thirty-six heirloom mango varieties, of which, twenty four genotype belongs to eastern parts of the country and specifically Kushinagar district and TamkuhiRaj. These heirloom mango varieties have also been characterized using hyper-variable SSR markers designed from Amrapali genome sequences. The molecular characterization of 36 heirloom mango varieties was attempted using 43 polymorphic SSRs. SSR profiling data revealed amplicons in the range of 150 to 400 bp with an average allele number of 2.60 per locus. Gene diversity ranged from 0.30 to 0.62. UPGMA analysis broadly grouped heirloom mango varieties into two major clusters. Cluster II comprises 27 varieties followed by cluster I possessing 9 varieties. Model based structure analysis revealed two gene pools. Analysis of molecular variance indicated that higher variation in individuals is observed within the individuals (99 %). It is concluded that 36 heirloom mango varieties have been characterized based on novel hyper-variable SSRs. The information generated has significance in conservation, protection and utilization of heirloom mango varieties.

Development and validation of genome-wide SSR markers in guava (*Psidium guajava* L.)

Guava (*Psidium guajava* L.) is one of the economically important fruit crops. To improve breeding efficiency and initiate molecular breeding, the self-sufficiency of genomic resources is of utmost importance for any crop species. The novel genome-wide SSR markers were developed by utilizing chromosome assembly (GCA_016432845.1) of "New Age" Chinese guava using GMATA, a comprehensive software. The most prevalent motif was dimers, accounting for over 75% of the total available motifs, while trimers comprised more than 15% of occurrences. A total of 55 g-SSR markers were chosen to screen 35 guava genotypes, encompassing wild *Psidium* species and five jamun genotypes. Of the 55 validated novel g-SSR markers (FHTGSSRs), 35 showed polymorphism, suggesting significant genetic variation among the guava genotypes, including wild species. The 35 FHTGSSR markers had an average of 2.69 alleles per locus. The major allele frequency was 0.79, the gene diversity was 0.30, the observed heterozygosity was 0.10, and the polymorphic information content was 0.27. Among the wild *Psidium* species studied, the transferability of these novel g-SSR loci across different species was 57.14 to 100%. Furthermore, only seven SSRs were successfully amplified in the jamun genotypes, of which only one SSR (FHTGSSR) showed polymorphism. In addition, the study of population structure classified the guava genotypes into two distinct genetic groups, which the PCoA largely supported. In addition, the AMOVA and PCoA analyses also deciphered substantial genetic diversity among the chosen guava genotypes, including wild species. Hence, the developed novel genome-wide genomic SSRs could enhance the availability of genomic resources in guava and assist in molecular breeding of guava.

Morpho-chemical and molecular diversity studies in pomegranate genotypes

The current investigation was conducted to analyze the characteristics of the 60 pomegranate genotypes. Ganesh took least time for sprouting with maximum sprouting and final cutting success. In contrast to this Goliath and G-2 took almost double time for sprouting and least sprouting success was also observed. Early sprouting was observed in most of the cultivated varieties, while late sprouting in indigenous wild genotypes. High sprouting was noticed in cultivated varieties and few exotic genotypes. In similar way high cutting success was also found in most cultivated and exotic genotypes. Maximum leaf blade length and width was observed in Solapur Lal and Jodhpur Red. Higher membrane stability index was noticed in Jodhpur Red with similar statistical values in Bhagwa. The highest *A* was observed in indigenous wild genotype G-2, *Ci* in IC-318737, *E* in Kandhari Red Bud Sport and g_s in EC-676968. Pertaining to phenol content EC-676964 was found significantly superior. Genotype EC-937333 exhibited higher caretonoid, chlorophyll *a*, *b* and *a* + *b* contents. Molecular analysis revealed that the genotypes studied are diverse and 21 out of 26 publically available SSRs used for diversity analysis showing high PIC value >0.5, being highest in PgSSR6 (0.57) with highest discriminating power (0.64). The 60 genotypes were grouped into three main clusters with first cluster contained 23 genotypes, second cluster included 18 genotypes and third cluster also comprised 19 genotypes. In our analysis, 3 major clusters were found with cluster 1 majorly consisting of exotic genotypes. The cluster 2 comprised mostly wild genotypes and mixture of cultivated, exotic and wild genotypes, while in cluster 3 it mostly consisted cultivated varieties. The findings confirm that the studied genotypes confirm high genetic diversity indicating that their inclusion into future crop breeding programmes.

Insights into the nut and food qualities of selected walnut (*Juglans regia* l.) genotypes

The present study was conducted to determine the superior genotypes (out of 44 Nos) for export related traits and consumer preference, collected from six locations of Himachal Pradesh and UT of Jammu and Kashmir. Based on export related traits, a total of 35 genotypes were selected. In terms of morphological characteristics, ovate nut shape, round nut shape in cross section, and smooth shell surface were found most predominating. The nut size related traits like nut length, nut diameter, nut weight, shell thickness, and thickness of dividing membrane varied from 30.42-50.04 mm, 28.93-47.87 mm, 8.74-21.68 g, 1.40-2.73 mm, and 0.16-1.42 mm, respectively, whereas kernel recovery varied from 30.43-61.42%. Bhushan genotype excelled for shell whiteness index, kernel size (along with CITHW-1), kernel weight and kernel recovery (61.42%). A huge range of biochemical constituents was observed in respect of moisture content (1.61-6.12%), ash content (1.04-4.12%), total phenolic content (TPC) (641-4762.07mg GAE/ 100 g), total flavonoid content (TFC) (64.75-235.88 mg QE/100 g), anti-oxidant activity (AOX) (48.73-83.8%), total carbohydrates (7.99-22.72%), total proteins (9.63-25.38%) and oil yield (34.13-63.23%). Polyunsaturated fatty acid namely linoleic acid ranged between 49.13-69.83%, while monounsaturated fatty acid i.e. oleic acid ranged between 18.50-41.18%. The saturated fatty acids (SFA) palmitic and stearic acid varied between 5.16-11.38% and 1.71-6.56%, respectively. A wide range of mineral nutrients concentration (K, P, Ca, Mg, Fe, Zn, Mn, and Cu), which were higher in defatted kernel than whole kernel. Overall, Bhushan, PAD 1-23, CITH-W-1, CITHW-6, CITH-W-8, CITH-W-10, CITH-W-12, Mandi Selection, Pusa Khor, Amartara Selection-1, Amartara Selection-2, and Gumma Selecton-1 were found most promising from export, nutritional and consumer standpoints.

Characterization and quality assessment of interspecific citrus hybrids

The present investigation was undertaken to characterize and evaluate the twenty-four interspecific citrus hybrids and four parents. Significant variation was observed in interms of leaf (leaf and leaf lamina shape) and fruit traits. Most of the hybrids showed spheroid fruit shape, while > 85% hybrids witnessed green- yellow (RHS-YOG-18B) fruit juice colour at maturity. The seeds per fruit varied from 6 to 70. Most of the hybrids (95.83%) were monoembryonic, however, 4.17% hybrids had polyembryonic nature. The higher juice recovery (> 40%) was recorded in SCSH 6-6, SCSH7-3, SCSH8-11, SCSH 8-18, SCSH 11-16, SCSH 13-4, sweet orange cv. Mosambi. Higher TSS/acid ratio (>8) was recorded in SCSH 2-2, SCSH 3-6, SCSH 7-2 and SCSH 7-4, and all parents except tangerine. The maximum total antioxidants contents (>5 DPPH µmol Trolox/g) found in SCSH 8-18. Majority of the fruit quantitative characters were positively correlated with each other. Study showed that out of 24 interspecific citrus hybrids, four hybrids (SCSH 3-10, SCSH 4-13, SCSH 8-18, and SCSH 13-6) showed excellent qualitative characters. Bio-active compounds such as naringin, hesperidin and limonene, also showed variation in citrus hybrids. Among the parents, tangerine showed highest naringin content (15.90 mg/L), while mosambi showed 0.43 mg/L and white pummelo showed 0.40 mg/L. Hesperidin content in hybrids varied from 0.1 mg/L (SCSH 4-13) to 193.8 mg/L (SCSH 8-18). Red pummelo showed highest limonene content (98.54%), while tangerine showed lowest (4.07%). Key findings from this study that Tangerine as one of the parents could resulted in enhancing juice content as well bio-active compounds like naringin and hesperidin in citrus hybrids. Moreover, white pummelo could enhance the limonene content. Citrus hybrids, evaluated were significantly different for macro-and micro-nutrients in fruit juice.

In-situ characterization and diversity analysis of custard apple (*Annona squamosa* L.) germplasm of Chotanagpur plateau region

The present study was conducted to characterize and genetic analysis of custard apple germplasm of Chotanagpur plateau region. In study involved 69 genotypes and one Arka Sahan variety as a reference variety. High variability was found in the morphological traits of the fruit, seeds, leaves, and trees. Spreading plant habit with ovate leaf shape, acute leaf apex, green leaf colour and crimson green petiole colour were recorded as predominant traits among 70 genotypes. The plant height, plant girth, leaf length, leaf breadth, petiole length in the studied genotypes ranged from 2.10-6.90 m, 16.78-50.65 cm, 5.97-14.33 cm, 2.40-6.47 cm and 0.80-1.73 cm, respectively. The fruit length, diameter, weight, peel thickness, core length, seeds per fruit, seed weight, seed length, seed width, seed weight, peel weight, pulp weight, pulp percent and pulp/ seed ratio varied from 4.95-7.04 cm, 5.24-7.59 cm, 70.67-216.00 g, 0.30-0.64 cm, 2.10-3.43 cm, 5-36, 16.30-46.34 g, 1.03-1.57, 0.60-0.83 cm, 2.28-7.93 g, 29.10-60.52 g, 29.53-150.07 g, 41.14-77.48 %, and 7.60-38.52 respectively. For biochemical traits, the variation range was recorded for TSS (12.60-29.37 ^{o}B), titratable acidity (0.26-0.67%), ascorbic acid (12.60-39.84 mg/100g), total antioxidant content (68.67-176.67 mg AEAC/100g), total phenol content (86-139.97 mg GAE/100g), total sugars (10.82-27.77 %), reducing sugars (9.92-25.82 %) and non-reducing sugars (1.08-4.51 %). The gallic acid was recorded high in 15 genotypes with an average of 37.74 mg/100g. The genotypes KCA03 (large fruit size and higher pulp weight) CCA03 (highest pulp percent and low peel percent), KCA21 (high pulp percent), CCA04 (high TSS) and RCA14 (low seed percent and highest TAC) were found superior genotypes with their respective quality traits.

Genetical studies for seedlessness and related traits in grape (*Vitis vinifera* L.) parents and its hybrids raised using *in vivo* and *in vitro* techniques

The evaluation of 12 grape genotypes revealed that seedless genotypes exhibited superior bunch and berry traits. Of the seedless genotypes, Pusa Purple Seedless had the highest TSS, however seeded genotypes like Pearl of Csaba had the larger berry size with lower TSS than former. Genotypes were classified into four phenotypic classes based on seed traits analysis: completely seedless (Beauty Seedless, Flame Seedless, Centennial Seedless, Perlette and Pusa Trishar), semi-seedless (Pusa Purple Seedless and Pusa Urvashi), semi-seeded (Pusa Aditi, Pusa Swarnika, Pearl of Csaba), and completely seeded (Cardinal). Promising genotypes (Pusa Aditi, Pusa Trishar, and Pusa Urvashi), were found suitable as female parents, while Perlette and Beauty Seedless emerged as excellent male parents for hybridization. For embryo rescue, the ideal ovule age for embryo rescue was genotypes/cross specific ranging from from 23-38 days after pollination (DAP). Nitsch and Nitsch medium with IAA (1.0 mg L^{-1}) and GA_3 (0.5 mg L^{-1}) was optimal basal medium for embryo culture, while WPM medium with BA (0.2 mg L^{-1}) + IBA (0.1 mg L^{-1}) enhanced the embryo germination and plantlet recovery. Basal MS medium supplemented with IBA (2.0 mg L^{-1}) + BAP (0.1 mg L^{-1}) proved effective for multiplication and rooting. Recovery rates of 21.37% for Pusa Aditi, 20.78% for Pusa Aditi × Beauty Seedless, 10.51% for Pusa Urvashi × Perlette and 8.59% for Pusa Trishar × Perlette was achieved through embryo rescue protocol. The hybridity of *in-ovulo* embryo rescue raised plantlets were validated through SSR markers, with primers VVS2, VMC1b11, VVIn16, VVMD32, VVMD21, VVMD24, VVMD8, and VrZAG62 confirming hybridity. RNA-Seq analysis provided insights into the molecular basis of seedlessness. Differentially expressed genes related to cell wall metabolism (*VIT_18s0001g03160*), hormone transport (*VIT_18s0001g11280*), seed development (*VIT_16s0022g02090*; *VIT_02s0025g04630*), and gibberellin biosynthesis (*VIT_07s0151g01040*; *VIT_16s0022g02310*) were identified.

Characterization of powdery mildew resistance in grapevine genotypes and identification of markers for resistance

In this study, the resistance of various grapevine genotypes, assessed to powdery mildew (*Erysiphe necator*), revealed the significant variation in disease severity under field conditions, enabling to classify the genotypes into 7 categories, based on their Disease Severity Index (DSI) values. *V. parviflora* and Male Hybrid proved highly resistant (DSI: 5.88-7.83), while Pusa Trishar was extremely susceptible (DSI: 90.56). The peak development of pathogen was at T_{max} between 26°- 29°C and T_{min} between 10°- 13°C, with disease severity peaking in August. Under *in-vitro* screenings Pusa Trishar and Alumwick behaved as highly susceptible, while Male Hybrid and 110 Richter were highly resistant (without observable mycelium). Correlation analyses among tissue necrosis, hyphal growth, and OIV scores revealed strong relationships, with increased necrosis correlating with reduced hyphal growth. Physiologically, Salt Creek recorded the highest *A*, although reduced further due to infection. Male Hybrid exhibited an unusual resilience with an increase in *A,* when infected. The highest and lowest *E* were recorded in *V. parviflora* and Pusa Seedless, respectively. Biochemically, total phenolic content increased in genotypes like Male Hybrid and Black Prince, which showed strong defence. Enhanced antioxidant enzyme activities were observed in PM-infected plants, suggesting an activation of various defense mechanisms against oxidative damage induced by the pathogen. The indigenous Himalayan species, *V. parviflora*, had the strongest PM resistance, characterized by a thicker waxy epi-cuticular layer on the abaxial leaf surface, which restricted pathogen infection and reduced necrotic tissue formation. Microscopic examinations using scanning electron microscopy confirmed significant differences in fungal hyphal growth between resistant and susceptible genotypes. *Vitis parviflora* had minimal hyphal growth and greater necrosis compared to the susceptible genotype Pusa Trishar.

Theme 2: Crop Improvement and Character Association

Evaluation of interspecific citrus scion hybrids for fruit quality and health promoting compounds

The biochemical changes during the maturity of 16 interspecific citrus hybrids (*C. maxima* [Burm. f.] Osbeck × *Citrus sinensis* [L.] Osbeck) were evaluated to determine the optimum harvest maturity of these novel hybrids. The TSS, TA, TSS/TA ratio, BrimA, and juice per cent corresponded to the highest organoleptic score, judged to determine the optimum harvesting stage. In the subtropical conditions of Delhi, the fruits attained the optimum maturity stage between the 15th of October and the 15th of November. The TSS, TA, TSS/TA ratio and ascorbic acid content at maturity varied from 8.93-11.47°B, 0.72-1.84%, 5.68-12.77, and 37.86-71.15 mg/100 mL in hybrid genotypes. The fruit weight, peel thickness, and juice content in new citrus hybrids varied from 282.00-584.77 g, 4.29-9.28 mm, and 22.91-48.24 %, respectively. The hybrids, SCSH-9-10/12, SCSH-11-15/12, and SCSH-17-19/13, were found superior, having better juice acceptability organoleptic score (≥5.0) and higher juice content (≥40%). The present study showed that the citrus fruits are a valuable source of supplementing essential mineral nutrients in healthy diets, and the genotypes evaluated were significantly different for macro- and micro-nutrients in fruit juice. A wide range of mineral nutrients concentration in the citrus fruit juice was observed including P (60.76-251.07 mg/L), K (574.67-1195.47 mg/L), Ca (153.6-736.0 mg/L), Mg (23.68-101.76 mg/L), Fe (1.65-7.37 mg/L), Zn (1.28-2.97 mg/L), Mn (0.51-1.24 mg/L), Cu (0.46-0.84 mg/L), Na (18.40-45.87 mg/L) and Cl (17.04-289.68 mg/L). The citrus hybrid genotypes namely, SCSH-9-6/12, SCSH-9-10/12, SCSH-11–9/13, and SCSH-7-2/12 were found to have superior micro-nutrients. The hybrids, SCSH-9-2/12, SCSH-9-11/12, and SCSH-11-9/13, were found to have very low limonin content (<1 mg/L) and higher organoleptic acceptability in the juice even after 24 h of storage.

Morphological, biochemical and molecular characterization of maternal half-sib progenies of Amrapali for identification of superior genotypes

A half-sib population of 125, phenotyped showed the significant variability in terms of growth, physiological and biochemical traits. Significant variation was noticed in terms of male flowers (525.0 to 3961.0), hermaphrodite flowers (74.75 to 854.00), incidence of malformation (2.00 to 100.0%) and inflorescence shape (broadly pyramidal: 41, pyramidal: 39 and conical: 20 half-sibs). The similar variations was also observed in biochemical attributes includingTSS (13.74 to 29.34 °brix), pulp titratable acidity (0.26 to 1.24 %) and pulp β-carotene (969.81 to 21,138.44 µg/ 100 g pulp). The scores of 42 HMSSR loci were used to determine the genetic diversity analysis and UPGMA tree generation in 119 maternal half-sibs of Amrapali, mother Amrapali and 14 probable male donor parents grouped into four clusters. The major allelic frequency ranged from 0.05 (HMSSR1917) to 0.49 (HMSSR458 & HMSSR1079) with an average of 0.30. The maximum expected heterozygosity (0.64) was noted in HMSSR_1305, while minimum (0.19) in HMSSR1923 with mean value of 0.37. In UPGMA, major share was in Cluster I which had 42 half-sibs (31.34 %). Cluster II had 14 maternal half-sibs of Amrapali and 14 probable male donor parents of half sibs. Cluster III consisted of 34 half-sibs (25.37 %) of population, and Cluster IV had 29 half-sibs and mother Amrapali (22.39 %). Out of 264 SSR markers studied, 10 primers exhibited polymorphism and were utilized to confirm parentage between Amrapali and 14 male donors. Various half-sibs demonstrated parentage combinations involving Amrapali with Mallika in HMSSR_760, St. Alexandrina in HMSSR767, Kesar (or) Sensation in HMSSR_2113 and HMSSR_1917, Elaichi in HMSSR_458, Olour in HMSSR_1079, Olour or

Mallika in HMSSR_1848, Kesar in HMSSR_640, Bahaduran in HMSSR_1111, Banganpalli (or) Totapuri in HMSSR_1164, respectively. Some half-sibs, like HS-12/5, HS-21/8, HS-24/1, HS-31/1, HS-31/2, HS-37/3 and HS-48/5 etc., exhibited improved traits over Amrapali.

In vitro screening of Vitis spp. for low moisture stress tolerance

In the present investigation, improved protocols for culture establishment and rooting media for two new hybrids namely, Pusa Swarnika and Pusa Purple Seedless grapes were standardized. Rapid multiplication of Pusa Swarnika was obtained with half-strength MS medium with 1.5 mg L^{-1} IBA, 0.25 mg L^{-1} BA, and 0.25 mg L^{-1} NAA. In contrast, higher IBA (4 mg L^{-1}) and BA (0.5 mg L^{-1}) concentrations worked for Pusa Purple Seedless. The impact of polyethylene glycol (PEG) induced drought stress (0% to 6%) on *in vitro* cultured nodal cuttings was evaluated over four weekson eight grape genotypes (110 R, Dogridge, St. George, Pusa Swarnika, Pusa Navrang, Perlette, Male Hybrid and *V. parviflora*). The LD_{50} values based on mortality percentages were 3.34% (110R), 3.1% (Dogridge), 3.24% (St. George), 3.16% (Pusa Swarnika), 2.34% (Male Hybrid), 1.86% (Pusa Navrang), 1.78% (*V. parviflora*), and 1.71% (Perlette) The average LD_{50} value for the eight grape genotypes was recorded at 2.57%. Proline, total soluble proteins, hydrogen peroxide levels, and antioxidant enzyme activity (superoxide dismutase, catalase, peroxidase, and glutathione reductase) increased with 3% to 4% PEG but declined beyond that. Of the eight genotypes, 110 R had the highest average explant survival, followed by St. George, Dogridge, and Pusa Swarnika. The genotype, 110 R demonstrated the highest survival rates and biochemical responses. Aquaporin gene (*PIP2;1*, *PIP2;2*, *TIP1;1*, and *TIP2;1)* expression analyses indicated significant regulation patterns across drought-tolerant (110 R, Dogridge, and St. George) and susceptible genotypes (*V. parviflora,* Perlette, and Pusa Navrang). The study concluded that 110 R, Dogridge, St. George, and Pusa Swarnika exhibited better *in vitro* drought tolerance as compare to Pusa Navrang, Perlette, *V. parviflora*, and Male Hybrid, providing a basis for their future field evaluations for drought tolerance.

Studies on inheritance of peel and pulp color in mango (*Mangifera indica* L.)

Color is a key quality attribute in fruit breeding. The fruit peel color plays crucial rolein international trade as it influence consumer perception. The present investigation aimed at studying the peel and pulp color among the progenies of Amrapali × Vanraj and Alphonso × Vanraj through morphological, genetical, biochemical and molecular aspects. The chi-square analysis revealed both epistatic and non epistatic governance of peel color. The pulp color inherited in 1:1 ratio. Biochemical profiling identified various compounds responsible for wide hues of peel and pulp. Red color of mango peel is primarily due to anthocyanins, with delphinidin being the prominent, followed by cyanidin, pelargonidin, and traces of malvidin. Additionally, five carotenoid compounds—β-carotene, α-carotene, neoxanthin, violaxanthin, and lutein — were identified in peel, contributing to its yellow color. In pulp, color was predominantlyattributed to β-carotene and lutein. The correlation between leaf and peel color serves as morphological marker for early selection of colored genotypes and correlation between colorimetric scales of peel and pigments serves as non destructive way for analyzing pigment concentration. Molecular characterization through gene expression using qRTPCR revealed the role of *Phenylalanine Ammonia Lyase* and *Flavonoid 3-O-Glucosyl Transferase* in red color formation. *Lycopene β-cyclase* and *Lycopene ε-Cyclase* were found out as the dominant genes responsible for carotenoid biosynthesis in peel while *Lycopene* β-*Cyclase* and *Carotene ε-Hydroxylase* are governing pulp carotenoid levels. Further QTL sequencing led to the identification of four QTLs for red peel color and a QTL for orange pulp color. Furthermore, candidate genes residing in respective QTLs were identified and validated. This study unveils the complex coloring pattern in peel and pulp of mango further facilitates, future mango breeding program.

Theme 3: *In vitro* Regeneration and Transformation

In vitro multiplication and conservation of endemic fruit-tree species *Garcinia gummi-gutta*

G. gummi-gutta commonly known as Malabar tamarind, is a tropical fruit of Clusiaceae family. Native to South India and Southeast Asia. The *in-situ* conservation of *G. gummi-gutta* is limited to the protected areas of the Western Ghats and the *ex-situ* conservation of this species through field gene banks (FGB) is undertaken only in a few sites. However, major threats under *in situ* conservation are deforestation, habitat destruction, and land conversion to agriculture. In the present study, *in vitro* shoot multiplication using 27 different media combinations including various concentration of 6-benzylaminopurine (BAP) and α-naphthaleneacetic acid (NAA) were tested in *G. gummi-gutta*. Of the media examined, *in vitro*-derived apical shoots cultured in MS media supplemented with 8.88 µM BAP and 2.68 µM NAA resulted in a maximum shoots per explant (12.50). Maximum shoot length (3.37 cm) was observed in media containing 0.53 µM NAA (T7). The treatments T13 (MS + 35.52 µM BAP + 0.53 µM NAA) and T20 (MS + 35.52 µM BAP + 2.68 µM NAA) recorded the shortest time to shoot initiation (37 days after subculture), demonstrating more rapid response compared to other media combinations. The survival rate of 2 mm apical shoots during dehydration with PVS2 using droplet vitrification (DV) declined with longer exposure times, from 81 ± 0.29% (control) to 35.56 ± 3.52% after 65 min. The highest survival was at 25 min, comparable to 15 and 35 min. Survival decreased significantly beyond 35 min PVS2 exposure, with only 57.78 ± 2.41% at 45 min PVS2 exposure. The highest post-thaw regeneration was achieved when explants were exposed to PVS2 for 35 min indicating the ideal PVS2 exposure duration for cryopreservation through droplet vitrification. Long-term conservation of *Garcinia gummi-gutta* can be achieved using Droplet Vitrification of 2 mm *in vitro*-derived apical shoots.

In vitro multiplication and rooting of an endangered endemic wild species of banana (*Musa indandamanensis* L. J. Singh)

The genus *Musa* L. includes three genera *viz*., *Ensete* (8 spp.), *Musa* (70 spp.), and *Musella* (1 sp.). *M. indandamanensis* L.J. Singh is a recently discovered wild species from the Andaman and Nicobar Islands, and is endemic to the region. According to The IUCN Red List of Threatened Species 2022 it is considered 'Endangered (EN)'. The present study was to carried out to develop an *in vitro* multiplication, and rooting protocol to safeguard this endangered endemic wild species of banana for *ex-situ* conservation. Various sources of cytokinins, including 6-Benzylaminopurine (BAP), Thidiazuron (TDZ), and Metatopolin (mT), were tested either alone or in combination with 1-Naphthalene Acetic acid (NAA) and Indole-3-acetic acid (IAA) at different concentrations. The highest number of shoots per explant (5.71±0.21) was recorded on Murashige and Skoog (MS) media containing 6 mg/L BAP + 1 mg/L IAA over other media combinations. Maximum shoot length (5.69±0.24 cm) was recorded on MS media containing no hormones over other media combinations. Minimum number of days for shoot induction (5.33±0.33 days) were recorded on MS media containing 6 mg/L BAP + 1 mg/L IAA and 8 mg/L BAP + 1mg/L IAA for earliest shoot initiation. Maximum number of roots per explant (6.25±0.62) were observed on half-strength MS medium supplemented with 1 mg/L NAA. Maximum root length (3.72 ± 0.14 cm) was achieved on full-strength MS medium with 1.5 mg/L NAA. The shortest time for root initiation (5.50±0.28 days) was recorded on half-strength MS medium containing 1.5 mg/L NAA, in comparison to other media combinations. Additionally, the genetic fidelity of the *in vitro* multiplied plantlets was assessed using 20 SSR markers, demonstrated no differences between mother plants and the *in vitro* multiplied plantlets, confirming their genetic stability during the tissue culture process.

Theme 4: Biotic and Abiotic stress Management and Crop Production

Effect of POLY4 (Polyhalite) on growth, yield and quality of Kinnow mandarin

The present study aimed to analyze the effects of POLY4 (Polyhalite), a multi-nutrient potassium fertilizer on the growth, yield, and quality of Kinnow mandarin. Seven treatments of different doses of fertilizers were applied on 12-year-old plants *viz*., Recommended dose of NP (T_1), NPK as per present fertilizer practice (T_2), NPK and application of calcium and magnesium sulphate (T_3), T_1 + 80% K: 35% Polyhalite + 65% MOP (T_4), T_1 +80% K :50% Polyhalite + 50% MOP (T_5), T_1 +100% K :35% Polyhalite + 65% MOP (T_6), T_1 +100% K :50% Polyhalite + 50% MOP (T_7). The canopy volume showed a positive response with T_7 (34.69 m^3). The treatment T_5 produced the highest fruit yield (50.20 kg / tree and 31.38 tons/ ha). Treatment T_7caused the highest TSS, total sugars and reducing sugars. Treatment T_5 exhibited the highest TSS to acidity ratio, while T_4 demonstrated superior antioxidant activity. Treatments incorporating polyhalite also contributed to improved phenolic content, flavonoid content and fruit firmness. Treatment T_7 exhibited the highest levels of P, Ca, and S, while T_4 had the highest N content in soil. Leaf nutrient status also improved, with treatment T_4 (N and Ca) before harvest, and T_5showed the highest F content. Soil microbial attributes further emphasized the benefits of POLY4. The economic analysis revealed that the treatment T_5 provided the highest net monetary returns (Rs. 274,328.43/-) and the best benefit-cost ratio (1.66). Treatment T_5 emerged as the most cost-effective and productive option for Kinnow mandarin cultivation.

Drought tolerance studies in *Citrus* species

Screening citrus rootstock genotypes for drought tolerance revealed significant differences in the tested traits. X639 exhibited superior drought tolerance with enhanced growth metrics and lowest leaf wilting scores (1.00). RLC-4 and RLC-1 demonstrated positive responses to rewatering, whereas Cleopatra mandarin exhibited poor performance. Stomatal traits highlighted X639 resilience, as evidenced by minimal alterations in the stomatal and potential conductance indices and lower percentage of closed stomata. Physiologically, X639 maintained elevated leaf relative water content, membrane stability, chlorophyll levels, and gas exchange parameters overother rootstocks. Plant bioregulator priming enhanced drought resilience in contrasting citrus genotypes (Cleopatra mandarin susceptible and X639 tolerant). In Cleopatra mandarin, foliar priming with proline, spermidine, and salicylic acid significantly mitigated leaf wilting (<1.66) and improved RWC (>70.00) under stress. Conversely, X639 exhibited stable physiological attributes with minimal variation owing to priming. Foliar application of proline and spermidine mitigated leaf wilting and abscission in Cleopatra mandarin comparable to normal irrigation, and augmented root and shoot biomass under drought stress in both genotypes. Priming treatment mitigated drought-induced declines in leaf K and Ca levels, reduced Na, and improved Mg and Ca in leaves and roots of Cleopatra mandarin. X639 exhibited superior nutrient allocation under drought stress compared with Cleopatra mandarin, particularly in terms of root potassium and calcium. Differential gene expression (DGE) analysis under drought stress revealed significant responses in X639 and Cleopatra mandarin. X639 exhibited 10,538 differentially expressed genes, with 9,938 up-regulated genes affecting 142 pathways. Cleopatra mandarin showed 4,984 differentially expressed genes, of which 978 were upregulated, influencing 137 pathways. Biological processes were less expressed in X639, but more prominent in Cleopatra mandarin.

Rootstock-mediated changes in mango (*Mangifera indica* L.) cultivars

Three mango cultivars-Pusa Surya, Amrapali, and Pusa Arunima, grown onto five polyembryonic rootstocks *viz*., Olour, Kurukkan, Pusa Aam Moolvrint-1 (PAM-1), Pusa Aam Moolvrint-2 (PAM-2), and K3 were evaluated. Of the evaluated rootstocks, PAM-1 and PAM-2, exhibited the least plant vigour, a highly desirable trait for high-density orchards. The maximum yield (80.46 kg/tree), number of fruits (484.33), and *E* (15.04 µmol H_2O $m^{-2}s^{-1}$) were found in the Amrapali/Kurukkan combination. The maximum fruiting density (3.72 m^3 cv), and yield efficiency (0.525 cm^2 TCSA) were found in the Amrapali/PAM-1 combination. Pusa Surya exhibited higher fruit weight, pulp content, and pulp/stone ratio in combination with PAM-2 rootstock, while combinations with Kurukkan and Olour resulted in smaller fruits of the same cultivar. PAM-2 rootstock consistently promoted superior pulp/stone ratios in all cultivars. Olour rootstock enhanced TSS and reduced acidity. Amrapali demonstrated higher TSS, total phenolics, flavonoids, and antioxidant activity, while Pusa Surya exhibited higher titratable acidity (TA). Rootstocks also influenced the nutritional and health-promoting properties of mango. Amrapali grafted onto Olour recorded the highest levels of ascorbic acid, phenolics, flavonoids, and antioxidant activity. Amrapali/PAM-2 and Amrapali/Olour combination exhibited high levels of phenolic compounds like rutin and catechin, contributing to enhanced antioxidant activity and improved fruit flavour. Mineral composition varied with rootstock-scion interactions, with Amrapali/K3 and Olour rootstocks combination had the higher high phosphorus, potassium, and calcium content. Pusa Arunima/ PAM-2 and Pusa Arunima/Kurukkan combinations exhibited the higher aroma volatiles such as isolongifolol and geraniol. Sensory evaluations showed that dwarf Amrapali/Olour and Pusa Arunima/ Kurukkan scored highest in overall acceptability.

Physiology of drought tolerance in citrus rootstock genotypes

The study was divided into two experiments: the first one involved the screening of nine citrus hybrid rootstock genotypes under 28 days of drought stress followed by 2 weeks of rewatering, while the second part focused on understanding the physiological responses of rootstock-scion interactions under induced drought stress. Of the genotypes, X639 showed the highest survival (41.75 days), followed by CRH 21-13, while SCSH 17-12 had the shortest survival (20.75 days). Canopy temperature rose in SCSH 17-12 (42.95°C), while X639 and US 812 maintained cooler canopy (<40°C). X639 also maintained minimal stomatal area reduction (1.38%), with significant increases in phenolic content (406.71%), proline (249.13%), and antioxidant enzyme activities (SOD, CAT, POD). High-throughput phenotyping (HTP) revealed that X639 and CRH 21-13 retained better leaf greenness and lower mean grey values under drought stress. In the second experiment, the rootstock-scion interaction was studied under drought stress, showing Redblush/X639 combination had the longest survival time (38.6 days), while Redblush/SCSH 17-12 had the shortest (18.8 days). Root length and root volume were highest in X639. The greatest reductions in LRWC (51.52%), chlorophyll (61.30%), carotenoids (32.65%), and gas exchange parameters, alongside the highest canopy temperature (39.40°C), were observed in Kagzi Kalan lemon/SCSH 17-12, while Redblush/X639 exhibited the least reductions. Proline and phenolic content increased significantly (84.40% and 189.81%, respectively), with X639 combinations showing the highest values. Antioxidant enzyme activities, including CAT and SOD, increased significantly in Redblush/X639. Nutrient analysis showed maximum reductions in potassium and calcium, but increases in sodium content (46.48%) in CRH 21-9. This study highlighted the rootstock CRH 21-13 as a promising rootstock for water-limited conditions, offering an alternative to X639, while SCSH 17-12 showed poor resilience, like Cleopatra mandarin.

Scion-rootstock interaction and osmolyte induced changes under water deficit stress in citrus

The responses of seedling *versus* self-grafted plants of *Jatti Khatti* (drought sensitive) and X639 (drought tolerant) citrus rootstock genotypes was assessed, grown on soilless media under 80%, 40% and 20% moisture levels in field conditions. Among X639 plant types, self-rooted plants exhibited least significant reduction in plant growth, and increased the root growth under 20% moisture levels. In contrast, in *Jatti Khatti,* self-rooted plants exhibited higher increments in root and shoot growth, became more pronounced in self-grafts under 20% moisture level over control (80 % moisture). X639 rootstock exhibited minimal diminish in RWC, MSI, Ch 'b' and starch, along with the moderate upregulation in stress indicators, as moisture deficit intensified compered to *Jatti Khatti*. In *Jatti Khatti*, self-rooted plants exhibited the greatest reductions in RWC and starch content, coupled with the highest upregulation of stress indicators and moderate upregulation of antioxidants. These findings indicate that self-grafted X639 demonstrated superior drought tolerance.Responses of self and reciprocal grafted combinations of *Jatti Khatti* and X639 rootstocks revealed that X639 adoptedgrowth-oriented strategies under WD, supported by enhanced root growth, antioxidants, and minimal oxidative damage, whereas *Jatti Khatti* focused on survival strategies, including early wilting. Reciprocal grafting of *Jatti Khatti* on X639 mitigated stress impacts, highlighting rootstock's influence scion performance. In another trial, conducted on sweet orange cv. Pusa Sharad grafted onto X639 rootstock to see the effects of chemical under different water regimes, the soil application of glycine betaine (GB) significantly improved the plant height, LN, LA, RDW, and ARD. Higher concentration of GB (2mM) alone resulted in significant improvements in plant growth compared to control (water application). Soil application demonstrated better mitigation of water stress than foliar application. This indicates the potential of GB, especially soil-applied, in enhancing resilience and productivity of citrus under water limited conditions.

Exploitation of *Psidium cattleianum* wild species for biotic stress tolerance in guava

Guava (*Psidium guajava* L.) is constrained by biotic stresses like root-knot nematodes (*Meloidogyne incognita*, *M. enterolobii*) and wilt (*Fusarium oxysporum* f.sp. *psidii*). To address these challenges, investigations were conducted using *P. cattleianum* in two approaches: screening hybrid progenies with *P. cattleianum* as the male parent and as a rootstock for guava. Results indicated that *P. cattleianum* var. *cattleianum* and *P. cattleianum* var. *lucidum* were immune to root-knot nematodes and wilt. Of the 300 hybrid progenies (Arka Poorna × *P. cattleianum* var. *cattleianum*), 17 were resistant to *M. incognita*, but all 200 screened progenies were susceptible to *M. enterolobii*. Additionally, 14 out of 190 progenies were resistant to wilt. Notably, four out of 40 hybrids (Arka Poorna × *P. cattleianum* and H12-5 × *P. cattleianum*) had combined resistance to *M. enterolobii* and wilt. Histopathological studies confirmed nematodes in the roots of susceptible plants, showing damaged cortex tissues, nematode eggs, and damaged vascular bundles. In plants inoculated with the wilt pathogen, blockage vascular vessels, disintegrated cortex and hyphal growth were observed. The roots of *P. cattleianum* var. *cattleianum* remained healthy. Using *P. cattleianum* as rootstock for Arka Kiran, graft success ranged from 13.33–46.67% (softwood) and 18.33–35.0% (approach grafting) at 120 days. Anatomical studies revealed a gap, necrotic layers, and improper vascular connection between rootstock and scion in Arka Kiran on *P. cattleianum*, indicating delayed graft incompatibility. *In vitro* grafts of Arka Kiran on *P. cattleianum* had a 33.67% survival rate at 90 days. *In vitro* shoot multiplication protocol for Arka Kiran was optimized, achieving optimal growth with ½ MS + 2 mg/L BAP. The best shoot multiplication from *in vitro* germinated seedlings of Arka Kiran, Arka Poorna, and *P. cattleianum* was achieved with ½ MS + 3 mg/L BAP.

List of the students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Raushan Vatshya (21870)	M. Sc.	Validation of new hyper-variable mango SSRs and diversity analysis of heirloom mango varieties.	Dr. Manish Srivastava	ICAR-IARI, New Delhi
2.	Kritidipta Pramanik (21872)	M. Sc.	Development and validation of genome-wide SSR Markers in guava (*Psidium guajava* L.)	Dr. A. K. Goswami	ICAR-IARI, New Delhi

3.	Swati Yadav (21873)	M. Sc.	*In vitro* multiplication and conservation of endemic fruit-tree species *Garcinia gummi-gutta*	Dr. Vartika Srivastava	ICAR-IARI, New Delhi
4.	Aanamika Rai (21874)	M. Sc.	Morpho-chemical and molecular diversity studies in pomegranate genotypes	Dr. O. P. Awasthi	ICAR-IARI, New Delhi
5.	Sahil (21875)	M. Sc.	Insights into the nut and food qualities of selected walnut (*Juglans regia* L.) genotypes	Prof. R.M. Sharma	ICAR-IARI, New Delhi
6.	Renu Chauhan (21876)	M. Sc.	*In vitro* multiplication and rooting of an endangered endemic wild species of banana (*Musa indandamanensis* L. J. Singh)	Dr. Vartika Srivastava	ICAR-IARI, New Delhi
7.	Dhrumeshkumar Chavda (21871)	M. Sc.	Characterization and quality assessment of interspecific citrus hybrids	Dr. Nimisha Sharma	ICAR-IARI, New Delhi
8.	Shiva Kumar N (21916)	M. Sc.	Effect of POLY 4 (Polyhalite) on growth, yield and quality of Kinnow mandarin	Dr. Kanhaiya Singh	ICAR-IARI, New Delhi
9	Shivam Kumar Rajpoot (60133)	M. Sc.	In-situ characterization and diversity analysis of custard apple (*Annona squamosa* L.) germplasm of Chotanagpur plateau region	Dr. Mahesh Kumar Dhakar	#ICAR-IARI, Jharkhand
10	Narendra Singh (11261)	Ph. D.	Evaluation of interspecific citrus scion hybrids for fruit quality and health promoting compounds	Prof. R.M. Sharma	ICAR-IARI, New Delhi
11	Amrut Sanjay Morade (11510)	Ph. D.	Drought tolerance studies in *Citrus* species	Prof. R.M. Sharma	ICAR-IARI, New Delhi
12.	Sreekanth H S (11518)	Ph. D.	Morphological, biochemical and molecular characterization of maternal half-sib progenies of Amrapali for identification of superior genotypes	Dr. Manish Srivastava	ICAR-IARI, New Delhi
13.	Mukesh Shivran (12060)	Ph. D.	Rootstock-mediated changes in mango (*Mangifera indica* L.) cultivars	Dr. Nimisha Sharma	ICAR-IARI, New Delhi
14	Amol Kailash Jadhav (11266)	Ph. D.	Genetical studies for seedlessness and related traits in grape (*Vitis vinifera* L.) parents and its hybrids raised using *in vivo* and *in vitro* techniques	Dr .S. K. Singh	ICAR-IARI, New Delhi
15	Anagha P K (11782)	Ph. D.	Physiology of drought tolerance in citrus rootstock genotypes	Prof. R.M. Sharma	ICAR-IARI, New Delhi
16	Mude Ramya Sree (11785)	Ph. D.	Characterization of powdery mildew resistance in grapevine genotypes and identification of markers for resistance	Dr. S. K. Singh	ICAR-IARI, New Delhi
17	Lal Chand (11787)	Ph. D.	Scion-rootstock interaction and osmolyte induced changes under water deficit stress in citrus	Dr. A.K. Dubey	ICAR-IARI, New Delhi
18	Bindu Praveena Ravipati (12214)	Ph. D.	*In vitro* screening of *Vitis* spp. for low moisture stress tolerance	Dr. Jai Prakash	ICAR-IARI, New Delhi

19	Sinchana Jain (11788)	Ph. D.	Studies on inheritance of peel and pulp colorin mango (*Mangifera indica* L.)	Dr. Murugan Sankaran	**ICAR-IIHR, Bengaluru
20	Ajay Kumar (11932)	Ph. D.	Exploitation of *Psidium cattleianum* wild species for biotic stress tolerance in guava	Dr. Vasugi Chinnaiyan	**ICAR-IIHR, Bengaluru

#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 post harvest management; development of appropriate storage protocols; valorization through processing and value chain of commercially important crops; advisory consultancy to both public and private sectors along with development of programmes for transfer of technology. The post graduate research findings have been grouped under various themes.

Theme 1: Post Harvest Management of Fresh Horticultural Produce

Ornamental plant extracts for management of postharvest diseases and quality of guava fruits

This study delves into the critical role of drying methods and extraction solvents in preserving the bioactive compounds of ornamental plant materials (rose and marigold leaves and petals) and their role in management of postharvest diseases and quality of guava fruits. Six drying methods, including microwave (MW) drying, shade drying (SD), and cabinet drying (CD) at various temperatures (40°C to 70°C) targeting rose leaves (RL), rose petals (RP), marigold leaves (ML), and marigold petals (MP) were tested. MW drying demonstrated the highest drying rates and methanol was most effective in extracting bioactive compounds, yielding the highest phenolic and flavonoid contents across RL, ML, and MP, while aqueous extracts performed best for RP. UPLC-QToF-ESI-MS/MS revealed the presence of quercetin, quercetin 3-O-rutinoside, and kaempferol acetyl disaccharide in rose leaves and petals while marigold extracts primarily comprised kaempferol, epicatechin gallate, and feruloyl-caffeoylquinic acid as the main constituents. Further, in-vitro studies established a minimum inhibitory phenolic concentration of 150 mg GAE/ 100 mL across all extracts, effectively controlling the selected pathogens. RL and MP extracts displayed enhanced inhibitory effects, showcasing superior potency in fungal growth inhibition. In-vivo antifungal efficacy assessments revealed that MP extract at 200 mg GAE/100mL phenolic concentration showed the highest efficacy, followed by RL extract, against selected fungi, highlighting the potential of natural plant extracts in controlling postharvest infections. Further, active edible coating formulations were made by incorporating ethanolic extracts of RL and MP at the concentration of 200mg GAE/100mL total phenolic content into the coating solutions of carboxy methyl cellulose (CMC) and gum arabic (GA). Maximum extension (18 days and 4 days) in shelf life of guava was observed for fruits coated with CMC+RL, CMC+MP and GA+RL under cold (10±1°C) and ambient (24±2°C) storage, respectively. Although physiological loss in weight increased with storage duration, but CMC+RL coated fruits exhibited least weight loss (6.51 %) compared to other coatings and control. In conclusion, the study underscores the effectiveness of MW and cabinet drying at 40°C in preserving the functional properties of ornamental plant extracts.

GABA content in tomatoes: Impact of genotype, maturity stage and processing regime

Gamma-amino butyric acid, widely known as GABA, serves as a major neurotransmitter inhibitor in the central nervous system of humans and animals. Tomato being its richest source of GABA among vegetables was focused to identify its best maturity stage for GABA accumulation as well as its best way of utilization through degradation studies under different processing and storage regimes. Seven tomato hybrids were evaluated for their GABA content at six different maturity stages: immature green, green, breaker, turning, pink, and ripe. In all the genotypes, GABA content was maximum at the green stage and declined as the fruit ripened. When processed into puree (approximately 14°B) using hot and cold break methods, the GABA content diminished over time and followed first order kinetics. Concentration of pulp during cold and hot break resulted in GABA degradation at the rate of 0.334 mg/gmin-1 and 0.359 mg/gmin-1, respectively. Different exposure conditions (natural light, dark, diffused light, and refrigeration) affected GABA content in tomato slices, in which diffused light exposure resulted in the least while natural light resulted in maximum degradation of GABA. The obtained results are helpful in the identification of best way of processing and consumption of tomato as a rich source of GABA.

Standardization of storage temperature and pre-treatments for extension of storage life of muskmelon

Climacteric type muskmelons are highly perishable and have very short storage life varies from 2 to 3 days at ambient temperature. Being a tropical crop, fruits are susceptible to chilling injury if stored at very low temperature conditions. Hence the present research work was conducted to standardize the optimum low temperature and to study the effect of different edible coatings and anti-ethylene compounds on various physiological, physical and biochemical parameters of muskmelon cv. Arka Siri at three different storage temperatures (7°C, 10°C and ambient temperature). The study revealed that the optimum low temperature for storage of muskmelon cv. Arka Siri was 10^0C where the fruits can be stored up to 14 days by maintaining highest physico-chemical and organoleptic properties. Among different edible coatings and storage temperatures tried, muskmelon fruits coated with shellac based formulation had storage life up to 21 days when stored at 7°C without any chilling injury symptoms. Among different ethylene inhibitors (synthesis and action inhibitors) tested, the pre storage treatment of muskmelon fruits exposed to ethylene action inhibitor, 1-MCP (500ppb) extended the storage life up to 21 days at 10^0C and 7 days at ambient temperature (27.0-34.3^{o}C and 47-50% RH).

Theme 2: Processing of Horticultural Crops

Studies on production of Kamalam/dragon fruit (*Hylocereus polyrhizus*) powder using tray drier and its value-added products

Dragon fruit (*Hylocereus sp.*), known as Kamalam in India, is an exotic fruit with growing domestic cultivation. Being highly perishable commodity, its storage life cannot be extended beyond 2–3 weeks using available preservation technologies. The present study aimed to standardize a cost-effective tray drying process for producing free-flowing dragon fruit pulp powder using additives, to evaluate its quality and storage potential and to develop value-added products. Dragon fruit pulp was blended with three different types of hydrocolloids-maltodextrins, corn starch and carboxymethyl cellulose (CMC) in various combinations and levels ranging from 2% to 64% of pulp weight. These mixtures were spread uniformly on SS 304 grade trays and dried in a tray dryer at 60±1°C. After cooling to ambient temperature, dried sheets were removed and powdered using a pulverizer. The resulting powder, when analyzed for various physico-chemical quality attributes showed that increasing additive levels reduced moisture, water activity, sugars and antioxidant properties while improving lightness and shelf stability. The free-flowing dragon fruit powder produced with 4% of additive combination-3 exhibited superior nutritional quality compared to other levels. Packaging and storage trials were conducted using powder made with 4% and 8% levels of additive combination-3. Results revealed that powder packed in aluminum laminate pouches stored at 13±1°C retained higher nutritional and microbiological quality over six months, with higher betalain content (323.15 mg BCE/100g), phenols (140.66 mg GAE/100g) and antioxidants (226.57 mg AEAC/100g). Value-added products like cookies, milkshake, and tea infusion made.

Utilization of tomato pomace powder for development of puffed extruded snack

Tomato pomace, a by-product of tomato processing, comprises mainly peel and seeds and contains significant amounts of fiber, protein, fat, and minerals. Being highly nutritious, tomato pomace is not utilized and is regarded as waste, and an environmental concern. Understanding the gaps, research work was conducted which included optimizing a foam mat drying protocol for developing tomato pomace powder and utilization of this powder as a functional additive for extruded snacks. Three factor three level Box Behnken Design (BBD) was used for the optimization of puffed extruded product made with tomato pomace and corn flour. The formulation comprising of 14.39% tomato pomace concentration at a screw speed of 213 rpm and feed moisture of 13.44% was optimized and validated with the values predicted by the model (0.716, desirability). The proximate composition of extruded snacks showed that the developed snack is a fair source of dietary fiber as well as lycopene content contributing to the antioxidant properties of puffed snack.

Ohmic heating for quality retention of citrus and tomato processed products

The study was carried out for preservation of citrus and tomato products through ohmic heating. To complete this research work two objectives were envisaged. First objective dealt with standardization of ohmic heating variables for processed sweet orange and tomato products. Four citrus (unsweetened juice, RTS, nectar and squash) and four tomato (juice, drink, pulp and concentrate) products were subjected to both ohmic and conventional heating upto 90° C temperature. Time and energy consumption and microbial reduction, were analysed for total eight products under this objective. Results were evaluated on the basis of different soluble solid content of products and the applied five voltages (120, 150, 180, 210 and 240 V). It was observed that as voltage increased, there was a corresponding reduction in time taken to achieve the desired temperature. Ascorbic acid, carotenoid content, antioxidant activity, phenol and lycopene content were retained maximum at 210 and 240 V as compared to other voltages applied during ohmic heating as well as conventional heating. Lowest colour change in processed products was observed at high ohmic voltage treatment. Similarly, PME activity was lowest during high electric field applied. Sensory attributes were superior for ohmically treated samples than conventional treated samples.

Innovative naturally coloured poshakprash: formulation and characterization

Poshakprash is a novel attempt of formulation of nutritionally dense product that possess health benefits from bioactives of horticultural produce and convenience and texture of a fruit bar. The formulation process was meticulously optimized through a 2x3 factorial experiment employing a Completely Randomized Design (CRD). Six treatments were formulated, varying the beetroot-aonla blend ratios and spice mix, while other critical ingredients were kept constant. The optimization was carried out based on physico-chemical, functional, and textural properties The optimized product was compared with two controls; C1 containing only aonla, while C2 containing a blend of aonla and beetroot. The comparative analysis revealed that the optimized poshakprash significantly ($p<0.05$) outperformed C2 in terms of total phenolic content, total flavonoid content, antioxidant activity, and carotenoid content. Additionally, it exhibited superior proximate composition and sensory attributes, including enhanced flavor, color, appearance, and overall sensory score. The product also demonstrated excellent thermal stability and hydrodynamic friction properties studied through thermogravimetric analysis and tribology, respectively. In-vitro simulation studies further confirmed its bio-functional efficacy, with intermediate cell viability observed across various concentrations, except at 10 µg/ml. All the samples possessed insulinotropic effect.

Pectin extraction from carrot pomace: Application in emulsion with bael (*Aegle marmelos* Correa) fruit powder

Carrot pomace is a by-product that is usually discarded as industrial garbage or fed to animals. However, it contains a wealth of healthy components, including carotenoids and pectin. Pectin was recovered from carrot pomace utilizing a surfactant in conjunction with ultrasound. Using 33 factorial experiment of completely randomized design and 3-way ANOVA, pectin was extracted from carrot pomace with variables being surfactant concentration, solid solvent ratio, and time; and making 27 treatment combinations. The optimal conditions for extraction were obtained with treatment 15 and 17 based on yield, GalA, content and degree of esterification. The pectin obtained from carrot pomace was compared with that obtained from whole carrot. Because of their less than 50% esterification, carrot pomace pectin (CPP) and whole carrot pectin (WCP) were classified as low molecular weight pectins (LMPs). Carrot pectin has shown significant levels of total flavonoid content (TFC) and total phenolic content (TPC), suggesting that it may be a valuable source of health-promoting bioactive chemicals. FTIR and TGA were used to characterize the pectin. Carrot pomace pectin showed better emulsifying activity (54.74 ± 0.65 %) than whole carrot pectin. The extracted carrot pectin has been effectively utilized in formulating emulsion in conjunction with bael powder. The findings indicate that carrot pomace is a valuable source for pectin with improved emulsifying and rheological properties, beneficial for food formulations.

Valorization of pummelo (*Citrus grandis*) peel for nanocellulose extraction

Nanocellulose is an exceptional biomaterial whose industrial applications are widely distributed. Pummelo peel is considered as waste produced in tons together by juice processing industries in every year. Also, pummelo peel contains many bioactive compounds and is one of the good natural reservoirs of cellulose source. Cellulose was extracted by subjecting peel powder to alkaline ($Mg(OH)_2$ - 6, 8, 10%) treatment, followed by acid hydrolysis using three different organic acids (formic, citric and malic acids at 70, 80, 90%). Among three tested organic acids, citric acid was emerged as best hydrolyzing agent with a yield of 27.24±0.05%, extracted cellulose was underwent ultrasonication for nanocellulose production. In this study pummelo peel was valorized for nanocellulose extraction by chlorine free/ green method was achieved using ultrasound assisted alkaline organic acid hydrolysis process. The optimum conditions were alkali 10% $Mg(OH)_2$, 90% citric acid as hydrolyzing agent and ultrasonication power of 800W for 30 minutes, resulted maximum cellulose and nanocellulose yields were 27.24% and 22.76%. The extracted nanocellulose was characterized to assess its functional properties, morphology, thermal behavior, crystal dimensions and surface charge by using FTIR, SEM, TGA, Color and particle and zeta potential analysis. FTIR confirmed the absence of non-cellulosic material and presence of O-H stretching functional group. PSA results depicted the average particle size ranging from 30 nanometers in diameter and 2-6 nm in length and negative zeta potential (-17.7mV), results are also consistent with SEM images. This study offers valuable insights to production of nanocellulose from pummelo peel which was earlier considered as waste.

Effect of vacuum frying on bioactive compounds retention and shelf-life extension of red cabbage and broccoli

Red cabbage and broccoli, cool-season cruciferous vegetables, are rich in vitamins, minerals, pigments (anthocyanins in red cabbage and chlorophyll in broccoli), glucosinolates, antioxidants, phenolics, carotenoids, and other bioactive compounds. To make these nutrient-dense vegetables available year-round in a convenient form while retaining their nutritional composition, vacuum frying was employed to produce healthy veggie crisps. Microwave blanching effectively inactivated peroxidase and minimized nutrient and color loss compared to hot water blanching. Freezing pretreatment enhanced crispiness and reduced oil uptake, while 70°C was identified as the optimal vacuum frying temperature for pigment retention. Additives like maltodextrin (0, 25, and 40%) and calcium lactate (0, 1, and 2%) improved structural integrity, nutrient retention, and sensory quality. Calcium lactate significantly enhanced sensory ratings. Fat content, however, remained high, necessitating hydrocolloid coatings. Coatings of 1% guar gum on red cabbage and 0.5% CMC on broccoli resulted in the lowest fat uptake. These coatings also improved color and retention of bioactive compounds, with bright red appearance in red cabbage crisps and vivid green in broccoli crisps. The crisps retained high levels of ascorbic acid, anthocyanins, chlorophyll, and glucosinolates. Vacuum frying preserved pigments, antioxidants, phenolics, and glucosinolates better than stir frying and atmospheric frying. LC/MS/MS and HPLC analyses identified key bioactives like cyanidin-3-(sinapoyl)-diglucoside-5-glucoside, quercetin, glucoraphanin, and β-carotene in the crisps. Vacuum frying achieved superior retention of bioactives, with notable retention percentages of anthocyanins (48.05%) and chlorophyll (4.67%) and slight enhancement of phylloquinone. Storage studies in vacuum-sealed laminates demonstrated slower degradation of quality attributes over 120 days compared to untreated controls, with free fatty acids remaining below 1%. Vacuum frying proved effective in producing nutrient-rich, sensory-appealing veggie crisps, ensuring the year-round availability of red cabbage and broccoli in an attractive and healthy form.

Theme 3: Processing of Arable Crops

Development and characterization of finger millet based functional food through extrusion processing

In recent years, there has been a growing awareness of the importance of incorporating functional foods into our diets to promote health and well-being. A successful formulation of a low glycemic ready-to-eat (RTE) extruded snack using finger millet, green banana flour and defatted soya flour was attempted. To develop an optimized blend formulation, a series of experiments was designed using response surface methodology. The extrusion process of the blend was conducted under specific conditions viz. barrel temperature 120°C, screw speed 300 rpm, feed rate 24 rpm, die diameter 3 mm, and feed moisture content 15% (wet basis). The ER, BD, hardness, crispness, WAI, WSI, ΔE, Calorific value and estimated glycemic Index of extruded products were found to vary in the range of 2.87-3.57, 0.114-0.148 g cm^{-3}, 30.16-57.18 N, 18.5 to 28.75, 2.31-3.79 g g^{-1}, 19.24-42.14 %, 5.77– 10.79, 287-349 calories and 56.82 to 67.96, respectively. Composite blend comprising of different ingredients in the ratio of 85:10:5 (FM: GB: DS) was found to be an optimum with a desirability function of 0.82. Product developed with this blend composition exhibited encouraging values of the quality indicators viz., ER = 3.57, BD = 0.115 g cm^{-3}, hardness = 29.98 N, Crispness =27.85, WAI = 3.70 g $g^{-1}$and WSI = 40.06%, Total colour difference (ΔE) =7.51, Calorific value=328 kcal and eGI = 57.5. Following optimum composite blend formulation, Central composite rotatable design (CCRD) was used to determine the effect of varying levels of process variables on different quality indicators of the extruded product (product moisture (PM), expansion ratio (ER), bulk density (BD), hardness, crispness (Cr), WAI and WSI) & Browning Index and fine tune them. The range of variables considered for the experiments were as barrel temperature (100-140°C), screw speed (200-400 rpm) and feed moisture (15-21% wb). The values of different attributes were found to be in the range- expansion ratio 2.85-3.65; bulk density 0.121-0.193 g cm^{-3}; hardness 25.53-35.52 N; crispness 20-29 fractures; WAI 3.79-4.43 g g^{-1}, WSI 22.13-28.11% and browning index 31.77-39.79, respectively.

List of contributing students and Chairperson of their advisory committee

S.No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Akshat Jain (21342)	M.Sc.	Ohmic heating for quality retention of citrus and tomato processed products	Dr. Shruti Sethi	ICAR-IARI, New Delhi
2.	Shakshi Kumari (21878)	M.Sc.	Innovative naturally colored poshakprash: formulation and characterization	Dr. Neelam Upadhyay	ICAR-IARI, New Delhi
3.	Avinash Kumar (21879)	M.Sc.	Utilization of tomato pomace powder for development of puffed extruded snack	Dr. Alka Joshi	ICAR-IARI, New Delhi
4.	Sasira D. (21917)	M.Sc.	Pectin extraction from carrot pomace: Application in emulsion with bael (*Aegle marmelos* Correa) fruit powder	Dr. Neelam Upadhyay	ICAR-IARI, New Delhi
5.	Manisha Bhardwaij (21961)	M.Sc.	GABA content in tomatoes: Impact of genotype, maturity stage and processing regime	Dr. Alka Joshi	ICAR-IARI, New Delhi
6.	Pavankumar T. (21967)	M.Sc.	Valorization of pummelo (*Citrus grandis*) peel for nanocellulose extraction	Dr. Dinesh Kumar	ICAR-IARI, New Delhi
7.	Sreenatha A. (11112)	Ph.D.	Development and characterization of finger millet based functional food through extrusion processing	Dr. Shalini Gaur Rudra	ICAR-IARI, New Delhi
8.	Bindu H. (11591)	Ph.D.	Standardization of storage temperature and pre-treatments for extension of storage life of muskmelon	Dr. D. V. Sudhakar Rao	**ICAR-IIHR, Bengaluru
9.	Harish T. (11594)	Ph.D.	Studies on production of kamalam/dragon fruit (*Hylocereus polyrhizus*) powder using tray drier and its value added products	Dr. C. K. Narayana	**ICAR-IIHR, Bengaluru
10.	Lekshmi S.G. (11856)	Ph.D.	Ornamental plant extracts for management of postharvest diseases and quality of guava fruits	Dr. Shruti Sethi	ICAR-IARI, New Delhi
11.	Sukanya Mam (11922)	Ph.D.	Effect of vacuum frying on bioactive compounds retention and shelf-life extension of red cabbage and broccoli	Dr. Shalini Gaur Rudra	ICAR-IARI, New Delhi

*******Outreach institute*

VEGETABLE SCIENCE

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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. The research findings of post graduate students have been grouped under the following themes:

Theme 1: Genetic Diversity, Heterosis and Nutritional Studies

Studies on nutritional and biochemical diversity in brinjal (*Solanum melongena* l.) genotypes

The study aims to identify nutritionally rich brinjal genotypes and to determine the diversity of nutrients and biochemical traits and correlation among different quality traits in brinjal. The data were subjected to statistical analysis for genetic variability, analysis of variance (ANOVA), analysis of correlation coefficient, exploration of genetic divergence and principal component analysis (PCA). Both at genotypic and phenotypic correlation study total anthocyanin had positive and significant correlation was found with fruit diameter. Zinc had positive and significant correlation with manganese. Calcium had positive and significant correlation was found with magnesium, but negative and significant correlation was observed with copper. Iron had positive and significant correlation was found with potassium. Magnesium had positive and highly significant correlation was found with phosphorus. Sodium had positive and significant correlation was observed with fruit length, and total carotenoid but negative and significant correlation was found with phosphorus. Potassium had negative and significant correlation was found with fruit weight. fruit diameter had positive and significant correlation with fruit weight. chlorophyll-a had positive and highly significant correlation with total chlorophyll, and total carotenoids. chlorophyll-b had positive and significant correlation with total chlorophyll. Ten principal components were derived which collectively explaining about 83.117% of the variation. Based on the D^2 analysis, a total of forty genotypes of brinjal were classified into five clusters based on twenty-three quantitative characters. The majority of genotypes were grouped into cluster III, which included 23 genotypes. Based on this study, it was revealed that the genotypes varied widely, indicating that there was opportunity for selection-based improvement of the brinjal genotypes. G-175 genotype was highlighted as promising ones for zinc and calcium content attributes, Pusa Purple Round & G-57 for high antioxidant and high ascorbic acid trait respectively. The promising genotypes have the capability to be employed in upcoming breeding initiatives.

Heterosis and combining ability study for yield and quality traits in bitter gourd (*Momordica charantia* L.)

Sixty-four bitter gourd hybrids along with 16 lines and 04 testers were evaluated during spring-summer, 2024 to study the heterosis, combining ability and gene action. The mean values of F_1 hybrids were higher than that of lines and testers for all the characters studied, except node number for first female flower, days to first female flower anthesis and days to first fruit harvest. In order of merit, PVGy-201 (1740.98 g), G-16-2 (1764.16 g) and DBGS-21-06 (1740.98 g) were identified as best performing lines for total yield per plant. Combining ability analysis of 20 parents and 64 F_1 showed significant GCA and SCA effects for all the characters studied. This indicated the importance of both additive and non-additive gene action for the characters studied. DBGS-21-06 appeared to be good general combiner for early maturity, yield components and quality traits. The F_1 hybrids PVGy-201 G-16-2 and DBG-38 × S-43 showed highest and significant desirable sca effect for fruit yield per plant. DBGS-21-06 × S-43 (52.5%) was best heterotic combination for yield per plant and PVGy-201 × G-16-2 (61.58%) for highest charantin content over the standard check (Pusa Hybrid-6). For many traits, like days to first female flower anthesis, days to first fruit harvest and various fruit, antioxidants and minerals, non-additive gene action indicated by higher dominance variance (σ^2D) compared to additive variance (σ^2A) was more influential. The variance due to SCA often exceeds that due to GCA, reinforcing the importance of non-additive interactions in these traits. Traits such as node number of first female flower, vitamin-C are more influenced by additive genetic effects. Some traits including chlorophyll a, chlorophyll b, iron, saponins and calcium showed both additive and non-additive effects. Out of twenty-eight SSR markers employed for testing genetic purity, AVRDC_BG-66 confirmed the hybridity of seven hybrids, whereas, MCSSR-11, S-32, AVRDC_BG-1 and AVRDC_BG-74 confirmed the hybridity of four hybrids. Mr. Theja M.J.

Genetic studies for yield and quality traits in advanced breeding lines of brinjal (*Solanum melongena* L.)

The study aimed to estimate the genetic variability for yield and quality traits and understand the associations between horticultural traits and yield among 45 advanced breeding lines of brinjal at the experimental farm, ICAR-IARI, Hazaribagh, Jharkhand. The ANOVA revealed significant differences among the genotypes for all the studied traits, indicating substantial genetic variability. High estimates of GCV and PCV were observed for fruit length, fruit diameter, fruit length: diameter ratio, ascorbic acid, total phenol and total antioxidant capacity. High heritability with genetic advance was observed for plant height, number of branches, fruit yield and ascorbic acid, suggesting that these traits are controlled by additive gene action and can be improved through selection. The number of fruits per plant, fruit weight and fruit diameter showed positive associations with fruit yield, emphasizing their importance in breeding programs. Path analysis indicated that the number of fruits per plant, fruit weight and fruit diameter had the most significant positive direct effects on fruit yield, emphasizing their importance for selection in breeding programs. Qualitative trait characterization revealed diverse plant growth habits (erect, semi-spreading and spreading), fruit shapes (round and long) and colours (light green, purple and white), contributing valuable information for the development of new brinjal varieties. The genotypes BWT-44 (28.43 t/ha), BWT-16 (28.01 t/ha) and BWT-3 (26.85 t/ha) were identified as high-yielding and they can be recommended as elite lines for future brinjal breeding programs. In conclusion, the findings from this study highlight the broad genetic diversity within the advanced brinjal breeding lines, the significance of specific traits for yield improvement and the potential for selection to enhance both yield and quality in brinjal cultivars.

Morphological and molecular characterization of male sterile and maintainer lines in onion (*Allium cepa* L.)

The aim of this study was to characterize 21 combinations of male sterile and maintainer lines of onion (*Allium cepa* L., 2n=2x=16), using flowering traits and molecular markers. Observations were recorded on 14 morphological traits in fresh onion. Significant variability was found among genotypes for different characters. All the seed traits viz., number of tillers, leaf colour (intensity), bolts per plant, bolt length (cm), umbel height (cm), umbel diameter (cm), flowers/umbel, umbels/plant, first flower open (days), 50% flower open (days), 100% flower open (days), anther colour, sterility and seed yield per plant (gm) exhibited significant variation. For cytoplasm determination the chloroplast based *InDel* primer *accD* determined 17 out of 21 (80.95%) combinations possessing S and N type of cytoplasm in their respective male sterile and maintainer lines. Molecular identification of fertility restorer *Ms* locus in the selected genotypes exhibited that 100 percent plants possessed homozygous recessive locus using the marker AcPMS1. But other markers AcPMS-1-1, predicted 78.6 % (33/42) homozygous recessive genotypes (*msms*) and 21.4 % (9/42) heterozygous genotypes (*Msms*). The male sterile and maintainer lines were genotypes with 43 Microsatellites or Simple Sequence Repeat (SSR) primers. Nine markers exhibited polymorphism. ACM124 showed high PIC index (0.525) and major allele frequency per locus. ACM004, ACKI088 and ACKI141 detected highest number of alleles (3). Cluster analysis using molecular markers revealed 3 distinct clusters. Evaluation of genetic diversity using more accessions and more markerswill lead to accurate estimate of genetic diversity among these male sterile and maintainer lines.

Studies on genetic diversity and expression of triterpenoid biosynthetic genes in bitter gourd genotypes (*Momordica charantia* L.)

In this experiment, 46 bitter gourd genotypes from various geographical regions were evaluated for agro-morphological and biochemical traits including antioxidants and dietary nutrients and expression of triterpenoid biosynthetic genes (charantin and beta-carotene). These genotypes displayed significant variability for leaf, fruit, flower and fruit tubercles, fruit skin colour, and also for fruit ridgeness characteristics. Most plants exhibited yellow flowers, with a few showing light-yellow blooms. Two genotypes, DBGS-21-06 and DBGS-48-00, exhibited predominantly gynoecious sex expression. The genotypes also exhibited variability in fruit colour, with unique creamy white fruits found in some genotypes. The study highlighted that PVGy-201 had the shortest time to the first female flower opening, while DBGS-2 (Sel-2) showed the longest fruit length and Pusa Rasdar had the maximum fruit diameter. DBGS-21-06 recorded the highest fruit weight and yield per plant. A significant correlation was found between yield and various traits, including fruit weight, length, vine length, and number of fruits per plant. Principal component analysis revealed that traits like days to first female flower opening and first fruit harvest contributed significantly to genetic diversity. Antioxidant analysis revealed variability in key compounds like carotenoids, vitamin C, saponins, and charantin. Pusa Do Mousami had the highest carotenoid content, while DBG-33-2 exhibited the highest vitamin-C levels. Sel-32 had the highest saponin content, and PVGy-201 showed the highest charantin content. The mineral nutrient analysis indicated wide variability in dietary nutrients such as magnesium, iron, manganese, calcium, and zinc. *Momordica balsamina* having the highest magnesium content and DBGS-100-0 recorded the highest iron content. Gene expression studies for charantin and beta-carotene biosynthesis revealed notable variability. PVGy-201 showed the highest gene expression for charantin, while DBGS-2 (Sel-2) demonstrated promising expression for *McHMGR* and *McPMK* genes. Genotypes like DBGS-21-06, NBH002, and Pusa Rasdar exhibited high expression for beta-carotene-related genes, indicating potential for increased beta-carotene content.

Genetic diversity studies in sponge gourd [*Luffa cylindrica* (Roem.) L.]

Diverse sponge gourd [*Luffa cylindrica* (Roem.) L.] genotypes were evaluated for yield attributes, quality parameters, and yellow mosaic disease resistance. ANOVA showed significant genetic variation among genotypes. VRSL 12 showed superior performance for fruit yield/plant, quantity of fruits/plant and vine length. Kashi Jyoti produced earliest female flower. VRSL 19 had the maximum phenol content and DPPH assay value. The PCV values were superior than the GCV values. High heritability (>60%) was exhibited for all characters and high genetic advance (>20%) was noted for fruit yield/plant, fruit weight and primary branches number. Fruit yield/plant exhibited significant and positive association with vine length, vitamin C, primary branches number and FRAP at both genotypic and phenotypic levels. Fruit girth, diameter and vine length had the maximum positive direct impacts on fruit yield/plant at the genotypic level and fruit weight, vine and petiole length at the phenotypic level. The accessions were divided into 5 groups. Clusters III and V exhibited superior performance for key traits, with highest inter-cluster distance (7458.0) exhibited between cluster III & cluster IV, indicating significant genetic diversity. First eight principal components exhibited 76.42% of the overall variation and Higher allelic richness in fruit skin and color and seed color reflect substantial genetic diversity with many unique alleles. VRSL 2 showed moderate resistance to yellow mosaic disease and high vitamin C content. The study suggests prioritizing fruit yield-related traits and yellow mosaic disease resistance in sponge gourd breeding initiatives.

Theme 2: Biotic and Abiotic Stress Tolerance

Studies on genetics and molecular mapping of downy mildew resistance in cucumber (*Cucumis sativus* L.)

To determine the source of downy mildew resistance in cucumbers and investigate the inheritance of downy mildew resistance, 174 cucumber genotypes including 3 check varieties (Pusa Long Green, Pusa Uday, Pahari Harit), were screened under natural field conditions at the ICAR-IARI, New Delhi. It was observed that none of the genotypes were immune to downy mildew, but genotypes IC 613461, IC 613461-A, and DC-92 showed resistance to the disease. A total of 150 genotypes recorded susceptibility with a Percent Disease Index (PDI) between 41 and 60 percent, while 20 genotypes were highly susceptible with a PDI of over 60 percent. Statistical analysis indicated that genotype IC 613461 had the lowest PDI value (1392.07 ± 164.52), highlighting its resistance to downy mildew disease. The mode of inheritance of resistance, involving the F_2 progenies of the DC-773 x DC-61 cross, revealed that downy mildew resistance in the DC-61 genotype is governed by a single recessive gene. The QTL-seq approach identified one genomic region spanning 5.5 Mb on chromosome 7 closely associated with downy mildew resistance. Within this QTL-region, numerous variants were detected, showing promise for fine mapping of the downy mildew resistance trait. Notably, several candidate genes were identified within the QTL-region, including Defensin-like protein 3, WRKY domain-containing protein, Heat shock protein (putative), NBS-LRR type resistance protein, Protein kinase domain-containing protein, NAC domain-containing protein, and Serine-rich protein-related (putative). These genes are potential candidates linked to downy mildew resistance expression in cucumber due to their known roles in plant defense mechanisms across various crops. Through additional mapping efforts and functional validation of the discovered genes, the study's findings provide useful insights into the expression of downy mildew resistance in cucumbers, paving the path for more accurate identification of candidate genes and finer mapping. In the end, this study advances our knowledge of the molecular and genetic basis of cucumber downy mildew resistance.

Understanding biochemical and molecular basis of differential response against downy mildew in cauliflower (*Brassica oleracea* var. *botrytis* L.)

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is one of the most popular vegetables in the Brassicaceae family due to its high nutritive value and its importance in processing sector. Downy mildew, caused by the oomycete *Hyloperonospora parasitica*, poses a significant threat to cauliflower production. Understanding the mechanisms underlying resistance to this disease is crucial for developing more resilient cultivars. This study investigated the morphological, biochemical, and molecular responses of three cauliflower genotypes including the downy mildew susceptible (Pusa Meghna and Pusa Sharad) and resistant (BR-2). Disease progression at different time points post inoculation with the pathogen (12hpi to 30dpi) was monitored, and histopathological analyses were conducted to assess pathogen invasion. Further, the activity of reactive oxygen species (ROS) scavengers and phenol content were also measured to evaluate antioxidant defense in the genotypes under study. These changes include the production of enzymes, secondary metabolites, and signalling molecules that help in combating the infection. Additionally, gene expression analysis was performed to identify defense-related genes involved in resistance. The results revealed that the resistant genotype BR-2 exhibited lower disease severity, reduced pathogen invasion, higher levels of ROS scavengers and phenols, and consistent upregulation of defense-related genes compared to the susceptible genotypes. These findings suggest that the enhanced antioxidant defense and activation of defense genes in BR-2 contribute to its resistance to downy mildew. This study provides valuable insights into the mechanisms of resistance to downy mildew in cauliflower.

Genetic and molecular analyses for root knot nematode resistance in brinjal (*Solanum melongena* L.)

Brinjal (*Solanum melongena* L.) is one of the important Indo-Burma region originated solanaceous vegetable. The brinjal production and productivity is rigorously affected by numerous biotic and abiotic stresses that have a substantial influence on brinjal crop production. Among them, plant parasitic root knot nematodes (RKN) cause primary damage and also pre-disposes soil borne pathogens. So far, no work has been reported on genetic and molecular basis of RKN resistance in brinjal. This study aimed to identify stable RKN resistance sources, investigate the genetics of resistance, and identify molecular markers linked to RKN resistance loci. The research, conducted from 2020-2024 at ICAR-IIHR Bengaluru and CHES Bhubaneswar, screened 126 brinjal accessions (111 cultivated, 15 wild species) through artificial inoculation. Four accessions—IIHR-824, VI046103 (*S. melongena*), IIHR-803 (*S. torvum*), and IIHR-792 (*S. seaforthianum*), exhibited resistance at high soil temperatures (36-38°C). Genetic studies using F_2 and backcross populations revealed a single dominant gene controlling RKN resistance in IIHR-824, supported by segregation ratios of 3(R):1(S) in F_2 and 1(R):1(S) in backcrosses. Six-generation mean analysis indicated dominance and complementary gene action. Molecular marker analysis employed 400 SSRs and 5 SCAR markers, identifying 38 SSRs polymorphic between resistant and susceptible parents. The SSR marker 'emf11A04' showed polymorphism in resistant and susceptible F_2 bulks, with a segregation efficiency of 92.87% and PVE of 46.34%. In conclusion, heat-stable resistant accessions IIHR-824, VI046103, IIHR-803, and IIHR-792 can serve as donors in breeding programs or as rootstocks to manage RKN in brinjal. The single dominant gene controlling RKN resistance facilitates the development of resistant F_1 hybrids, while the 'emf11A04' marker enables marker assisted selection for RKN resistance, advancing sustainable brinjal cultivation.

Molecular and biochemical basis of resistance to phomopsis fruit rot in eggplant (*Solanum melongena* L.)

The study was conducted at the Division of Vegetable Science, ICAR-IIHR, Bengaluru, from 2022-2024. Eggplant, a key Solanaceous vegetable, suffers yield losses due to phomopsis fruit rot caused by

Diaporthevexans, affecting all growth stages. This research aimed to identify resistance sources, investigate biochemical resistance mechanisms, and analyze transcriptomes of resistant (IIHR-629) and susceptible (BBR-54) genotypes. Field surveys in Karnataka, Maharashtra, and Uttar Pradesh yielded 24 isolates, with IIHR PV-2 identified as the most virulent through pathogenicity tests. Morphological and molecular characterization revealed minor intraspecific variations among isolates. Screening 114 genotypes via artificial inoculation identified highly resistant genotypes (IIHR-629, JB-7, *S. torvum*) and classified others into resistance categories based on PDI and AUDPC values. Biochemical analysis showed elevated levels of defense enzymes (PPO, β-1,3-glucanase, chitinase), total phenols, flavonoids, epicuticular wax, and solasodine in resistant genotypes, highlighting their defensive roles. Transcriptomic analysis identified Differentially Expressed Genes (DEGs) linked to secondary metabolite biosynthesis, signalling pathways (MAPK, Toll-like receptor, NF-kappa B), and pathogen recognition, which were enriched in the resistant genotype. In contrast, the susceptible genotype displayed compromised metabolic responses. GO and KEGG analyses emphasized the critical roles of these pathways in immunity and defense. This study identified resistance sources and provided insights into host-pathogen interactions, highlighting key genes, metabolites, and enzymes essential for developing resistant eggplant hybrids/varieties against *Diaporthevexans.*

Incorporation of multiple virus resistance into male sterile genetic background in chilli (*Capsicum annuum* L.)

Chilli (*Capsicum annuum* L.) is an essential crop used in food, cosmetics and pharmaceuticals. However, its production is significantly impacted by viral diseases, including cucumber mosaic virus (CMV), chilli venial mottle virus (ChVMV) and chilli leaf curl virus (ChLCV). The present aimed to develop breeding lines resistant to CMV (Guntur isolate), ChVMV (Bengaluru isolate) and ChLCV (Raichur isolate) in a cytoplasmic male-sterile maintainer background. Resistant donor lines, IHR 4597 (ChLCV-resistant) and IHR 2451 (CMV and ChVMV-resistant), were used to introduce resistance loci into the male sterile maintainer line background (IHR 3905). A double-cross strategy, ((MS_3B × IHR 2451) × (MS_3B × IHR 4597)), was employed with MS_3B as the recipient parent. Standardised sequential screening revealed inoculation of CMV at the cotyledonary stage, while the 2-leaf and 4-leaf stages were optimal for ChVMV and ChLCV infections, respectively with inoculation intervals ranging from 12 to 14 days.The double-cross F_1 ((MS_3B × IHR 2451) × (MS_3B × IHR 4597)) showed a 1:1 segregation (Resistant: Susceptible) for ChLCV, indicating single dominant gene action. Among the 5,010 double-cross F_2 plants screened sequentially, 2,731 were resistant to CMV, 945 to CMV and ChVMV and 473 to all three viruses. In the DF_3 (18,481 plants), a total of 2,100 plants exhibited combined resistance.Molecular markers validated the presence of resistance loci in the DF_4 families. Artificial screening against the three viruses of the 50 shortlisted families showed resistance ranging from 73.33–100%. Two advanced breeding lines (DF_4-32, DF_4-171) displayed combined genotypic and phenotypic resistance to all three viruses, whereas 12 families demonstrated high phenotypic resistance while retaining the homozygous recessive loci (*rfrf*). Thus, these lines hold potential for virus-resistant, male-sterile chilli breeding programs.

Assessing genetic diversity in brinjal genotypes for resistance against *Fusarium oxysporum* f. sp. *melongenae*

Brinjal (*Solanum melongena* L.), an important solanaceous vegetable widely cultivated in tropical and subtropical regions, faces significant challenges from soil-borne pathogens. Fusarium wilt, caused by multiple *Fusarium* species, has become increasingly severe and persistent, exacerbated by climate change. Traditional control methods, such as cultural, biological, and chemical practices, have proven inadequate, highlighting the urgent need for developing resistant cultivars. Therefore, the present study aimed to identify Fusarium wilt-resistant brinjal genotypes by screening under three growing conditions (sick-plot, pots and hydroponics) and validating disease reactions using molecular markers. A total of 90 diverse genotypes, comprising released varieties, local landraces, exotic collections and related wild *Solanum* species, were evaluated for resistance in a Fusarium wilt-endemic field. The causal agent isolated from infected plants was identified as *Fusarium oxysporum* f. sp.*melongenae,* through morpho-cultural characterization, molecular sequencing and pathogenicity assays. The isolate was then used for artificial inoculation in pots and hydroponic systems for confirmatory evaluation of disease reactions using different scoring techniques. Nine genotypes (Swarna Mani, G-17, Pink, CH-151, Sidhasar Local, Special Muktakeshi, H-183, *S. sisymbriifolium*, *S. torvum*) were identified resistant under all three growing conditions. Additionally, distinct variations in disease progression patterns, changes in host phenotypic traits, and delayed infection in vascular tissues were observed in resistant genotypes using the rapid hydroponic phenotyping approach. This underscores its broad applicability to screen diverse plant species against root pathogens. Furthermore, molecular marker analyses using SCAR and SSR markers validated the observed resistant reactions. With good polymorphism and phenotypic variation rates, the novel SSR markers hold significant potential for marker-assisted selection within the germplasm. Biochemical analysis also examined differential responses among resistant and susceptible accessions upon infection. The resistant genotypes identified, along with the phenotypic, anatomical, molecular and biochemical insights, will contribute to advancing brinjal improvement programs aimed at enhancing resistance to Fusarium wilt.

Understanding genotypic variation and biochemical changes during low temperature induced parthenocarpy in sweet pepper

A total of 23 genotypes were evaluated under optimum and low-temperature conditionsto explore the morphological and biochemical traits of capsicum genotypes. None of the genotypes produced parthenocarpic fruits under optimal temperatures, highlighting that parthenocarpy is not solely genotype-dependent but is significantly influenced by environmental stress. Under low-temperature conditions, 18 genotypes set fruits, with the majority producing parthenocarpic fruits. Genotypes such as DCapBL-31-5 and DCapBL-1 showed high fruit set percentages, indicating strong potential for parthenocarpy, while others like DCapBL-38-1 and DCapBL-35-5 exhibited limited fruit set. Parthenocarpic fruits displayed diverse morphologies, including knotty, deformed, beak-like, carpelloid and normal shapes. Morphological traits such as fruit weight, length, volume, diameter, cavity volume and firmness were significantly reduced under low-temperature stress while pericarp thickness increased suggesting an adaptive response to chilling temperatures. Biochemical analysis revealed a significant increase in antioxidant and phenolic content under low temperatures, while carotene, iron, and zinc levels decreased. Chlorophyll-a, chlorophyll-b, and total sugar levels remained stable across temperature regimes. Hormonal profiling of flowers leading to parthenocarpic versus fertilized fruits revealed auxin levels were notably higher in parthenocarpic fruits under low temperatures, while genotype-specific variations in gibberellins and ABA were observed within temperature regimes. The study underscores the multifaceted impacts of low-temperature-induced parthenocarpy on fruit morphology and biochemical properties, alongside the hormonal mechanisms driving this process. Breeding efforts could target the development of genotypes with enhanced parthenocarpic potential and resilience to cold stress, paving the way for improved productivity in challenging environments.

Theme 3: Breeding for Quality Traits

Development of mapping population and identification of QTLs associated with extended shelf-life in cucumber (*Cucumis sativus* L.)

125 F_2 progenies from a cross between two cucumber genotypes, namely DC-48 (with extended shelf life) and DC-83 (Pusa Long Green) were evaluated over three consecutive crop seasons-Kharif-2022, Summer-2022 and Summer-2023 at IARI, New Delhi. The goal was to analyze and map QTLs related to shelf life and flowering traits, such as: fruit firmness, fruit shrinkage, retention of green color, days to the first female flower, and node of the first female flower. A survey of 1,200 SSR markers revealed 106 polymorphic markers between the parental lines. Using QTLIciMappingV4.0software, a chromosomal linkage map was constructed, covering a total length of 1,175 cM with an average marker interval of 25 cM. The Inclusive Composite Interval Mapping of ADDitive (ICIM-ADD) method identified 32 QTLs for five traits across seven chromosomes over the two years of testing. For fruit firmness at the bottom (pedicel region), three QTLs (*qBF7.3, qBF7.1*) were mapped. Two QTLs (*qMiFF7.3,qMiFF6.1*) affecting fruit firmness in the middle were located on chromosomes 7 and 6 during the rainy and summer seasons of 2022. Additionally, three QTLs (*qMeFF7.3, qMeFF7.1, qMeFF7.1.1*) were identified for overall fruit firmness (top, middle, and bottom) on chromosome 7 across both summer and rainy seasons. For fruit shrinkage, seven QTLs were mapped on chromosomes 1, 3, and 4, with most showing consistency over both seasons. Three QTLs (*qRGC7.1, qRGC7.2, qRGC7.3*) were identified for retention of green color in the summer and rainy seasons of 2022-23.In terms of days to the first female flower, two QTLs (*qDFFF3.3.1, qDFFF3.1*) on chromosome 3 showed significant consistency, with LOD values of 10.46 and 7.71. For the node to the first female flower, two QTLs (*qNFFF2.1, qNFFF2.2*) were identified across two summer seasons (2022 and 2023). The QTL detected on chromosome 2 (*qNFFF2.2*) was major, with a PVE of 13.05%, while the other (*qNFFF2.1*) was minor, with a PVE of 6.95% during the summer season of 2022.

Genotyping and phenotyping of ToLCD resistant backcross lines of tomato for processing traits

Forty six genotypes including checks were genotyped with molecular markers linked with multiple disease resistance including ToLCD and fruit quality traits. Simultaneously, the genotypes were subjected for fruit quality traits including juice recovery (%), puree (9 ºBrix) and paste (25 ºBrix) and yield. Minerals (Zn, Mg, Ca and Fe) and phyto nutraceutical (lycopene and beta carotene) were also analysed from paste samples. Genotypes having superior promising processing qualities along with *Ty-3*and *Ph-3* resistant gene for ToLCD and late blight (PTH-6 and DTH-162) superior over the check (Punjab Chhuahra). The *ovate* gene mutant allele in Pusa Prasanskrit, DTK-91, DTH-507 and Punjab Chhuhara for oval fruit shape. Among the genotypes evaluated Pusa Tomato Hybrid-6 (PTH-6) with high yield (986.7 q/ha), juice recovery (84.31%) puree and paste recovery of 37.2% and 16.7% respectively and found most promising for dual purpose segment. Other promising genotypes includes DTK-128 for fewer locules (2), DTK -91 with firmness of (6.0 kg/cm^2), DT-396 for thick pericarp (9 mm), DTK-103 for high fruit shape index (FSI) (1.9), high acidity present in DTK-137 (0.6%), DT-904115 (5.2 °Brix), DTK-1 (SPS-6) for high viscosity (61.4 cP) from the fruits. Paste samples having superior biochemical properties include PTH-6 for high lycopene content (15.8 mg/100g), Punjab Chhuhara for beta carotene (4.4 mg/100g), titratable acidity in DTK-134(1.2 mg/100g), DTK-135 for high ascorbic acid content (78.0 mg/100g), high total antioxidant activity in DT-411-1-6-11-15 (27) (505.5 µmol Trolox/100g) , total phenolic content in DT-411-1-6-11-15(27) (167.0 mg/100g), highest flavonoid in DTK-117 (142.3mg/100g) and DTPVB-2 for colour value (2.6). Significant genetic diversity was found for processing traits along with multiple disease resistance for boosting indigenous Indian tomato-based processing industry.

Genetic and molecular analyses for pungency related traits in *Capsicum* species

The pungency of peppers is one of the main attributes of quality in *Capsicum*, which depends on the accumulation of capsaicinoids (mainly, capsaicin and dihydrocapsaicin). Analogous non-pungent compounds, called capsinoids (mainly, capsiate and dihydrocapsiate) are also present in peppers. In the present study, fruits of 65 accessions of varied *Capsicum* spp., such as *C. annuum, C. chinense, C. baccatum and C.frutescens* were used to estimate capsaicinoid and capsinoid contents using high performance liquid chromatography (HPLC). The results showed the presence of wide variability among accessions for all the studied compounds, ranged as nordihydrocapsaicin (0.00−10,081 SHU), capsaicin (0.00−549,099 SHU), dihydrocapsaicin (0.00-183,317 SHU), total capsaicinoids (0.00−742,497 SHU), capsiate (26.77−474.39 **µg/g**), dihydrocapsiate (6.00−215.99 **µg/g**) and total capsinoids (36.11−690.38 **µg/g**). Among accessions, highest content of nordihydrocapsaicin, capsaicin, dihydrocapsaicinand total capsaicinoids was found in IHR 4550 followed by IHR 4652 and IHR 4501. Total capsinoids, capsiate and dihydrocapsiate were highest in IHR 4651 followed by IHR 4550 and IIHR 4649. The nature and magnitude of gene action for capsaicinoids and capsinoids content was also estimated through six generations (P_1, P_2, F_1, F_2, BC_1P_1, BC_1P_2) mean analysis obtained from IHR 4604 × IHR 4550 cross. Among gene effects, dominance and additive × additive type of gene interaction were predominant for capsaicin, dihydrocapsaicin, total capsaicinoids, capsiate, dihydrocapsiate and total capsiate, whereas additive and additive × additive type of gene interaction were predominant for nordihydrocapsaicin. Out of Twenty-six molecular markers linked to chilli pungency, all the markers (except BF7+ BR9, dominant markers) were able to differentiate non-pungent IHR 4604 from pungent IHR 4550 accession. The designed InDel marker (MAPS F2/R2) showed polymorphism between parent IHR 4604 and IHR 4550, further validated in F_2 segregating population which showed 67.88 percent of phenotypic variance. Designed co-dominant InDel marker (MAPS F2/R2) could be used in marker- assisted selection for pungency genotyping.

Exploring antioxidant vitamins and pigments diversity in chilli accessions through metabolomic and genomic approach

Chilli is a versatile commercial value, serving as a spice and vegetable. Recent trends show a high demand for consumer products based on bioactive compounds. Population in the present study revealed significant diversity in fruit morphological traits, especially for the intensity of ripe fruit colour. Principal Component Analysis of biochemical traits indicated that carotenoids, ASTA colour value, and vitamin E traits contributed 65% of the total variability—notably, Acc. IHR4432 exhibited the highest vitamin C (291.56 mg/100g FW), Acc. IHR4650 had the highest vitamin K (151.37 µg/100g DW), and Acc. IHR3455 excelled in vitamin E (126.84 mg/100g DW), total carotenoids (448.78 mg/100g DW), ASTA colour value (250.43 ASTA units), and capsanthin (166 mg/100g DW). Acc. IHR-B-HP-81 was prominent for total anthocyanin (59.69 mg/100g FW) and delphinidin content (321.6 µg/g FW). Acc. IHR4613-1A had the highest zeaxanthin (21.96 mg/100g DW), while Acc. IHR4677 was rich in lutein (18.99 mg/100g DW). Seasonal variations played a significant role in biosynthesis, with genotype × environment interaction effects being significant ($p<0.01$) for all traits except vitamin K. Carotenoids and vitamin synthesis was favourable at an average temperature of 27.11°C and 175.5 total sunshine hours in summer. For anthocyanin accumulation, an average temperature of 24.5°C and 137.1 total sunshine hours during the rainy season were ideal. Stability analysis indicated that accessions IHR4613-1A and IHR2452 performed reliably for vitamin C across both seasons, IHR4430 and IHR4429 for total carotenoids and vitamin E, and IHR-B-HP-56 and IHR IIHR-B-HP-137 for anthocyanins. Allelic variations among carotenoid biosynthetic genes revealed that in the *PSY-1* gene, no variations were observed except in IHR4569, which had a low ASTA colour value. The *CRTZ-2* gene showed consistent coding across all accessions, matching HPLC-MS carotenoid profiling results where zeaxanthin was predominant. The *CCS* gene exhibited distinct disruptions among yellow and orange-yellow accessions, including full-length deletions, 17 bp deletions, transverse mutations, and frameshift mutations. Whereas, red accessions showed no allelic variations, indicating gene dominance.

Theme 4: Standardization of Production Technology and Regeneration Protocol

Standardization of *in vitro* regeneration protocol through callus culture in okra (*Abelmoschus esculentus* [L.] Moench.

The study aims to refine explant selection and media composition for improved callus induction and plant regeneration in okra. Three okra cultivars, namely Pusa Sawani, Pusa Bhindi-5, and Pusa Lal Bhindi-1 were employed for study. Culture establishment was optimized using 0.1% $HgCl_2$ for 5 minutes, achieving the highest establishment rate of 81.01%. Higher concentrations or longer exposure times reduced the success rate. For callus induction, cotyledonary leaf, hypocotyl, and leaf segments as were tested. Hypocotyl explants demonstrated superior callus induction, while cotyledonary leaves had moderate potential and leaf segments had the lowest success rate for callus induction.MS medium supplemented with 2.0 mg/L 6 - benzylaminopurine (BAP), 0.2 mg/L (naphthalene acetic acid)NAA, and 200 mg/L activated charcoal was found to be the most effective for callus induction across all explants. This combination maximized callus induction (up to 93.26%) and reduced the time required for initiation. In vitro shoot regeneration was evaluated using BAP, kinetin, and thidiazuron (TDZ). BAP was most effective for shoot initiation from hypocotyl-derived callus. The optimal combination was 2.0 mg/L BAP and 0.2 mg/L NAA, which yielded shoot initiation in shortest time and maximum shoot length. For in vitro rooting, MS medium with 0.2 mg/L NAA provided the best results, producing the longest roots, highest root volume, and weight, while reducing the time needed for rooting. Hardening strategies tested included plastic pots with polythene covers and glass jars with PP caps. Plantlets hardened in plastic pots showed superior survival rates, shoot length, root length, and chlorophyll content. The highest total chlorophyll content was found in plantlets hardened in glass jars. This study establishes a robust in vitro culture and regeneration protocol for okra, offering key insights into the effects of growth regulators and media conditions. It provides a strong basis for further research in enhancing regeneration efficiency, genetic transformation, and crop improvement in okra.

Generation and characterization of doubled haploids (DHs) in onion (*Allium cepa* L.)

Gynogenesis is crucial for generating haploid and doubled haploid plants in onion (*Allium cepa* L.), as it can produce completely homozygous lines in a single generation. Gynogenic response of ten onion genotypes was studied with different combinations of MS medium along with impact of heat and cold shock treatments on gynogenesis efficiency. The results demonstrated that genotypes Bhima Safed (9.52%) and Bhima Dark Red (9.14%) exhibited the highest gynogenesis efficiency. Among media, OGH8 outperformed OGH4 and HFM in inducing direct embryogenesis. A 2-day cold pretreatment was comparable to the control, while extended cold treatment enhanced callogenesis. In contrast, heat treatment was found ineffective for gynogenesis induction. Thereafter, based on the cytology and flow cytometry, 51.39% of plants were found haploid, 26.39% were spontaneous diploids, and 22.22% were mixoploids. Stomatal characteristics of confirmed haploids and doubled haploid plants were compared with diploids. The study found that haploids exhibited smaller stomatal sizes and higher stomatal densities compared to diploids. Likewise, doubled haploids displayed reduced vigour relative to their diploid counterparts. In doubled haploids, all horticultural traits, including plant height, leaf length and width, pseudostem length and width, as well as bulb weight, length, and diameter, was observed to be reduced compared to their diploid counterparts. SSR markers effectively confirmed the homozygosity of the diploid regenerants produced through in vitro gynogenesis. Furthermore, this study also examined the associations between flower bud length and diameter, anther length and diameter, and the developmental stages of the male gametophyte across ten onion genotypes. The optimal stages for anther culture (late uninucleate and early binucleate) was observed in flower buds measuring 2.5 to 3.5 mm in length and 2.0 to 2.7 mm in diameter. In anthers, these stages were found at length of 1.2 to 1.6 mm and diameter of 0.55 to 0.75 mm, thereby, serving as useful markers for identifying microspore developmental stages.

Effect of mulching and fertigation doses on growth, yield and quality of summer squash (*Cucurbita pepo* L.) varieties under low tunnels

An experiment was conducted in factorial randomized complete block design using 2 mulching conditions (silver/black polythene mulch (M1) and non-mulch (M0)), 3 fertigation doses (50% (F1) , 75% (F2) , and 100% (F3) with the RDF being 100:50:60 kg NPK/ha), and 7 varieties of summer squash i.e., 4 long type (Pusa Alankar (V1), Australian Green (V2), Yellow Zucchini (V3), Green Zucchini (V4)), 3 round type (Gol-2 (V5), Latto (V6), and Pusa Pasand (V7). The results showed significant variations in growth, yield, and quality parameters of summer squash due to mulching, fertigation and their interactions across the varieties. Pusa Alankar (V1) exhibited the highest plant height, number of branches, stem diameter and plant spread, while Gol-2 (V5) had the highest number of leaves, when grown under mulching (M1) combined with the F3 (100% RDF) fertigation dose. Yellow Zucchini (V3) exhibited the earliest flowering, fruit set, and Pusa Alankar (V1) had taken shortest time from flowering to fruit harvest under mulching (M1) with the F3 (100% RDF) fertigation dose. Pusa Alankar (V1) had the highest fruit weight, fruit length, fruit yield per plant and yield per square m, under the combination of mulching and 100% RDF (F3) fertigation doses. Additionally, the maximum fruit diameter was observed in Gol-2 (V5) and Pusa Pasand (V7), while Yellow Zucchini (V3) produced the highest number of fruits per plant under mulching (M1) with 100% RDF (F3), which was statistically at par with the 75% RDF (F2) fertigation dose. Quality analysis indicated that Latto (V6) had the highest total soluble solids (TSS), Yellow Zucchini (V3) showed the highest carotenoid and ascorbic acid content, Pusa Alankar (V1) had the highest total sugars, Pusa Pasand (V7) had the highest antioxidant content, Pusa Alankar (V1) and Yellow Zucchini (V3) had the highest phenol content, Australian Green (V2) had the highest flavonoid content, and Pusa Pasand (V7) had the highest firmness under mulching with 100% RDF (F3), followed closely by 75% RDF (F2). Furthermore, Pusa Alankar (V1) in M1F3 91 combinations had the highest economic returns, indicated by a benefit-cost ratio of 3:1 under low tunnels, which was statistically at par with B:C ratio observed with the 75% RDF (F2) fertigation dose. In comparison to the 100% RDF (F3), the 75% RDF (F2) dose demonstrated more economic viability and environmental sustainability, while still promoting optimal growth, yield, and quality of the summer squash varieties under low tunnel conditions.

List of contributing students and Chairperson of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the Thesis	Chairperson	Institute
1.	Ananya P Kumar (21862)	M.Sc.	Assessing genetic diversity in brinjal genotypes for resistance against *Fusarium oxysporum* f. sp. *melongenae*	Dr. Jeetendra Kumar Ranjan	ICAR-IARI, New Delhi
2.	Anupam Saha (21865)	M.Sc.	Studies on nutritional and biochemical diversity in brinjal (*Solanum melongena* l.) genotypes	Dr. Bhoopal Singh Tomar	ICAR-IARI, New Delhi

3.	Balkrishna Nayak (21863)	M.Sc.	Genotyping and phenotyping of TOLCD resistant backcross lines of tomato for processing traits	Dr. Zakir Hussain	ICAR-IARI, New Delhi
4.	Banoth Tharun (21721)	M.Sc.	Studies on genetic diversity and expression of triterpenoid biosynthetic genes in bitter gourd genotypes (*Momordica charantia* L.)	Dr. Gograj Singh Jat	ICAR-IARI, New Delhi
5.	Chaithra M (21861)	M.Sc.	Effect of mulching and fertigation doses on growth, yield and quality of summer squash (*Cucurbita pepo* L.) varieties under low tunnels	Dr. Awani Kumar Singh	ICAR-IARI, New Delhi
6.	Taniya Shit (21860)	M.Sc.	Studies on genetics and molecular mapping of downy mildew resistance in cucumber (*Cucumis sativus* L.)	Dr. Shyam Sundar Dey	ICAR-IARI, New Delhi
7.	Theja M J (60126)	M.Sc.	Genetic studies for yield and quality traits in advanced breeding lines of brinjal (*Solanum melongena* L.)	Dr. Krishna Prakash	ICAR- IARI, Jharkhand#
8.	Vinod Raj H J (21864)	M.Sc.	Understanding genotypic variation and biochemicals changes during low temperature induced parthenocarpy in sweet pepper	Dr. Arpita Srivastava	ICAR-IARI, New Delhi
9.	Vishal Sunartiya (21867)	M.Sc.	Heterosis and combining ability analysis for yield and quality traits in bitter gourd (*Momordica charantia* L.)	Dr. Gograj Singh Jat	ICAR-IARI, New Delhi
10.	Yogita Yadav (21866)	M.Sc.	Understanding biochemical and molecular basis of differential response against downy mildew in cauliflower (*B. oleracea* var. *botrytis*)	Dr. Manisha Mangal	ICAR-IARI, New Delhi
11.	Manu A N (21868)	M.Sc	Standardization of in vitro regeneration protocol through callus culture in okra (*Abelmoschus esculentus* [L.] Moench.	Dr. Suman Lata	ICAR-IARI, New Delhi
12.	Pushpraj (50090)	M.Sc	Morphological and molecular characterization of male sterile and maintainer lines in onion (*Allium cepa* L.)	Dr. Anil Khar	ICAR-IARI, New Delhi
13.	Selvakumaran. B (21869)	M.Sc	Genetic diversity studies in sponge gourd [*Luffa cylindrica* (Roem.) L.]	Dr. Sabina Islam	ICAR-IARI, New Delhi
14.	Pooja Belwal (11891)	Ph.D.	Generation and characterization of doubled haploids (DHs) in onion (*Allium cepa* L.)	Dr. Anil Khar	ICAR-IARI, New Delhi
15.	Pradeepkumara N (11886)	Ph.D.	Development of mapping population and identification of QTLs associated with extended shelf-life in cucumber (*Cucumis sativus* L.)	Dr. Chander Parkash	ICAR-IARI, New Delhi
16.	Gujjala Narayana Swamy (11919)	Ph.D.	Genetic and molecular analyses for root knot nematode resistance in brinjal (*Solanum melongena* L.)	Dr. Tejavathu Hatiya Singh	**ICAR-IIHR, Bengaluru

17.	Koushik Saha (11133)	Ph.D.	Genetic and molecular analyses of pungency related traits in chilli (*Capsicum annuum* L.).	Dr. Madhavi Reddy Kambham	**ICAR-IIHR, Bengaluru
18.	Meghana D (11933)	Ph.D.	Exploring antioxidant vitamins and pigments diversity in chilli accessions through metabolomic and genomic approach	Dr. Madhavi Reddy Kambham	**ICAR-IIHR, Bengaluru
19.	PYD Roshni (11625)	Ph.D.	Incorporation of multiple virus resistance into male sterile genetic background in chilli (*Capsicum annuum* L.)	Dr. Madhavi Reddy Kambham	**ICAR-IIHR, Bengaluru
20.	Sulochana K.H (12192)	Ph.D.	Molecular and biochemical basis of phomopsis fruit rot resistance in eggplant (*Solanum melongena* L.)	Dr. Tejavathu Hatiya Singh	**ICAR-IIHR, Bengaluru

***Outreach institute*

Session VI: School of Social Science

Thesis Summary

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Agricultural Economics	06	06
Agricultural Extension	11	02
Agricultural Statistics	10	07
Bioinformatics	05	02
Computer Application	06	01
Total	**38**	**18**

SCHOOL OF SOCIAL SCIENCE

Chairperson: Dr. N.P. Singh, Former Member (Official), CACP, Ministry of Agriculture & Farmers Welfare, Govt. of India, New Delhi

Dr. N.P. Singh served as Member (Official) & Chairman, Commission for Agricultural Costs & Prices (CACP), Ministry of Agriculture & Farmers Welfare, New Delhi from October, 2020-January, 2025. He completed B.Sc. Agriculture (1991) from G.B Pant University of Agriculture and Technology, Pantnagar, India; M Sc. Agricultural Economics (1993) from NDRI, Karnal and Ph.D. in Agricultural Economics (1999) from ICAR-IARI, New Delhi. Dr. Singh also completed Post-Doctoral under CIMMYT Economics Program, Mexico (2001). Dr. Singh has more than 26 years' experience of working in various countries of Asia including China. He has expertise in Participatory Research and Adaptation Strategies to Climate Change, Price Policy, Agricultural Development, Futures Market, Impact Assessment, Priority Settings and Conservation Agriculture with a sound empirical knowledge. He has practical experience and knowledge of a wide range of agricultural systems, diversification and other agricultural development issues in Semi-Arid Tropics of South Asia, South East Asia and China. He has good theoretical and applied knowledge in various econometric techniques suiting to the policy framework. The experience of working with Asian NARS and knowledge of the intricate issues of socio-economic research critical for uplifting the livelihood of rural poor is a distinct edge. Dr. Singh has published 112 research articles (including 21 international) in various NAAS accredited journals, 37 research reports (including 12 international), 20 policy paper/working paper/ discussion paper (including 10 international); 2 books (Springer, CABi), 9 policy briefs, 27 popular articles/mass media articles, five technical bulletins, twelve book chapters and has two softwares to his credit.

AGRICULTURAL ECONOMICS

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Prof. Pramod Kumar

The Division has achieved excellence in post-graduate education and research as an ICAR-UNDP Centre of Excellence through a faculty exchange program for human resources development and strengthening of infrastructure facilities. Since 1995 it has been functioning as an ICAR Centre of Advanced Faculty Training (CAFT) to strengthen the capacity for agricultural economics and policy research in the national agricultural research system. 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 Division has maintained good academic liaison with other divisions at IARI and other national and international agricultural research institutions The research focus of the Division has been continuously reoriented to address contemporary development challenges. The significant research findings of postgraduate students are enlisted under the following themes.

Theme 1: Technology, Resource and Environment

Impact of climate change on rice based cropping systems: an analysis in the east coastal zone of Andhra Pradesh

The impact of climate change on the crop sector is a reality, and the manifestation is multifaceted. Climate change poses a significant threat to rice-based cropping patterns. The study attempted to investigate the climate change impact on rice cultivation in the eastern part of India, specifically, eight districts that represent three subzones viz., Godavari, Krishna, and North Coastal Zone of the east coastal belt of Andhra Pradesh. Here the occurrence of natural disasters is frequent, hence varying crop yield levels. The first objective used climate data to analyze the long-term (1960-2023) climatic trend and variability. The results from Mann Kendall and Sen's slope estimators revealed that there had been a significantly increasing trend of maximum temperature across all eight districts. The Pettitt test identified a significant seasonal climatic shift for the Northeast monsoon (NEM)/*rabi*season temperatures in the region after the mid-1990s. However, the late 1970s and early 1980s were identified as the shift years for the *kharif*season. The seasonal rainfall distribution around the climatic shift points confirmed that the climate change in the East Coastal Zone resulted in an increase in the Southwest monsoon (SWM) rainfall and a decline in NEM during the study period. The Just and Pope mean yield function provided a positive and significant impact of non-climacteric factors such as the irrigated area under paddy and the quantity of fertilizer used. Climatic factors, both maximum and minimum temperature impacts, were estimated to be having significantly negative effect on paddy yields. However, the rainfall showed a positive and significant relationship with the rice yields. Pre-structured survey schedules were used to accomplish the third and fourth objectives. One hundred eighty farmers were personally interviewed from three districts-East Godavari, Krishan and Srikakulam representing the three subzones. The livelihood vulnerability analysis using the weighted average and the LVI-IPCC methods revealed that Krishna and East Godavari are the most vulnerable, respectively. Adaptive capacity scores were lowest in the case of East Godavari, followed by Krishna and Srikakulam.Most rice growers agreed/ strongly agreed with a reduction in rainfall, increased occurrence of erratic and unseasonal rainfall, dip in night temperature, and increased daytime temperature. The major perceived impacts of changing climate by farmers are unavailability of quality irrigation emanating from excessive groundwater depletion, increased incidence of pests and diseases, uncertainty in yield levels, and thereby rising farm operational costs.

Climate change and food security of farm households: A case study of Kuttanad region of Kerala

Climate change, characterized by long-term alterations in the mean state of the climate, has been significantly influenced by human activities, leading to increased global temperatures and frequent extreme weather events. Kerala has recently experienced severe weather events, resulting in substantial loss of lives and property. Kuttanad region, known for its unique below-sea level farming is a vital rice-producing region and often referred to as the "rice bowl of Kerala,". However, farmers face recurrent flooding and climate change-related challenges. Therefore, this study was undertaken, to assess the long-term climatic trends and variability in Kerala; to examine farm household food security and its interaction with climate change vulnerability in the Kuttanad region; to evaluate the impact of major adaptation technologies on productivity, profitability, and food security; and to identify the socio-economic factors and constraints affecting the adoption of these adaptation technologies. Secondary data on temperature and rainfall was used for the study. The study revealed significant increase in maximum, minimum, and mean temperatures across all districts in Kerala, with the highest increase being observed in southern districts. Rainfall patterns indicated significant positive trends in July and September. The southwest monsoon, accounting for about 70% of Kerala's rainfall, showed a significant decreasing trend during the winter season. In the Kuttanad region which is spread between southern districts of Kerala, viz. Alappuzha, Kottayam, and Pathanamthitta recorded the highest magnitude of temperature increase. Most farm households in this region displayed medium levels of food security. Key factors influencing food security included access to credit, extension contact, off-farm income and farm assets. Technologies such as drum seeders (D), short-duration varieties (S), and eco-friendly pest and disease management (E) were identified as most preferred climate-smart adaptation technologies in the study area. The adoption of these technologies was higher among large farmers and was significantly influenced by variables such as age, education, farming experience, credit, extension contact, and landholding size. It is revealed that the adoption of a combination of three technologies led to a significant increase in yield (5.5 q/acre) and net farm income (Rs. 17,000/acre). It also ledtosignificant reduction in production costs compared to control, with ATT ranging ofRs. 683/q, and significantly improved food security (21%). Further, the most important constraint in adopting climate-smart adaptation technologies was the delayed disbursement of the paddy procurement price, and the knowledge about the technology. Thus it is suggested to enhance early warning systems and promote proven technologies like drum seeders and short-duration varieties through demonstrations and training. Further, addressing financial constraints through improved credit facilities and through efficient price disbursement system for the produce procured by state government.

Economic valuation of kole wetland agroecosystem in Kerala

Agricultural wetlands, also known as wetland agroecosystems, are managed wetlands where there is a balance between human use and the ecosystem's condition. Proper management practices, including appropriate water and agricultural practices in both wetlands and their surrounding areas, can lead to increased benefits for wetlands. However, it's essential to be aware that such management practices can also have significant impacts on the ecology and functioning of wetland ecosystems. The present study explored the economic value of ecosystem services in wetland agro-ecosystems located in developing countries, with a focus on the Kole Wetland agro-ecosystem situated in Kerala. The study determined the challenges and vulnerabilities of ecosystem services due to the interaction between wetlands and human activities. The Kole Wetlands located in Kerala spans in an area of 13,636 hectares. These wetlands are one of the rice granaries in Kerala. The meta-analysis revealed that in developing countries, wetland agroecosystems emerge as pivotal contributors to economic and social security, giving a substantial total economic value of US$ 46,162.75per hectare per year (2012 US$, PPP adjusted). The highest economic value was attributed to climate regulation (US$ 10160.55/ha/year), followed by disturbance regulation (US$ 9026.68/ha/year) and food production (US$ 7983.74/ha/year). Various methodologies, such as market price, replacement cost, and contingent valuation, were used to conduct a primary study of the economic valuation of ecosystem services in Kole Wetlands. The study found that the Kole Wetland agro-ecosystem generates a total economic value of ₹ 1,676.81 crores per year, and 84.89% of the value is currently non-marketed. Population growth & urbanization were identified as the factors affecting changes in the ecosystem services and disservices, followed by unscientific wetland management and climate change. The study employed the Driver-Pressures-State-Impacts-Responses (DPSIR) framework approach and observedthat the major drivers or threats to the Kole Wetland agroecosystem which includes population growth and urbanisation, agricultural intensification, land management and infrastructure, policies, and climate variability. Vulnerability assessments based on this framework revealed that the regulating services and supporting services were the most vulnerable. It is also observed that urbanisation& population growth and climate variability act as primary stressors. Across provisioning, regulating, supporting, and cultural services, the most vulnerable were water provision, flood regulation, habitat maintenance, and aesthetic value, respectively. Thus the need for targeted conservation and management strategies is emphasised.

A study on land use change and ecosystem services valuation in Maharashtra

Over the past decade, India has experienced dramatic land-use changes, including a decline in cropland, increases in forests and accelerated expansion of urban areas (Sajjad&Iqbal, 2012). Land use change is the primary force driving changes in agro-ecosystem service (Crossman et al., 2012). The valuation of ecosystem services helps in providing a solid platform for compensating the land managers for protecting, nurturing, and maintaining Ecosystem Services (ES). Maharashtra state has been witnessing massive losses of its agricultural land over the past decades. Hence, research on “A Study on Land Use Change and Ecosystem Services Valuation in Maharashtra” was undertaken with the following objectives: To examine the spatio-temporal changes of land use in India; To estimate the value of ecosystem services at various land use scenarios and explore the relationship between them in Maharashtra; and To analyse the stakeholder’s perspectives on land use change and willingness-to-pay (WTP) for preserving the agro-ecosystem in Maharashtra. The study used primary data of 240 farmers collected during Feb 2023. The Study also utilized multi-temporal remote sensing images to investigate urban growth, quantifying urban sprawl and agriculture areas over time and identifying agricultural land loss with remote sensing data. The results showed that areas under non-agricultural use increased by about 71 per cent during the last three decades in Maharashtra. GIS data analysis showed that 40 thousand ha of cropland had been converted to the built-up area between 2005 and 2020. The valuation of carbon sequestration and soil loss prevention ecosystem services revealed that net carbon stock Mg C ha-1 from cropland decreased from 59.35 to 40.72 during the study period, and the highest Net Carbon stock was found in tropical wet evergreen forests (409.50 Mg C ha-1). The soil loss prevented by cropland was 21.4 tons ha-1 year-1 during 2019-20. The economic value of carbon sequestration and soil loss prevention were 442 and 20 $ha-1year-1 respectively, during 2019-20. The panel data regression between ecosystem services and economic development variables showed a negative relationship between ecosystem service and per capita income. The results of the soil sample show that, on average, forest soil (69.10 Mg C ha-1) has the highest carbon stock (51.86 Mg C ha-1), followed by Conservative Agriculture (CA). The CA offers opportunities for increasing farmers' income by linking to carbon credit markets. Around 98 per cent of farmers showed a willingness to enroll in conservative agriculture. Single-bound contingent valuation analysis found a mean compensation of Rs.5,645 per ha is required for practicing conservative agriculture by the farmers. The consumers are willing to pay an extra Rs.10.45 per Kg of sustainably sourced rice. Thus, Strategic planning that avoids land use conflict by identifying areas for non-agricultural activities such as urban and industrial expansion and protecting prime agricultural land is necessary. The land use management strategies of agriculture and other non-agricultural land use have to be made by accounting for the value of ecosystem services.

A gender-based study on varietal adoption, trait preference and value addition by paddy farmers: A case of selected stress prone districts of Odisha

Rice (*Oryza sativa*) serves as a vital source of sustenance and income for millions of farming households. In Odisha, where rice occupies more than 75% of the gross cropped area under cereals, the adoption of improved and resilient rice cultivars remains limited despite numerous efforts to promote them. The gender-specific constraints and preferences play a significant role in determining the acceptance and success of improved rice varieties. Without addressing these differences, the potential of new technologies may not be fully realized. The study focused on three main objectives: to analyze the adoption of improved rice varieties and the factors influencing adoption, to assess gender-based differences in rice varietal trait preferences among farming households, and to examine the extent of value addition by farmers and its impact on income. The study used data collected from 880 farmers across three climate-vulnerable districts of Odisha—Bolangir, Ganjam, and Mayurbhanj—where both male and female paddy farmers were surveyed. The study revealed a general trend of non-adoption of improved rice varieties, particularly among female farmers, with male headed households showing a higher adoption rate. Adopters of improved varieties tend to have larger households, higher education levels, more land under cultivation, and greater annual incomes. Key determinants of adoption include caste, gender, education, operational land area, non-farm income, and asset ownership. The adoption of improved varieties is associated with only a marginal increase in income, however,asignificant increase in household income is observed through value addition (₹2306.53). Gender-specific preferences also show notable differences: women tend to prioritize traits related to stress tolerance, marketability, and culinary convenience, while men focus on economic returns. Both men and women, however, value high yield and good taste. Male participation in value addition activities is higher than female participation, further emphasizing a gender disparity in agricultural engagement. Overall, the adoption of improved rice varieties, driven by socio-economic factors and gender-specific preferences, results in modest income gains but has a significant positive impact on value addition activities.

Theme 2: Agricultural Markets and Value Chain

Economics of contract farming in India: A case of vegetable production in Karnataka

Contract farming ensures better prices for agricultural produce for farmers and high-quality raw materials for agro-based processing industries it also reduces crop production risk and lowers produce price volatility (Tripathi*et al*., 2005; Singh, 2000). It needs to be empirically evaluated whether contract farming is advantageous to small and resource-constrained farmers in increasing yield and income at the farm level.The study used primary data collected from 240 farmers, comprising 120 contract farmers and 120 non-contract farmers, utilizing a multistage sampling method and also with input from other stakeholders. The secondary data were compiled from the "Land and Livestock Holding of Households and Situation Assessment of Agricultural Households" NSS 77th Round, 2019(January 2019 – December 2019) and APEDA. It is estimated that a total of 4,53,688 agricultural households were involved in contract farming in India, with the highest number of households associated with contract farming were found in Punjab (25.77 %), followed by Uttar Pradesh (21.48%). In the study area of Karnataka two predominant contract farming models were identified: the centralized model and the intermediary model, focusing on specific crops like gherkin, baby corn, and jalapeno pepper. In cucumber and gherkin production in India, Karnataka stood out as the predominant producer contributing 1,11,606.88 metric tons of production with 49.02% share of overall production. The exports witnessed substantial growth during the study period 1987-2023 exhibiting a CAGR of 24.30% in quantity and 31.94% in value. The contract farmers of gherkins on average reported a higher Technology Adoption Index (TAI) of 84.07% as compared to non-contract farmers (65.78%). Financial returns underscored the economic advantages of gherkin cultivation with a B:Cratio of 1.56, surpassing both jalapeno (1.35) and baby corn (1.26). Comparing output and financial returns across gherkin grades, the low-grade farmers exhibited significantly higher yields at 69.04 qtl/acre. The data envelopment analysis (DEA) revealed superior technical efficiencies of contract farmers who scored on an average overall Technical Efficiency (TE) of 84.25%, surpassing that of non-contract farmers (76.39%). In Scale Efficiency the contract farmers scored an average of 89.93%, compared to 80.31% for non-contract farmers. The financial assessment of the firms reveled that they annually handled 10,375 MT of produce andgeneratedincome of Rs. 7,306.25 Lakh. The B:C ratio revealed was 1.39, and the net present worth (NPW) averaged at Rs. 2,444.48 Lakh, revealing the firm's profitability.

Potential impact of FTA between India and UK on Indian agriculture

International trade plays a crucial role in driving economic development, providing consumers with a variety of goods, enhancing firm efficiency, and fostering competition among local producers. Since India's 1991 economic reforms, trade agreements have been instrumental in promoting its global trade, particularly by reducing tariff barriers. India currently participates in 13 Regional Trade Agreements (RTAs), including those with Japan, South Korea, and ASEAN nations, all of which have seen significant export growth. The 2016 Brexit referendum presented India with an opportunity to negotiate a bilateral RTA with the UK, independent of the EU. This research study fills gap in understanding India-UK agricultural trade patterns post-Brexit. The study was taken up with three objectives: to analyze agricultural trade patterns using compound annual growth rate (CAGR); to assess trade intensity and competitiveness using the trade intensity index and symmetric revealed comparative advantage (SRCA); and to evaluate the impact of tariff liberalization using the SMART model. The trade data for the period 2004-2023 from ITC Trade Map, EXIM Bank, and UNCOMTRADE were used. The study showed that India's agricultural exports to the UK grew at a CAGR of 4.87%, primarily in cereals, rubber, coffee, tea, and marine products. The UK's exports to India, which is dominated by beverages, grew at 9.15%. While the UK had a higher trade intensity index from 2004-2008, India's index has since risen, signaling stronger bilateral ties. India exhibited a strong SRCA in products like meat, crustaceans, tea, and spices, while the UK showed a negative SRCA in most agricultural products except beverages. The tariff liberalization is projected to result in an 8% revenue loss for India and 6% for the UK, though India's export revenue may rise by 3.8%, compared to a 100% increase for the UK, largely due to India's higher initial tariffs. So, while negotiating with UK, India has to consider the adverse effects on tariff revenue, trade diversion from partner countries, and on domestic industries and Indian Farmers to mitigate the future implication of Free Trade Deal with UK .

India's trade policies on cereals: Economic assessment of its effects on export and welfare

In India, food production, which stood at 72 million tonnes in 1965-66, rose to 315.6 million tonnes in 2021-22. With the widespread introduction of modern varieties of wheat and rice, India transformed itself from a food deficit country and a net importer of food to a country that is not only self-sufficient but is also a major exporter of foodgrains. Export of Cereals in India averaged 4056.59 USD Million from 1996-2023, reaching all time high of 13857.95 USD Million in 2022. With improved food supply, the country has become self-sufficient. The demand for foodgrain has not increased with same speed, due to both a decline in share of food expenditure and diversification of diet towards non-cereal food items, which is to be expected with rising income levels. India continues to export the surplus and hence, became the largest exporter of rice in the world. India accounted for about 40 per cent of total rice exports (56 million tonnes) globally in calendar year 2022. Against this backdrop, the study assessed the impact of the existing trade policy with the **following objectives:** to analyse the growth and instability of supply and utilization components for major cereals; to measure the trade competitiveness and trade intensity of major cereals by destination of India; and to simulate the welfare effects of trade policies on rice and wheat. The study shows rice, wheat, and maize production in the sample period have increased at the compound annual growth rates (CAGR) of 1.92%, 2.29%, and 4.51%, respectively. The wheat and maize saw moderate expansion in acreage, with 1.19% and 1.97% respectively, rice area declined slightly at -0.14%. In terms of export performance, rice achieved an impressive expansion at 11.8%, followed by maize at 9.42% and wheat at 4.54%. Yield improvements were also observed during the study period, with rice, wheat, and maize yields increasing at 1.77%, 1.44%, and 2.54%, respectively. The trade intensity index for basmati rice shows that Saudi Arabia was India's major partner, followed by Iraq and Iran. In terms of comparative advantage, India consistently showed a strong RSCA in rice exports. For wheat, the RSCA showed considerable volatility, with values occasionally turning negative. Maize, on the other hand, showed a more stable RSCA compared to wheat, although it has also shown negative values in recent years. These results emphasize India's competitive strength in rice exports and the challenges the country faces in maintaining stable competitiveness in wheat and maize. The analysis of the welfare effects of the most recent trade policy measures for the most important cereals, such as the export ban and the export tax, was evaluated. The impact of the export ban on non-basmati rice and wheat shows that domestic prices can be reduced by 13% and 5% respectively as more commodities are available in the domestic market. The export tax on basmati rice increases export costs and reduces export demand by 9 per cent. This in turn increases domestic availability by 10 per cent and lowers the domestic price by 14 per cent.

Theme 3: Institutional Innovations and Rural Livelihood

Agricultural credit, indebtedness and farm income linkages in India

Access to credit plays a key role in improving the livelihoods of rural households that are majorly agriculture based. The study explored the access to institutional credit, its sources, Incidence of Indebtedness (IOI) and the role of institutional credit in improving the resource use efficiency, technology adoption and income of agricultural households in India. This study is based on the unit level data of "Land and Livestock Holdings of Households and Situation Assessment of Agricultural Households, 2019" NSS 77th Round Survey (Jan- Dec 2019). The results showed that more than 90 per cent of the agricultural households had access tobank. The coverage of Kisan Credit Card (KCC) was low at 19.12 %. About 50% of the Indian agricultural households were found to be indebted. The Extent of Indebtedness (EOI), measured as the average outstanding amount per agricultural household, was estimated at ₹74,121 at the all-India level. The IOI was highest in Andhra Pradesh (93%), Telangana (92%), Odisha (61%) and Rajasthan (60%) states. Andhra Pradesh also had the highest EOI (₹ 2,45,553) followed by Kerala (₹ 2,42,490) and Punjab (₹ 2,03,255) states, while, the lowest EOI was observed in the Jharkhand state (₹ 8,415). The access to institutional credit was higher in the western and southern regions, at around 34 %, compared to the Central (20.28 %), North-Eastern (22.16 %), Eastern (23.31 %) and Northern (23.89 %) regions. More than 60 per cent of the loans were accessed through institutional sources mainly Scheduled Commercial Banks (SCBs), Regional Rural Banks, cooperative societies and microfinance agencies such as Self Help Groups (SHGs) and bank linked Joint Liability Groups (JLGs). The role of SHGs/JLGs was higher in case of female headed households and those belonging to marginalized socio-economic groups. Non-institutional sources mainly professional and agricultural moneylenders, friends and relatives enabled consumption smoothing by meeting consumption credit needs of the households. Heckman probit model estimates showed a positive effect of age, membership of farmers' organization, land ownership, share of non-farm income, information and institutional credit facilities on institutional credit access. Households with access to institutional credit and KCC incurred higher level of input expenditure in paddy production. Stochastic frontier analysis showed the positive effect of institutional credit as well as access to KCC on the efficiency of paddy production. The application of Cragg's Double Hurdle model revealed positive effect of access to KCC on adoption of bio-fertilizers among the paddy farmers. The Multinomial Endogenous Regression Model (MESR) showed a positive impact of institutional credit on crop, livestock, total net income, consumption expenditure and expenditure on productive assets by the agricultural households. The study highlights positive impacts of agricultural credit on income, consumption and also on farm and non-farm investment of agricultural households. Creating opportunities in the non-farm sector, improved social networking, and information services would also increase households' access to institutional credit.

Economic evaluation of Kisan Credit Card scheme in Latur district of Maharashtra

Credit plays a pivotal role in the advancement of agriculture within India. The Kisan Credit Card scheme represents a significant initiative within the banking sector aimed at fostering agricultural credit and facilitating financial inclusion. This research was conducted with objectives: 1. To study the growth and performance Kisan Credit Card in India; 2.To analyse the impact of KCC on farm income; 3. To identify the determinants and constraints in the adoption of the KCC. The study utilized secondary data onKisan Credit Cards issued and the outstanding amounts was compiled from publications and websites of NABARD, RBI, and indiastat.com. Primary data were gathered from 180 farmers through personal interviews in the Latur district of Maharashtra, alongside insights from 30 key informants within the study region. The scheme has demonstrated positive growth in both the number of cards issued and the outstanding amounts. By the end of 2022-23, the scheme had issued 7.35 crore KCCs, with an annual growth rate of 11.73 per cent, and an outstanding credit amount reaching ₹8.86 lakh crore, indicating a robust CAGR of 21.72 per cent. Among the issuing agencies, Cooperative Banks have distributed the highest number of KCCs, followed by Commercial Banks and Regional Rural Banks (RRBs), with RRBs exhibiting the highest growth in credit issuance. State-wise analyses reveal significant variations, with Chhattisgarh, Assam, and Bihar leading in adoption and credit growth, while states like Orissa and Jharkhand show relatively slower yet steady progress. In Maharashtra, the scheme has demonstrated substantial growth across Cooperative Banks, RRBs, and Commercial Banks, with an overall CAGR of 12.85 per cent for card issuance and 22.11 per cent for the outstanding amount. KCC adoption positively impacts farm profitability, leading to higher yields, increased investment in productive areas, and improved net returns. In soybean cultivation and livestock farming, KCC beneficiaries show higher net income compared to non-beneficiaries, highlighting its role in financial stability and agricultural productivity. Key factors influencing farm income include labour, input costs, landholding, family size, and KCC adoption. The adoption of KCC is driven by education, proximity to banks, cooperative involvement, and farming experience. The barriers to KCC are insufficient loan amounts, delays in disbursement, complex documentation, and perceived bank bias. Addressing these constraints is essential for enhancing the scheme's reach and effectiveness, ultimately fostering greater financial inclusion and productivity within India's agricultural sector. The Cooperatives and RRBs are situated in close proximity to the farmers and should increase the issuance of KCC loans. The loan disbursement process could be streamlined to improve access to institutional credit. There is a need to increase the loan limits to correspond with the escalating costs associated with agricultural production. There exists scope for simplification of application procedures coupled with the introduction of a digital platform. The monitoring of KCC loan utilization for agricultural investments would optimize its efficacy in augmenting farm productivity and ensuring financial stability.

An analysis of electricity tariff policies for irrigation and its implications on groundwater use and irrigation cost in India

Groundwater has become the backbone of irrigation in India. Over the past four decades,India's reliance on ground water has surged, making the country the world's largest consumer of this resource. The study examined groundwater irrigation andenergy usagetrends using data from the Minor Irrigation Censuse and Land Use Statistics. Districts are categorized based on their stage of groundwater development. The state-wise electricity tariff rates for irrigation are documented. The study also employs the Mann-Kendall test and Sen's slope estimator to analyze groundwater level trends from 1996 to 2020.The study estimates the electricity subsidy given for agriculture and analyses its variation along states, crops, and farm size categories.The results reveala significant increase in India's irrigation coverage, from 19%of the netsown area in 1960- 61to 55% in 2021-22.The netirrigated area has grown by1.89%,while the number of wells has increased by 3.17%, highlighting the growing reliance on groundwater. Telangana, Punjab, and Andhra Pradesh show high well densities.The share of deep tubewells rose from 2% in 1993- 94 to17% in 2017- 18 indicating depleting groundwater levels. The analysis of groundwater extraction stages shows that many districts in Punjab (91%), Rajasthan (88%), Haryana(86%), and TamilNadu (61%) fall into the"non-safe"category. States with significant reliance on deep tubewell stend to face more acute groundwater depletion. A shift toward more powerful motors (6-12HP) has also been observed, suggesting that farmers are either extracting water from deeper levels or irrigating intensively. Agricultural electricity consumption has surged from 84,000 GWh in 2000-01 to 228,000 GWh in 2021-22, with Telangana,Punjab,Tamil Nadu, and Haryana consuming the most electrici typer hectare. States providing free electricity for agriculture, suchas Punjab and Haryana, have experienced the steepest declines in groundwater levels, as shown by the Mann-Kendall and Sen's slope analyses.Haryana's groundwater levels are declining by 0.468m/year, while Punjab seesa drop of 0.499m/year, far steeper than in states with higher electricity tariffs like Kerala and Maharashtra. There exist regional disparities in electricity subsidies, with Punjab, Haryana, and Karnataka farmers getting the highest subsidy. In Punjab and Haryana, maximum subsidy is given for paddy crops. Small and marginal farmers receive more subsidy per hectare as compared to large farmers.The price elasticity of irrigation is estimated at-0.262 for Punjab and-0.363 for Haryana, indicating that while irrigation demand is relatively in elastic, Haryana farmers are more responsive to tariff changes than Punjab.This is large lydue to Punjab'sheavydependence on paddy cultivation, which offers limited opportunities for crop diversification. The study recommends the adoption of energy-efficient irrigation technologies, such as drip and sprinkler systems, to reduce groundwater use and electricity consumption.The key policy recommendation is for states likePunjab and Haryana, which offer free or heavily subsidized electricity to incentivizing sustainable irrigation practices.

Impact assessment of SaaS based startups on price realisation by Indian farmers

Agriculture in India has evolved significantly, moving beyond essential food grain cultivation to achieve self-sufficiency and reduce import dependency. While earlier initiatives were effective, the current challenge lies in ensuring that plans focus on elements that empower farmers with cost-effective solutions for future growth. Startups have introduced innovative solutions and disruptive technologies to the agricultural sector, transforming traditional farming practices. These enterprises bridge gaps between producers and consumers while addressing supply chain inefficiencies. The adoption of new agricultural technologies has improved the economic welfare of farming communities, benefitting all income groups without disadvantaging any. Software as a Service (SaaS) in agriculture addresses growing demands for agri-products while tackling critical concerns like resource depletion, environmental damage, carbon emissions, and water wastage. SaaS enables sustainable farming, efficient supply chains, and transparent food systems, with significant implications for price realization by Indian farmers. The impact of SaaS extends across crop farming, livestock management, and other domains, reshaping the agricultural landscape. The benefits and challenges of adopting SaaS-based platforms for farmers and startups warrant detailed assessment, alongside the need to quantify these platforms' impact on farmer earnings. This study aims to overview SaaS-based agricultural startups globally and in India, assess user challenges and benefits, and evaluate the impact on price realization. Data collected via interviews and Traxcn technologies analyzed using NVIVO 15 and DID methodology reveals that the USA leads globally in SaaS agriculture, while Karnataka is a frontrunner in India. Farmers using these platforms earned Rs 1.8/kg more than mandi prices, benefiting from better rates, technical support, and quicker payments. Challenges include delayed procurement, quality concerns, and high onboarding costs. Nevertheless, SaaS startups foster competitive pricing, market access, and support services, driving positive transformation.

List of students and Chairpersons of their advisory committee

S. No.	Name of student & roll no	Degree	Title of thesis	Chairperson	Institute
1.	Harshit Gupta (21833)	M.Sc.	Potential Impact of free trade agreement between India and UK on Indian agriculture	Dr. Shiv Kumar	ICAR-IARI, New Delhi
2.	Athulya S. (21834)	M.Sc.	A gender-based study on varietal adoption, trait preference and value addition by paddy farmers: A case of selected stress prone districts of Odisha	Dr. Praveen K.V.	ICAR-IARI, New Delhi
3.	Sagar Umesh Kolkur (21835)	M.Sc.	Impact analysis of SaaS based startups on price realization by Indian farmers	Dr. Akriti Sharma	ICAR-IARI, New Delhi
4.	Anukriti Raj (21836)	M.Sc.	An analysis of electricity tariff policies for irrigation and its implications on groundwater use and irrigation cost in India	Dr. Shivendra Kumar Srivastava	ICAR-IARI, New Delhi
5.	Vishwanath (21837)	M.Sc.	Economic evaluation of Kisan Credit Card scheme in Latur district of Maharashtra	Dr. P. Anbukkani	ICAR-IARI, New Delhi
6.	Neha Sannyasi (21838)	M.Sc.	India's trade policies on cereals: Economic assessment of its effects on export and welfare	Dr. Kingsly Immanuelraj	ICAR-IARI, New Delhi
7.	Pavithra Srinivasamurthy (11388)	Ph.D.	Agricultural credit, indebtedness and farm income linkages in India	Dr. Alka Singh	ICAR-IARI, New Delhi
8.	Jobin Sebastian (10732)	Ph.D.	Impact of climate change on rice based cropping systems: an analysis in the east coastal zone of Andhra Pradesh	Dr. Pramod Kumar	ICAR-IARI, New Delhi
9.	Omprakash Naik N. (11385)	Ph.D.	A study on land use change and ecosystem services valuation in Maharashtra	Dr. Dharam Raj Singh	ICAR-IARI, New Delhi

10.	Geetha M.L. (11381)	Ph.D.	Economics of contract farming in India: A case of vegetable production in Karnataka	Dr. Dharam Raj Singh	ICAR-IARI, New Delhi
11.	Ajmal S. (11669)	Ph.D.	Economic valuation of kole wetland agro-ecosystem in Kerala	Dr. Dharam Raj Singh	ICAR-IARI, New Delhi
12.	Jamaludheen A. (10940)	Ph.D.	Climate change and food security of farm households: A case study of Kuttanad region of Kerala	Dr. Nalini Ranjan Kumar	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 mandated activities 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. The post graduate research findings have been grouped under various themes.

Theme 1: Assessment of Government Centric Programmes, Schemes and Practices

An analytical study of self-help groups under *Deendayal Antyodaya Yojana*-national rural livelihood mission in Andhra Pradesh

SHGs play a crucial role under DAY-NRLM in bringing financial inclusion, empowering women and promoting socio-economic development. A study was conducted in Kurnool, East Godavari, NTR and Vishakhapatnam districts of Andhra Pradesh state. The data were collected from 150 randomly selected respondents, comprising 60 members of SHGs, 60 non-SHG members and 30 officials. Ex-post facto and exploratory research designs were applied. Seventeen independent variables along with two dependent variables *viz*., financial inclusion and livelihood security were studied. Indices were developed to measure financial inclusion and livelihood security of members. SHG members showed better financial inclusion and livelihood security when compared with non-SHG members. Overall financial inclusion index for SHG members is 0.742 and for non-SHG members it is 0.375. Overall livelihood security index for SHG and non-SHG members is 0.811 and 0.446, respectively. Independent t-test was conducted to test the difference of two group means and t-value is 17.921 and 18.950, respectively for financial inclusion and livelihood security, and it is significant at 0.001 level. The predictors explain 85.5 percent and 85.4 percent of variance in the financial inclusion and livelihood security, respectively. The members of SHG have moderate (66.7%) to high (33.3%) financial inclusion, while members of non-SHGs have low (46.7%) to moderate (53.3%) financial inclusion. The members of SHG have moderate (61.7%) to high (38.3%) livelihood security, while members of non-SHGs have low (45%) to moderate (55%) livelihood security. Annual income, social participation and consumption expenditure contributed significantly to both financial inclusion and livelihood security. While distance to bank and educational qualification, contributed significantly to financial inclusion only. Major problems perceived are untimely loan repayment, insufficient savings and inadequate credit. AHP tool prioritized the strategies and top three being designing flexible repayment schedules, promote social inclusion and empowerment among SHG members¸ linking SHGs with banks.

Effectiveness of micro irrigation under *Pradhan Mantri Krishi Sinchayee Yojana* (PMKSY) in rained areas of Rayalaseema region in Andhra Pradesh

The study assessed the effectiveness of micro-irrigation under the *Pradhan Mantri Krishi Sinchayee Yojana* (PMKSY) in the rainfed areas of Rayalaseema, Andhra Pradesh. The focus was on farmers access to information, knowledge levels, adoption factors, and constraints faced by beneficiaries. A descriptive and exploratory research design was employed. The study was conducted in the semi-arid, drought-prone Rayalaseema region, specifically in Anantapuramu and YSR Kadapa districts, which have the highest micro-irrigation area coverage. Two blocks from each district, BukkarayaSamudram and Singanamala in Anantapuramu, and Veerapunayuni Pally and Proddatur in YSR Kadapa, were selected. From each block, two villages were randomly chosen, with 30 respondents (15 beneficiaries and 15 non-beneficiaries) per village, total 240 respondents. Results showed that both beneficiaries and non-beneficiaries had medium access to information and a medium level of knowledge about micro-irrigation. The benefit-cost ratio of crops like groundnut, tomato, and banana under micro-irrigation was significantly higher compared to conventional methods. Farmers reported greater satisfaction with micro-irrigation, with mean scores of 23.31 compared to 18.76 for conventional methods. Multiple regression analysis revealed that 69% of the variance in micro-irrigation adoption was explained by independent variables ($R^2 = 0.69$). Garrett's ranking analysis identified major constraints, including damage to irrigation lines (technical), low-quality materials (infrastructural), high installation costs (financial), lack of expert contact (institutional), and unsuitability in saline water areas (climatic).The study concluded that while micro-irrigation under PMKSY offers significant economic and satisfaction benefits, addressing key constraints can enhance its adoption and effectiveness.

Theme 2: Nutrition and Health

A study on consumer behaviour towards bio fortified products and their willingness to pay

Biofortified foods, enriched to enhance nutritional content, are gaining popularity for their health benefits. This study examines consumer behaviour toward biofortified products, focusing on awareness, perception, willingness to pay (WTP), and adoption barriers. In New Delhi, 240 respondents were selected through simple random sampling from five districts. The survey revealed that 45% had moderate awareness of biofortified foods, 28% had low awareness, and 27% were well-informed. Urban respondents exhibited the highest awareness of biofortification techniques, despite lingering misconceptions about nutrient addition. Perceptions, measured using a validated scale, reflected generally positive but mixed views on availability, accessibility, and affordability. Urban respondents showed the most favourable perceptions, while semi-urban respondents were less optimistic. Education and income significantly influenced purchase intentions, with health benefits and marketing playing key roles. Using the Double Contingent Valuation Method, the study found that 88.75% of respondents were willing to pay for biofortified products, with many willing to pay a premium, although price sensitivity was evident.

Principal Component Analysis (PCA) identified enhanced nutrition, health benefits, branding, and affordability as primary drivers of consumption, explaining 66.24% of the variance across 17 indicators. Binary logistic regression revealed that education, income, food expenditure, and family type positively impacted WTP, while gender had a minor negative effect. Constraints ranked through the Garrett Ranking Method highlighted economic and cognitive barriers as the most critical, directly affecting consumers' ability to purchase and consider biofortified foods. Market and policy barriers also influenced product availability and adoption. Strategies ranked via the Rank-Based Quotient (RBQ) method showed consumer education programs as the most preferred approach. The study concludes that addressing barriers through education, marketing strategies, and supportive policies is essential to boosting consumer acceptance and market penetration of biofortified foods.

Nudging healthy food choices among students: A choice architecture study

This study underscores the pivotal role universities play in shaping students behavior, focusing on the effectiveness of nudging—a concept rooted in behavioral economics in promoting healthier dietary decisions. It seeks to address key questions, including: current research trends in healthy food choices, the impact of nudging interventions, their effectiveness, and the factors influencing students food decisions. Adopting quasi-experimental and exploratory research designs, the study examined two university cafeterias in New Delhi, India, which cater to a significant segment of the student population. The findings offered a detailed profile of respondents, capturing demographic characteristics, dietary preferences, and key information sources shaping food choices. Global research trends revealed that United States as a leader in studies on healthy food behavior. Through a systematic review process, 738 records were rigorously evaluated, with 24 publications meeting the eligibility criteria. Nudging strategies were analyzed using Sunstein's classification system, shedding light on various approaches, their efficacy, and areas needing further exploration. A quasi-experimental component evaluated the impact of nudging on students' selection of millet-based products, yielding significant results that affirm the strategy effectiveness. It identified ten critical factors influencing food decisions with health, mood and social dynamics emerging as the most significant. The study results emphasized the importance of prioritizing health and mood within university settings and advocates for collaborative efforts among stakeholders to create environment that encourage healthy eating habits. Empirical evidence from the study supported nudging as a valuable tool for promoting healthier behaviors, particularly in university cafeteria contexts, while also highlighting the need for further research to address existing gaps and enhance the strategy's applicability.

A comparative study of conventional and organic farming in Telangana State

India is the country with the highest number of organic farmers and 6th in terms of World's Organic Agricultural land. Organic farming is picking up the steam and the government is also at the forefront in promoting it. The certified organic farming area increased by over 1.5 times in ten years, reaching 5550405 ha in 2011–12. The nation has significantly increased its share of organic commodity exports. India exported organic goods worth about 771.96 million dollars during the 2022 fiscal year. The realized value of organic food exports was approximately INR 5249.32 crore, or 771.96 million USD. The performance of Telangana state is even poorer as its total area under organic certification is also very less. Therefore, it is important to figure out the reasons such as factors behind adoption. It is also essential to assess the knowledge level and perception of farmers on organic farming and the constraints faced by them and suggest strategies to address them. For the present study, Telangana was purposively selected and two districts namely Warangal and Sangareddy were selected purposively based on the concentration of conventional and organic farmers respectively. Two blocks from each district were randomly selected. Two villages from each district were selected randomly and fifteen respondents from each village were randomly selected making the total sample size as 120 respondents. Majority of the respondents had medium level of knowledge on organic farming. Socio-economic factors such as allied agricultural activities, farmer group membership, and annual income, psychological factors such as innovativeness were major influencing factors in adoption of organic farming. The study gives an insight into the constraints faced by the farmers which could be used as a framework for developing training progammes for farmers and will also prove useful for policy makers.

Theme 3: Entrepreneurship Development

Professional competencies of agripreneurs in Madhya Pradesh: An exploratory study

Agri-entrepreneurship holds immense significance in India's agrarian economy by fostering innovation, economic independence, and entrepreneurial competence within rural communities. A detailed analysis of socio-economic and psychological profiles of selected agripreneurs reveals key insights. A considerable portion of agripreneurs (37.5%) were under 35 years old, with substantial educational qualifications (37.5%) having bachelor's degrees or higher. Caste-wise, the general category dominated (41.7%), and joint families formed the majority (73.3%). Most agripreneurs (43.89%) had less than four years of experience, with many benefiting from training programs. Their primary motivation comes from fellow agripreneurs (41.67%), followed by family (26.11%) and friends (21.22%). However, access to credit remained low for most (51.66%), and only 10.84% had received recognition or awards. Professional competencies in terms of managerial, executive, and collaborative were evaluated. Managerial competencies were notably strong (43.33%), especially among livestock and poultry entrepreneurs. Executive competencies were highest in horticulture, while fisheries excelled in collaborative skills. Key constraints included over-reliance on local money lenders, profit reductions due to competition, labour shortages, outdated technology, inadequate government support, and limited infrastructure. Marketing challenges, such as high retailer margins and a lack of marketing skills, further hindered growth. To enhance professional competencies, five data-driven strategies were recommended. Agripreneur conferences and fairs were the most effective, offering networking and knowledge-sharing opportunities. Market linkages and value chain integration ranked second, improving market access and competitiveness. Industry expert workshops ranked third, providing tailored learning experiences. Awareness of government schemes, ranked fourth, ensuring access to available support. Financial literacy programs empowering agripreneurs with critical financial management skills was ranked fifth. The research offers an empirically grounded understanding of agripreneurs in Madhya Pradesh, shedding light on their backgrounds, challenges, and pathways for growth. It provides practical insights for policymakers, researchers, and stakeholders aiming to bolster agripreneurship in the region.

A study on entrepreneurship development training in Kerala

This study assesses the effectiveness of entrepreneurship development training programmes in three selected institutions in Kerala: CPCRI-KVK, KAU-ABI, and RSETI. The primary objectives were to analyse the various training methods, evaluate their effectiveness, and identify constraints faced by trainees in setting up successful enterprises. Data were collected from 120 respondents using structured interviews. Findings reveal that CPCRI-KVK was the most successful, with 52.5% of respondents reporting high levels of training outcomes, suggesting a well-structured curriculum and effective support systems. KAU-ABI showed moderate success, indicating potential for improvement, particularly in applying training methods. Conversely, RSETI had the lowest effectiveness, with half of the respondents reporting poor outcomes, underscoring the need for a thorough re-examination of its training approach and follow-up support. The most frequently used method of instruction was the lecture format, with trainees rating demonstrations and experiential learning as the most relevant and comprehensible methods due to their hands-on experience and practical application of concepts. In contrast, simulations were perceived as the most complex, likely due to the technological and abstract nature of the exercises. Significant barriers to entrepreneurship included financial constraints, limited access to formal credit, high input costs, technical challenges, and marketing difficulties. Socio-cultural factors, including societal norms and family expectations, posed significant challenges, particularly for women and marginalized groups. The study concludes that addressing these issues by enhancing practical training elements, offering sustained post-training support, and alleviating financial constraints through better access to credit and financial incentives could significantly improve the success rates of entrepreneurship training programmes in Kerala, providing crucial insights for policymakers and training institutions to refine their approaches and foster a more conducive environment for entrepreneurial growth in the region.

A study on institutional interventions for agri-entrepreneurship development

Dalwai Committee advocates for agri-entrepreneurship promotion to enhance farmers' economic sustainability and drive innovation. The study was conducted with specific objectives including the analysis of entrepreneurship promoting institutions, assessment of extent of support and its effect, identifying factors for effective intervention, and exploring constraints and suggestions for promotion. Sixteen institutions were selected from Telangana and Rajasthan states, chosen purposively with a total of 200 entrepreneurs and 43 professionals as the respondents. Among the institutions majorly (56.25 %) affiliated with academic or research institutions, mostly emphasizing entrepreneurship development (50%) 56.25% operating on a national coverage. Various institutions offer support services catering to the diverse needs of agri-entrepreneurs, with a significant focus on women (93.75 %) and youth (62.5 %). There was a unanimous and robust emphasis on training & workshops with experts, certification support (68%), business and financial model development (56.25 %), indicating a recognition of the pivotal role played by sound business models. An analysis of institutional support using the Institutional Support for Agripreneurship Development Scale (ISAD-S) revealed satisfactory support in production and marketing (Rank-1) and technical (Rank-2) dimensions, albeit with room for improvement in legal and bureaucratic (Rank-3) and financial (Rank-4) dimension. An Index for Perceived Effect of Institutional Support for Agripreneurs (I-PEISA) was constructed to measure effectiveness of institutional interventions. Varying impacts across different dimensions viz. natural, physical, human, financial and social capitals for different categories of entrepreneurs *viz*., farm based, off farm and service/tech entrepreneurs were noticed. Support for project formulation, vocation-oriented syllabi, long term strategic involvement, Training Institute-Industry-Market-Entrepreneur (T-I-M-E) connect were emphasized. Lack of priority lending, delays and bias in grants, and a lack of prototype testing facilities were reported. Transparent evaluation processes, initiatives to attract venture capitalists, enhancing financial support post programme, streamlining administrative processes, and fostering an entrepreneurial culture among farmers were recommended.

Theme 4: Innovations in Extension Systems

A study of social networks and stakeholders in farmer producer organizations

An effective strategy to overcome the many challenges faced by small and marginal farmers is the formation of Farmer Producer Organizations (FPOs). A study of the information networks, stakeholders, and comparative performance of FPOs would help better understand the stakeholders and information networks of the farmers in FPOs. In this context, a comprehensive study on ten FPOs and 240 members was carried out in Maharashtra and Madhya Pradesh states of India. Social Network Analysis (SNA) was used to map the information network of farmers for the quantitative analysis while stakeholder analysis was used to map and rank the stakeholders of

FPOs. FPO officials were major actors of information for members of FPO while input dealers were important actors for non-members of FPO. The farmers were the most important stakeholders with first rank in the AHP priority ranking. Farmers, BOD, government institutes, input suppliers, official staff, and NGOs were classified in the key players category. Customers and traders were classified in the subject category. The funding agencies were identified as a context stakeholder and the processors were classified in the crowd's category by their level of interest and influence in stakeholder analysis. In high- performing FPOs, the area under high-value crops was more, scalability was greater, had their own brand and infrastructure were better, compared to low-performing FPOs. The study suggests that FPOs need to enhance their network of farmers and connections with stakeholders. Emphasis needs to be given to providing more training and capacity building for FPO officials in new technology and innovation. There is a need to integrate input suppliers into the extension and advisory system through new extension models or programs. The low performance of FPOs can be addressed by enhancing value-addition facilities, creating their own brand, increasing the cultivation of high-value crops, and improving marketing infrastructure.

Theme 5: Training and Education

An assessment of training needs and their determinants in communication skills among postgraduate students in Agricultural Universities

In a rapidly changing professional environment, agricultural graduates are expected to possess not only technical knowledge but also strong communication abilities. However, the current academic curriculum at agricultural universities often emphasizes scientific and technical aspects, while communication skills receive limited attention. The study investigates specific communication skill gaps among postgraduate students, the factors that influence skill development, and the constraints they face in acquiring these skills. The present study has adopted an exploratory and descriptive research design under which primary data was collected from 210 postgraduate students and 30 teachers across three prominent agricultural universities in India: ICAR-Indian Agricultural Research Institute (IARI) New Delhi, G.B. Pant University of Agriculture and Technology (GBPUAT) Pantnagar, and Banaras Hindu University (BHU) Varanasi. The determinants were studied under three dimensions, which include socio-personal, psychological, and institutional factors. The study found that academic performance, academic motivation, achievement motivation, empathy, self-esteem, financial support, self-confidence had significant negative correlation while Communication apprehension had significant positive correlation. The Borich Need Assessment Model was used to identify skill gaps, Garrett ranking was applied to analyze constraints, and regression analysis helped explore the relationship between communication skill development and influencing factors. The findings revealed significant communication skill gaps across five key areas: non-verbal communication, speaking, writing, listening, and reading. GBPUAT students had the highest training needs, while IARI students exhibited relatively lower gaps. Socio-personal, psychological, and institutional factors were found to influence skill development. Major constraints included heavy academic workloads, lack of systematic training programs, and limited exposure to diverse communication contexts. Based on these findings, the study recommends tailored training programs to bridge these gaps and enhance employability. Overall, the study has assessed the specific training needs for communication skills and provided an actionable insight to improve their employability and professional success.

Assessment of teaching effectiveness and it's determinants in the agricultural education system

Teaching effectiveness plays a pivotal role in shaping students' academic and professional development in agricultural education. This study evaluates the effectiveness of teaching at the postgraduate level in agricultural education across three prominent universities: ICAR-Indian Agricultural Research Institute (IARI) New Delhi, G.B. Pant University of Agriculture and Technology (GBPUAT) Pantnagar, and Banaras Hindu University (BHU) Varanasi. A comprehensive Teaching Effectiveness Index was developed based on three dimensions— Pedagogical Proficiency, Learning Engagement, and Educational Environment Dynamics— further divided into 75 sub-indicators. Principal Component Analysis (PCA) was employed to calculate the weightage of these sub-indicators, while constraints were ranked using the Analytic Hierarchy Process (AHP). The results showed IARI with the highest score of 0.74, indicating strong teaching effectiveness, followed by GBPUAT and BHU, both with scores of 0.71. The study also identified and analyzed the various factors that influence the effectiveness of teaching and learning processes using correlation and regression analysis. The study identified a positive correlation between teaching effectiveness and various psychological, professional, and institutional factors, highlighting the significance of factors like self-confidence, achievement motivation, verbal immediacy, non-verbal immediacy, instructional skills and classroom interaction in enhancing teaching quality. Institutional variables like the quality of teaching staff, facilities and infrastructure, financial support, and technology integration further underscored the importance of institutional support. The study also explored key constraints affecting teaching effectiveness, such as research-related challenges, limited exposure to technology, and insufficient software guidance. Based on student feedback, strategies to improve teaching effectiveness were ranked using the Garrett method. The top suggestions included incorporating software learning into the curriculum, encouraging interactive teaching sessions, and establishing industry partnerships for hands-on experience. The findings of the study provide valuable insights for policy development, curriculum improvement, and teaching strategies in agricultural education, with the aim of enhancing effectiveness of teaching-learning environment with respect to agricultural education.

Theme: 6. Contemporary Issues

A study on adaptive capacity and livelihood security of farmers in flood prone areas of Kerala

India, characterized by its diverse geo-climatic and topographical conditions, is highly vulnerable to natural disasters, particularly floods. With approximately 40 million hectares of land at risk of flooding, the country ranks seventh on the global Climate Risk Index, experiencing significant disaster-related fatalities and economic damage. Kerala, a southern state in India, has witnessed a troubling increase in flood frequency and intensity due to extreme rainfall, inadequate land-use practices, and poor water and forest management. The floods of 2018, 2019, 2020, and 2021 illustrate the escalating climate risks that have severely impacted local farming communities. In response to these escalating challenges, a research study was conducted in Kerala to evaluate the adaptive capacity and livelihood security of flood-affected farmers. Using an ex post facto research design, data were collected from 120 flood-affected farmers selected through simple random sampling. This study specifically focuses on the Alappuzha and Thrissur districts in Kerala. The research assessed adaptive capacity through dimensions of awareness, ability, and action. Findings reveal significant differences between the districts, with Alappuzha showing higher levels of awareness and Thrissur demonstrating greater ability. Overall, the majority of respondents exhibited a medium level of adaptive capacity. Adaptation strategies primarily include crop diversification and home-based measures such as food grain storage and constructing two-story houses. The study also evaluated livelihood security using indices of food, economic, health, educational, social, institutional, and infrastructural security, revealing medium levels of overall livelihood security among respondents with high social security and low economic security. Constraints hindering effective adaptation were categorized into technical, institutional, economic, infrastructural, and socio-cultural. Major issues identified include inadequate training, poor early warning systems, limited financial resources, and entrenched traditional beliefs. The study underscores the urgent need for enhanced adaptive capacity and proactive measures to mitigate climate change impacts and protect agricultural livelihoods in Kerala.

Rural women leadership in climate change adaptation and sustainable livelihood

Despite a higher workforce participation rate compared to urban women, rural women face significant challenges, including financial instability, poor socioeconomic conditions, unemployment, and climate variability. The gendered impacts of climate change are severe, with women being more vulnerable due to their higher poverty rates and dependence on threatened natural resources. The study aimed to seek insights into the climate change related vulnerabilities of rural women and their adaptation behaviours was conducted on 200 women farmers, with 100 linked to formal leadership groups (SHGs) and 100 without such influence in Uttarakhand, utilizing correlational design and qualitative methods. An index was developed from the dimensions of Exposure, Sensitivity, and Adaptive Capacity. SHG members (LVI = 0.355) were less vulnerable compared to non-members (LVI = 0.439), highlighting a greater risk among non-member women. To document Indigenous Technical Knowledge (ITK) related to climate adaptation, primary and secondary data, focus group discussions, and validation through the QuIK method were used. ITK practices such as water conservation and pest management were found significant and could be scaled up after further validation. Adaptation behaviour was analyzed using an extended Theory of Planned Behaviour (TPB) framework. Constructs such as risk perception, social network, and self-efficacy were assessed. Leadership competencies among rural women were evaluated through a scale that included variables like influencing, managing, and decision-making. Significant differences were found between SHG members and non-members, with higher competencies in SHG members (mean = 17.316.5) compared to non-members (mean = 9.49.8). The study underscored the importance of gender sensitive policies and strategies to address vulnerabilities and enhance adaptation. It also provided recommendations for promoting rural women's leadership. The findings are relevant to planners, policymakers, scientists, and extension workers for developing technological interventions and policies aimed at improving rural livelihoods and fostering climate resilience.

List of the students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Devanand Tripathi (21582)	M.Sc.	Professional competencies of agripreneurs in Madhya Pradesh: An exploratory study	Dr. J.R. Mishra	ICAR-IARI, New Delhi
2.	Suresh Kumar Bishnoi (21839)	M.Sc.	A study of social networks and stakeholders in farmer producer organizations	Dr. Vinayak Nikam	ICAR-IARI, New Delhi
3.	Fathimath Shibla K. (21840)	M.Sc.	A study on adaptive capacity and livelihood security of farmers in flood prone areas of Kerala	Dr. Sukanya Barua	ICAR-IARI, New Delhi
4.	Krishan K. (21841)	M.Sc.	A study on consumer behaviour towards bio fortified products and their willingness to pay	Dr. Satyapriya	ICAR-IARI, New Delhi
5.	Sreenanda S. Ananda (21842)	M.Sc.	Assessment of teaching effectiveness and it's determinants in the agricultural education system	Dr. Girijesh Mahra	ICAR-IARI, New Delhi

6.	Yogesh B.M. (21843)	M.Sc.	An assessment of training needs and their determinants in communication skills among postgraduate students in Agricultural Universities	Dr. Girijesh Mahra	ICAR-IARI, New Delhi
7.	Swetha Bandewal (21844)	M.Sc.	A comparative study of conventional and organic farming in Telangana State	Dr. Sukanaya Barua	ICAR-IARI, New Delhi
8.	Sakaray Vaishnavi (21845)	M.Sc.	An analytical study of self-help groups under Deendayal Antyodaya Yojana-National Rural Livelihood Mission in Andhra Pradesh	Dr. V. Lenin	ICAR-IARI, New Delhi
9	Bhukya Karthik (21846)	M.Sc.	Effectiveness of micro irrigation under Pradhan Mantri Krishi Sinchayee Yojana (PMKSY) in rained areas of Rayalaseema region in Andhra Pradesh	Dr. J.R. Mishra	ICAR-IARI, New Delhi
10	Sulthana Parveen (21953)	M.Sc.	A study on entrepreneurship development training in Kerala	Dr. J.R. Mishra	ICAR-IARI, New Delhi
11	Simran Pundir (21969)	M.Sc.	Rural women leadership in climate change adaptation and sustainable livelihood	Dr. R. N. Padaria	ICAR-IARI, New Delhi
12.	Sujay Basappa Kademani (11426)	Ph.D.	A study on institutional interventions for agri-entrepreneurship development	Prof. Manjeet Singh Nain	ICAR-IARI, New Delhi
13.	Juhee Agrawal (11427)	Ph.D.	Nudging healthy food choices among students: A choice architecture study	Dr. V Sangeetha	ICAR-IARI, New Delhi

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 (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: Design of Experiments

A study on efficient equivalent-estimation split-plot designs through algorithmic intervention

Agricultural, post-harvest, processing, engineering and industrial experiments often involved hardto-change factors which are expensive or time consuming in terms of level change. These factors restrict the use of complete randomization. One solution for these situations is the use of minimally changed factorial run orders. Although minimally changed factorial run orders are being extensively studied in different literature, analytical procedure based on these run orders remains a concern. Alternatively, one can use split plot designs which reduces the number of independent settings of the hard-to-change factors by allocating them to whole plots or main plots and the easyto-change factors to subplots. In general model estimation of split plot designs requires the use of generalized least squares (GLS). However, for some split-plot designs ordinary least squares (OLS) estimates are equivalent to generalized least squares (GLS) estimates. These types of designs are known as equivalent-estimation split-plot designs in literature. As the designs involve hard-to change factors, therefore the design run orders may be influenced by trend effects due to lack of randomization. In the present investigation, search algorithm has been developed to obtain balanced incomplete equivalent-estimation split-plot designs for different experimental setups as computer intensive algorithms can widen the search domain with modern age computational platform. The algorithm developed in the present investigation performs efficiently in terms of computational time. To obtain the best designs, the D-optimality aspects have also been investigated and a good number of D-optimal designs have been obtained for different experimental setups. Besides, the performances of the designs obtained under the present investigation have been evaluated in the presence of trend effects through the calculation of trend factors. Further optimal designs have also been obtained in the presence of trend effects for different experimental setup. The algorithm for the present investigation has been implemented by writing programmes using R software.

Orthogonal and sliced Latin hypercube designs for computer experiments in agriculture

Latin hypercube designs (LHDs) are widely used in developing complex computer models. While orthogonal LHDs offer the benefit of independent factor estimation, they are often constrained by the number of runs or factors. To overcome this limitation, a general method has been developed for generating nearly orthogonal LHDs, addressing existing research gaps and comparing to five alternative methods. When dealing with multiple computer models for collective evaluation, traditional LHDs are insufficient. Sliced Latin hypercube designs (SLHDs), a special class of LHDs, address this limitation by dividing the design into slices or smaller batches of LHDs. The sizes of these slices, which can either be equal or unequal, are crucial in experiments. Recognizing the need for SLHDs with varying batch sizes, a simple method has been proposed to obtain such designs, along with a catalogue to serve as a quick reference. In experiments requiring the orthogonal property for independent factor effect estimation, Sliced Orthogonal Latin Hypercube Designs (SOLHDs) become critical. These designs, especially with unequal run sizes, are valuable in situations where models vary in importance or accuracy. The research introduces two methods for generating SOLHDs with four and five slices, addressing gaps in the existing literature and paving the way for flexible designs with variable slices, runs, and factors. To simplify the generation of these advanced designs, an R package "SlicedLHD" has been developed, providing an accessible tool for researchers. This thesis thus bridges significant gaps in Latin hypercube design methods, focusing on orthogonality, flexibility, and practical utility in computer experiments in agriculture and allied fields.

Construction of statistical designs based on semi Latin rectangles

Semi-Latin Rectangles (SLRs) are a specific type of row-column design having wide-ranging applications. The primary objective of the study was to develop efficient and flexible methods for generating these designs for a variety of block sizes and parameter combinations.The study introduces new combinatorial methods and algorithms to generate BSLR and PBSLR designs for a range of block sizes, specifically k=2,3, 4 and extends to $k>4$ for BSLR designs.The study provides four different construction methods for generation of BSLR designs and four different construction methods for generation of PBSLR designs in block size 2 and 3. Two separate construction methods are also developed for generation of PBSLR designs in block size 4. Two different algorithms are developed out of which one can be used for generation of BSLR designs in block size 4 and other is for generation of BSLR designs in block size greater than 4. In total ten construction methods and two algorithms have been developed. A comprehensive catalogue of BSLR and PBSLR designs for $k+1\leq v\leq 10$, where k is the block size and vv is the number of treatments is presented. Additionally, the average efficiency factor (E) for each design has been calculated and presented. BSLR designs for block sizes k=2, 3, 4,…, 8 and treatment (v) ranges $k+1\leq v\leq 10$are catalogued as a ready reckoner solution.Similarly, we presentPartially Balanced Semi-Latin Rectangles (PBSLR) designs for block sizes k=2, 3, 4and treatment ranges$k+1\leq v\leq 10$. An R package named "slr" has been developed and can be accesible with URL as https://cran.r-project.org/web/packages/slr/index.htmlcan be used forgeneration ofBSLR and PBSLR designs. A web application has also been developed and is available at https://drsr.icar.gov.in/SLR/index.html. The application is capable of constructing designs for a broad range of parameters, specifically for $2\leq k\leq 4$ (block size) and $k+1\leq v\leq 20$ (number of treatments).

Designs for two-level factorial experiments in block size four

Block designs are useful for the experimental situations in which one-way heterogeneity is present in the experimental material. Recently many researchers emphasize block designs for two-level factorial experiments with block size two to estimate important factorial effects. However, experiments with block size four can be more useful than block size two. Often number of replications required to estimate main effects and two-factor interactions will be more while considering small block size like block size four hence obtaining such designs for factorial and fractional factorial experiments in minimum number of runs is a challenging task economizing time and cost of experimentation. Certain cases where it is not the choice of experimenters to estimate all two factor interactions or experimenter may be interested in estimation of all main effects and some selected two-factor interactions. To deal with the above experimental situations, the present study was undertaken to obtain block designs for 2^n factorial experiments for estimating the main effects and specific two factor interactions in single replications or minimum number of replications, and also efficient block designs for 2^nfactorial experiments in blocks of size four to estimate all main effects and two factor interactions with minimum number of replications. Economizing the experimental resources by considering a part (fraction) of the complete factorial set up, a general method for obtaining efficient block designs for 2^{n-k}fractional factorial experiments in block size 4 have been obtained with minimum number of runs enable estimation of all main effects and two factor interactions. All the designs developed using proposed construction methods were catalogued for $n< 10$with its efficiency factor and compared with the existing designs in literature. Catalogue of developed designs for 2^n ($n<10$) factorial and 2^{n-k} fractional factorial experiments is a ready reckoner solution for the NARES users.

Theme 2: Sample Surveys

Multiple frame survey estimators and resampling methods of variance estimation under two stage sampling

Multiple frame (MF) surveys are essential when a single frame is inadequate or cost-effective frames from different sources are available. Dual frame (DF) surveys, a subset of MF surveys, use two overlapping frames to ensure full population coverage. Despite their importance, limited research has addressed two-stage sampling in DF surveys, particularly when domain sizes are unknown. This study bridges that gap by proposing methods to estimate population totals and variances under two-stage sampling with unknown domain sizes. Simulation studies on generated univariate normal population evaluated the proposed estimator and variance estimation methods using metrics such as percentage relative bias (%RB), relative root mean square error (%RRMSE), percentage coefficient of variation (%CV), skewness, and kurtosis. Results show that the proposed estimator is efficient and approximately unbiased, with %RB and %RRMSE decreasing as sample sizes increase. Desirable skewness and kurtosis were also maintained, confirming robustness and reliability. Building on Hartley's (1962) observation that unbiased variance estimation in MF surveys is more complex than in single-frame surveys, the Post-Stratified Rescaling Bootstrap Method was introduced. This method applies frame-wise resampling with rescaling factors, significantly reducing %RB and improving relative stability (RS) compared to standard bootstrap methods. To address missing data, the Proportional Post-Stratified Bootstrap Method was developed to accommodate missing observations. Among imputation techniques, Multiple Imputation provided the most accurate and stable estimates, followed by Regression Imputation, while Zero Substitution showed high bias and instability. In conclusion, the proposed estimator and methods demonstrate superior performance in DF surveys with unknown domain sizes or missing data. These findings advance variance estimation methodologies under the DF framework. Future research could expand these methods to more complex scenarios, such as multiple frames across different sampling stages.

Geographically weighted ANN based model calibration estimation of finite population total

In sample surveys, calibration is widely used to integrate known population characteristics by adjusting design weights. The model-calibration approach extends traditional calibration by employing complex models to derive model-assisted estimators. Many surveys exhibit spatial dependency, where nearby observations are more similar, and spatial non-stationarity, where relationships between study and auxiliary variables vary by location. While Ordinary Least Squares (OLS) models fail to address spatial non-stationarity, Geographically Weighted Regression (GWR) accounts for it by capturing spatially varying relationships. Similarly, Geographically

Weighted Artificial Neural Networks (GWANN) model nonlinear spatial relationships, but do not consider survey sampling designs. To address this gap, a novel Geographically and Survey Weighted Artificial Neural Network (GSWANN) technique was developed for survey data to estimate population parameters. Within the framework of single-stage Simple Random Sampling Without Replacement (SRSWOR) and assuming availability of complete auxiliary information, two GSWANN-based model-calibration estimators for finite population totals were proposed. These estimators are asymptotically design-unbiased and approximately model-unbiased under specific regularity conditions. Approximate variances and variance estimators of the proposed estimators were also derived. A spatial simulation study using R software was conducted which evaluated the performance of these estimators against existing methods, including the Horvitz-Thompson, ratio, and regression estimators. Results showed that the proposed GSWANN-based model calibration estimators were asymptotically design-unbiased based on percentage relative bias (%RB) and more efficient in terms of percentage relative root mean square error (% RRMSE). The findings highlight the significant potential of GSWANN-based estimators in improving finite population parameter estimation under complex survey conditions characterized by spatial non-stationarity. This methodology effectively integrates auxiliary information and advances the precision of spatial survey data analysis.

Resampling variance estimation of finite population parameter under two stage ranked set sampling

In experimental settings where measuring an observation is costly, but ranking a small subset is comparatively easy, Ranked Set Sampling (RSS) can be used to improve the reliability of the estimators. Majority of the research work on Ranked Set Sampling has been focused on estimating unknown parameters, particularly the population mean, under the assumption of infinite population. The use of RSS approaches in the context of a finite population, however, has not received much attention. Very few authors have expanded this to two-stage sampling design, which is more practical in nature as in most national and international surveys, a two-stage sampling design is preferred over a single-stage sampling design. Estimating the variance in case of two-stage Ranked Set Sampling without replacement (RSSWOR) under finite population has been proven to be cumbersome. That's why in this research work, an attempt was made to develop unbiased variance estimation techniques using Rescaling Bootstrap method. Two rescaling bootstrap methods have been developed namely Strata Based Rescaling Bootstrap (SBRB) and Cluster Based Rescaling Bootstrap (CBRB) for two-stage RSSWOR under finite population framework. A simulation study has been carried out to assess the performance of the proposed rescaling bootstrap variance estimation techniques against standard bootstrap (without rescaling factor) and to compare the performance of two-stage RSSWOR with respect to two-stage SRSWOR. From the findings of simulation study, it is observed that the efficiency of two-stage RSSWOR is more in comparison to two-stage SRSWOR. Both the proposed variance estimation methods outperform standard Bootstrap in terms of Percentage Relative Bias and Relative Stability. Among the proposed bootstrap approaches, strata-based approach performs better.

Calibration estimation of population total in the presence of non-response under two stage sampling design

Sample surveys are subject to two types of errors: sampling errors and non-sampling errors. Among non-sampling errors, non-response is particularly problematic as it introduces bias by when non-respondents differ significantly from respondents. Hansen and Hurwitz (1946) pioneered a technique to address non-response by sub-sampling non-respondents and collecting data from this sub-sample through specialized efforts and introduced an unbiased and consistent estimator for the population mean. Recently, Raman *et al.* (2013, 2016) and Chaudhary *et al*. (2023) proposed new estimators as an improvement over Hansen and Hurwitz estimator for population total in uni-stage sampling design in presence of non-response using calibration estimation. Most of the existing estimators for non-response focus on single-stage sampling designs. However, real-world surveys typically employ multi-stage sampling designs, and non-response is a common challenge in such surveys involving human participants. Estimators designed for single-stage sampling cannot be applied in this context, hence there is a critical need for estimators dealing with non-response in multi-stage sampling designs. In this research, we have developed two novel calibration estimators for the population total under two-stage sampling in the presence of non-response with assumptions on two situations of availability of auxiliary information at the ultimate stage unit level. The mean squared error (MSE) and the estimator of MSE were derived for both estimators. A simulation study, employing both hypothetical and real data, compares the proposed estimators with the existing Horvitz Thompson type Hansen-Hurwitz estimator under two stage sampling design. The results consistently demonstrate the superior performance of the proposed estimators for estimation of population total in the presence of non-response within a two-stage sampling framework through calibration.

Crop yield estimation using machine learning technique for geo-referenced survey data

Accurate crop yield estimation is crucial for effective agricultural planning and policy-making. Approximately, around 8.5 lakh Crop Cutting Experiments (CCEs) are conducted annually under the General Crop Estimation Surveys (GCES) to estimate yield for major crops in the country. This number has significantly increased to approximately about 1 crore due to the Pradhan Mantri Fasal Bima Yojana. This study introduces a novel sampling methodology using machine learning techniques and geospatial data to reduce number of CCEs while maintaining the same level of efficiency of the yield estimates. The study was conducted in Barabanki district, Uttar Pradesh using the dataset obtained from the “Integrated Sampling Methodology for Crop Yield Estimation” project for wheat crop. In this study, machine learning models namely random forest (RF), support vector regression (SVR) and gradient boosting (GB) were used for model development and five spatial indices viz. NDVI, GNDVI, NDRE, SAVI, MSAVI obtained from satellite imagery of Sentinel II were used as input variables in the model. The entire dataset consisting of CCE data including spatial coordinates was divided into sampled and non-sampled part. The usual GCES estimator was considered as the estimator for sampled part whereas the estimator for non-sampled part was constructed using model-based frameworks. The proposed estimator was constructed using the combination of estimator for sampled and non-sampled part which outperformed the traditional Horvitz-Thompson estimator with respect to relative bias (% RB) and relative root mean square error (%RRMSE). Among the models, GB demonstrated the best performance with decreasing root mean square error (RMSE) as sample size increases. The proposed methodology provides more efficient, reliable and stable estimator of crop yield which can be obtained in timely manner with reduced number of CCEs using machine learning and geo-spatial techniques. The study recommends further validation of the proposed methodology in other regions, exploration of alternative indices and refinement of the approach using survey weights and additional machine learning techniques.

Calibration estimation of population total by double use of auxiliary information in two stage sampling design

Sample survey is a method that involves selecting a subset of individuals from a larger population to make inference about the entire population. The use of auxiliary information while estimating the population parameters are widely adapted due to its capability of obtaining efficient estimators. The Calibration approach is one of the most employed method for integrating auxiliary information into the estimation process. Rank-based calibration is a statistical method that leverages a single auxiliary variable in two different ways. Several researchers, including Haq et al. (2017) and Alam and Shabbir (2020) have successfully applied rank-based calibration to improve estimators for uni-stage sampling designs which were merely used in any real life surveys as in real life surveys commonly employed designs are multistage in nature. In this context, we have developed two new calibration estimators for two-stage sampling by utilizing auxiliary information in two different ways i.e. the auxiliary information self and its rank as another. We considered two cases of availability of auxiliary information i.e. when auxiliary is available for the entire population and when it's only available for selected clusters. The approximate mean square error and its estimator were also derived using Taylor Series linearization technique. To evaluate the performance of the proposed estimators, we compared them with existing estimators using both simulated and real survey data. In both the studies it was found that the proposed estimators have outperformed the existing estimators i.e. Horvitz-Thompson estimator, classical ratio estimator and Aditya et al. (2017) calibration estimator.

Kriging based spatial estimation of finite population total under complex surveys

In the field of geostatistics, kriging is widely recognized for its ability to incorporate spatial dependencies into prediction models, making it a cornerstone of spatial estimation techniques. This study focuses on the development of kriging-based spatial estimators for estimating the finite population total. These estimators were formulated within the framework of single-stage Simple Random Sampling without Replacement (SRSWOR), applying both model-based and model-assisted approaches. The theoretical properties of the proposed kriging-based estimators were rigorously evaluated. Under specified regularity conditions, the estimators were shown to be asymptotically unbiased with respect to the sampling design and approximately unbiased with respect to the underlying spatial working model. Additionally, the approximate variances of these estimators were derived, along with methods to estimate these variances. To assess the practical performance of these estimators, a detailed spatial simulation study and a design-based simulation were conducted. The study compared the proposed kriging-based spatial estimators with established methods, such as the Narain-Horvitz-Thompson estimator (Narain, 1951; Horvitz and Thompson, 1952) and the spatial estimator based on Inverse Distance Weighting (IDW) (Biswas et al., 2017). The results indicated that the kriging-based estimators achieved asymptotic design unbiasedness, as reflected in their percentage Relative Bias (%RB). With increasing sample sizes, the estimators converged to the true population total without systematic error due to the sampling design. Furthermore, the proposed estimator's demonstrated superior efficiency compared to existing methods, with lower percentage Relative Root Mean Square Error (% RRMSE). In summary, the kriging-based methodologies developed in this study represent a significant advancement in the estimation of finite population parameters. These methods are particularly valuable for single-variable complex surveys where spatial stationarity is a factor. The improved precision and reliability of these estimators underscore their potential to enhance spatial data analysis and decision-making processes across various applications.

Theme 3: Statistical Modeling

Deep learning approaches for cereal crops yield prediction using spectral indices

To address the challenges of climate change, rising population, and food demand, accurate crop yield prediction is crucial for crop management, food security, trade, and policymaking. Predicting crop yield is complex due to the interdependence of factors like crop genotype, environment, management practices, and their interactions. Proximal sensing and remote sensing, such as spectral vegetation indices (VIs), are increasingly used in agricultural and environmental monitoring. This study proposes deep learning frameworks that use spectral indices for improved crop yield prediction. We explore deep neural networks (DNN), convolutional neural networks (CNN), long short-term memory (LSTM), and hybrid CNN-LSTM models, enhanced with optimization techniques like artificial bee colony (ABC), genetic algorithm (GA), and particle swarm optimization (PSO). Among these, CNN and

LSTM models effectively capture nonlinear patterns and temporal dependencies, respectively. ABC optimization outperforms GA and PSO due to its efficient exploration and faster convergence. The models are tested in two scenarios: non-sequential and sequential data. For non-sequential data, DNN and optimized CNN models predict wheat yield in Delhi and Pune, using NDVI, canopy temperature, and plant height. For sequential data, DNN and optimized CNN-LSTM models predict paddy yield in Krishna district, Andhra Pradesh, using NDVI, NDWI, and weather variables. The performance of these models is compared with LASSO, random forest regression (RFR), and support vector regression (SVR) through various metrics. Additionally, a ranking technique, TOPSIS, is used. The results show that hyperparameter-optimized models, especially those tuned with ABC, provide superior performance in terms of R-square, RMSE, and computational efficiency. ABC-optimized CNN and CNN-LSTM models are found to be robust tools for crop yield prediction. NDVI was identified as the most influential factor for predicting crop yield.

A study on copula approach for time series forecasting

The present study develops and evaluates Copula-based time series models to capture complex interdependencies among multiple agricultural commodity prices. Three innovative Copula-based models have been proposed, each tailored to address specific objective. The first model, the Bivariate ARIMA-GARCH-Copula model, is designed to model interdependencies between two time series, and a simulation-based forecasting algorithm for this model has also been proposed. Empirical analysis for this model is conducted on the price data of key oilseed crops and pulses across two markets in India for each commodity. Comparative assessments against conventional models, including the MGARCH-DCC and Univariate ARIMA-GARCH models, demonstrate the superior forecasting performance of the Bivariate ARIMA-GARCH-Copula model, as evidenced by lower value of different accuracy measures and ensured by the DM test, which indicates a statistically significant improvement in forecast accuracy. The second model, the Trivariate ARMA-GARCH-Vine Copula model, is developed to capture dependencies across three interrelated time series, with a simulation-based forecasting algorithm proposed. This model is applied to examine the price series of major vegetable crops across three different markets in India for each crop. Comparative analysis reveals that the proposed Trivariate ARMA-GARCH-Vine Copula model significantly outperforms MGARCH-DCC and Univariate ARIMA-GARCH models, as shown by different error metrics and DM test results. Furthermore, the third model, the Vine Copula (VC)-Based Optimal Multivariate Deep Learning model (MDL), with Genetic Algorithm (GA) optimization, a robust approach for multivariate time series forecasting has been introduced. This model, termed as the optimal GA-MDL-VC model, is benchmarked against GA-MDL models using daily price data for soybean across 15 major Indian markets. Empirical results indicate that the optimal GA-MDL-VC model achieves highest forecast accuracy as compared to other models. The study highlights the superior predictive power of Copula-based models in capturing spatial and temporal dependencies in agricultural price forecasting.

Modeling agricultural price through deep learning techniques

This research delves into the advancement of deep learning models for vegetable price forecasting, with a focus on three distinct domains: metaheuristic algorithm-based models, exogenous variable-driven models, and the Wavelet-Transformer algorithm.Integration of Metaheuristic Algorithms (MHAs) like Particle Swarm Optimization (PSO), Grey Wolf Optimizer (GWO) and Whale Optimization Algorithm (WOA) with various neural network architectures such as Multilayer perceptron (MLP), Recurrent Neural Network (RNN), Long Short Term Memory (LSTM), Gated Recurrent Unit (GRU) and Transformer results in 15 unique model combinations, including innovative *"Meta-Transformers"* like PSO-Transformer, GWO-Transformer, and WOA-Transformer.

These models exhibit competitive performance among themselves, showcasing excellence in capturing intricate patterns within agricultural commodity price data. Furthermore, exogenous variable-driven models like NBEATSX and TransformerX incorporate external factors such as weather data, thereby enhancing forecasting accuracy. The Wavelet-Transformer algorithm, combining wavelet analysis with transformer architectures, effectively decomposes nonlinear price time series into multi-resolution levels, adeptly capturing both global trends and localized information. Leveraging feature augmentation and self-attention capabilities, the Wavelet-Transformer surpasses baseline and other wavelet-based models, offering novel methodologies and insights into agricultural economics and deep learning for forecasting vegetable prices across diverse market conditions. Evaluation of model performance across objectives employs metrics such as RMSE, MAE, sMAPE, MASE, and Quantile loss, with the model exhibiting the lowest values of error metrics being deemed the best-performing one.

Bivariate empirical mode decomposition based models for agricultural price forecasting

The multifaceted nature of agricultural price series, characterized by nonstationary and nonlinear behaviours, poses a challenge to conventional mono-scale smoothing methods, which struggle to capture these complexities. Empirical Mode Decomposition (EMD) has emerged as a widely used tool in time series forecasting, offering an adaptive, data-driven approach to decompose nonstationary signals into intrinsic mode functions (IMFs) that reveal valuable temporal patterns. However, EMD is inherently limited when processing bivariate data, as it cannot capture the intrinsic relationships or dependencies between paired signals. To address this limitation, Bivariate Empirical Mode Decomposition (BEMD) was introduced. BEMD processes bivariate data as complex-valued signals, effectively capturing interdependencies between two variables. In this study, two BEMD-based neural network models are proposed for interval-valued agricultural price forecasting. Daily minimum and maximum prices of Potato of the Delhi market obtained from the website of 'Agmarknet' (https://agmarknet.gov.in) are used to construct an interval-valued bivariate series, transformed into a complex time series, with lower and upper bounds represented as real and imaginary parts, respectively. The complex-valued signal is then decomposed into several intrinsic mode functions (IMFs) and a residue, each with distinct frequency characteristics. The real and imaginary components of these complex-valued IMFs and residues are extracted as separate lower and upper bound series, which are then modelled independently using TDNN and LSTM models. Forecasts of each IMF and residue component are ensembled to yield interval forecasts for the original series. Empirical results demonstrate that the proposed BEMD-TDNN and BEMD-LSTM models outperform traditional EMD-based counterparts (EMD-TDNN and EMD-LSTM) in terms of Theil's U statistic, interval mean squared error (IMSE), and interval mean absolute error (IMAE). These findings underscore the advantages of BEMD-based approaches in handling the complex, interval-valued nature of agricultural price data, delivering enhanced predictive accuracy and stability compared to standard decomposition techniques.

Ensemble based forest cover trend estimation

Forest is one among the major resources that take crucial role in sustaining the ecological equilibrium and environmental system. Deforestation is increasing greenhouse gas emissions and aggravating the loss of biodiversity and wildlife habitat. Remote sensing is essential in mapping the occurrence of forest disturbance and quantifying its extent and severity. Several spectral indices are very effective to analysing the forest cover trends. For estimating the forest cover change, Mann-Kendall (M-K) test, Sen's Slope estimation methods are common.The accuracy of change detection using these methods is dependent on the ideal images. To get the ideal images, the integration of several pixels is used instead of using a single pixel. In the study, the forest cover change has been estimated in the 9 major districts (>50% of forest area) of Assam state, India. The satellite raster images for the study area have been collected from the processed MODIS (2001–2023) and Sentinel-2 (2016–2023) satellite, and the Normalized Difference Vegetative Index (NDVI) has been used. In an average 20 random individual areas of 500 meters radius have been selected in each of the districts. To estimate the forest cover trend of each district, an ensemble trend estimation procedure has been developed using modified M-K test and a p-value combination function. The significant combined p-value has determined the presence of the positive or negative overall trend, and the slope coefficient has been used to indicate the vegetative trend, i.e. a positive coefficient indicates vegetative regrowth and a negative coefficient represents vegetative degradation.From the study, the positive forest cover trend has been found in 5 districts using MODIS datasets and 3 districts using Sentinel-2 datasets, and for 2 districts, no significant trend has been observed in Sentinel-2 datasets.

CNN-Transformer hybrid deep learning model for time series forecasting

Time series forecasting plays a vital role in understanding how phenomena evolve over time, making it, a crucial tool for predicting future values based on historical data. This technique is essential across various domains, including finance, meteorology, and agriculture, where it helps forecast crop yields, commodity prices, and other factors crucial for decision-making. Deep learning models, with their advanced capabilities for handling complex, high-dimensional data and capturing both short-term and long-term dependencies, have transformed time series forecasting. This study introduces a hybrid deep learning model integrating Convolutional Neural Networks (CNNs) with Transformers, specifically designed for predicting one-dimensional price data. Using Potato price data from Delhi's Azadpur market, the CNN-Transformer hybrid model effectively combines CNNs' ability to extract detailed features and Transformers' strength in capturing long-range dependencies. The model demonstrated impressive performance, with RMSE values of 121.91 (training) and 130.92 (test), MAPE values of 8.36 (training) and 9.66 (test), and MAE values of 85.07 (training) and 92.55 (test). Compared to other deep learning methods, including CNN, Transformer, CNN-LSTM, LSTM, Bi-LSTM, GRU, and Stacked LSTM, the CNN-Transformer model consistently delivered superior results across all metrics. This research addresses a significant gap in the literature by showcasing the effectiveness of hybrid deep learning models in agricultural price forecasting and offers actionable insights for key stakeholders such as farmers and policymakers. It highlights the potential of combining different neural network architectures to enhance time series analysis and forecasting accuracy, paving the way for more informed decision-making in the agricultural sector.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1	Umesh T.H. (21847)	M.Sc.	Geographically weighted ANN based model calibration estimation of finite population total	Dr. Ankur Biswas	*ICAR-IASRI, New Delhi
2	Rounak Kumar (21848)	M.Sc.	Bivariate empirical mode decomposition based models for agricultural price forecasting	Dr. Girish Kumaar Jha	*ICAR-IASRI, New Delhi
3	Swarup Bera (21849)	M.Sc.	Resampling variance estimation of finite population parameter under two stage ranked set sampling	Dr. Tauqueer Ahmad	*ICAR-IASRI, New Delhi
4	Safeela Nasrin M. (21850)	M.Sc.	Calibration estimation of population total in the presence of non-response under two stage sampling design	Dr. Kaustav Aditya	*ICAR-IASRI, New Delhi

5	Ayub Aktar (21852)	M.Sc.	Crop yield estimation using machine learning technique for geo-referenced survey data	Dr. Prachi Misra Sahoo	*ICAR-IASRI, New Delhi
6	Vyshna I C (21853)	M.Sc.	Calibration estimation of population total by double use of auxiliary information in two stage sampling design	Dr. Kaustav Aditya	*ICAR-IASRI, New Delhi
7	Suman Kalyan Barman (21854)	M.Sc.	Ensemble based forest cover trend estimation	Dr. A.K. Paul	*ICAR-IASRI, New Delhi
8	Punuru Lingamma (21855)	M.Sc.	Kriging based spatial estimation of finite population total under complex surveys	Dr. Ankur Biswas	*ICAR-IASRI, New Delhi
9	Anurag Rawat (21856)	M.Sc.	Designs for two-level factorial experiments in block size four	Dr. Sukanta Dash	*ICAR-IASRI, New Delhi
10	Varshini B.S. (21857)	M.Sc.	CNN-transformer hybrid deep learning model for time series forecasting	Dr. Wasi Alam	*ICAR-IASRI, New Delhi
11	Lokeshwari M. (11709)	Ph.D.	Deep learning approaches for cereal crops yield prediction using spectral indices	Dr. Girish Kumar Jha	*ICAR-IASRI, New Delhi
12	Bijoy Chanda (11712)	Ph.D.	A study on efficient equivalent-estimation split-plot designs through algorithmic intervention	Dr. Arpan Bhowmik	*ICAR-IASRI, New Delhi
13	A.Anil Kumar (11717)	Ph.D.	Orthogonal and sliced latin hypercube designs for computer experiments in agriculture	Dr. B.N. Mandal	*ICAR-IASRI, New Delhi
14	Harish Nayak G.H. (11999)	Ph.D.	Modeling agricultural price through deep learning techniques	Dr. Wasi Alam	*ICAR-IASRI, New Delhi
15	Moumita Baishya (11714)	Ph.D.	Multiple frame survey estimators and resampling methods of variance estimation under two stage sampling	Dr. Tauqueer Ahmad	*ICAR-IASRI, New Delhi
16	B. Manjunatha (11992)	Ph.D.	A study on copula approach for time series forecasting	Dr. Ranjit Kumar Paul	*ICAR-IASRI, New Delhi
17	Kaushal Kumar Yadav (11995)	Ph.D.	Construction of statistical designs based on semi Latin rectangles	Dr. Sukanta Dash	*ICAR-IASRI, New Delhi

**Sister institute*

BIOINFORMATICS

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Prof. Sarika

The Division of Agricultural Bioinformatics, ICAR-IASRI, New Delhi, is the youngest discipline of the institute, which is a sister institute of ICAR-IARI. It hosts ASHOKA (Advanced Supercomputing Hub for OMICS Knowledge in Agriculture), the first supercomputing hub in agriculture dedicated to the nation. With a mandate to advance research, teaching, and training in computational biology and bioinformatics, its focus includes priority research, analytical support, database, genomic resource and web-tool development, human resource training and fostering interdisciplinary collaboration to enhance global agricultural research and innovation. So far 53 students have received M.Sc. degree and 23 have received Ph.D. degree in Bioinformatics. Significant research findings of M.Sc. and Ph.D. students are enlisted under the following themes:

Theme 1: Computational Tools and Genomic Resource Development for Agricultural Applications

Development of artificial intelligence based fish specific long non-coding RNA biomarkers discovery tool and web genomic resource

Long noncoding RNAs (lncRNAs) are RNA molecules over 200 nucleotides in length that do not encode proteins but play vital roles in regulating gene expression and cellular processes. Despite their importance, predicting and characterizing lncRNAs in fish is challenging due to limited data. This study addresses the gap by developing advanced machine learning/ deep learning models to identify and analyze lncRNAs in fish, contributing to improved aquaculture through genetic insights. A curated dataset from the Ensembl database, containing 48,006 RNA sequences from 14 fish species, balanced between lncRNAs and coding RNAs, was used. Feature extraction combined traditional sequence-based methods with advanced techniques like TF-IDF (Term Frequency-Inverse Document Frequency), yielding six key features for ML training and testing. Two feature selection techniques—Random Forest (RF) and Univariate Selection (Mutual Information)—along with their combination (RFMI), were employed. Twelve ML, seven DL, and three hybrid methods were used for classification. The Light Gradient Boosting Machine (LGBM) model with RFMI on 45 features achieved the highest accuracy of 98.36%. Its robustness was validated against six popular lncRNA prediction tools using an independent dataset from *Salmo trutta*. To enhance accessibility, the FishLncPred web server (http://46.202.167.198:5000/) was developed, enabling real-time lncRNA prediction. A case study on common carp (*Cyprinus carpio*) identified 33,990 lncRNAs and 22,854 circRNAs, validated through RNA-seq data. Additionally, the CCncRNAdb resource (http://ccnrnadb.daasbioinformaticsteam.in/) was created, providing comprehensive genomic data for common carp. This research advances computational lncRNA identification, offering tools and resources to support sustainable aquaculture practices, ultimately enhancing productivity and resilience in fish farming.

A study on development of artificial intelligence-based methodology for identification of copy number variation in crops

Copy number variations (CNVs), encompassing deletions and duplications of DNA segments, are critical genomic features that influence gene expression, adaptation, and phenotypic variation. These structural variations play a pivotal role in genome evolution, trait expression, and environmental adaptability across plants. This research introduces MLDeCNV, a novel machine learning-based framework for the accurate detection and interpretation of copy number variations (CNVs) in genomic data, specifically targeting next-generation sequencing (NGS) data. CNVs, which involve alterations in the number of DNA copies, can significantly influence gene expression and contribute to phenotypic diversity. Traditional CNV detection methods often struggle with small CNVs or those in regions with low read-depth signals, leading to incomplete detection. To overcome these challenges, MLDeCNV integrates 32 features derived from NGS data and combines outputs from multiple CNV detection tools with experimental validation using PCR and aCGH. A key aspect of the framework is the application of the Smote-TomekLinks data-balancing technique, which enhances the model's accuracy by addressing class imbalances commonly found in CNV prediction. MLDeCNV outperforms existing CNV detection tools like Delly, CNVnator, and Manta, demonstrating robust performance across different species, including rice, Arabidopsis, and pomegranate, with an impressive AUC of 0.96. The study also highlights the practical utility of MLDeCNV by developing a web-based tool that simplifies CNV detection for researchers by accepting standard genomic inputs and offering an intuitive interface for classifying CNVs into deletions, duplications, or no CNV. Additionally, the research presents a genome-wide analysis of CNVs in black pepper and bitter gourd, uncovering thousands of CNVs and mapping them to critical agronomic traits such as stress resilience and pathogen defense. This work contributes significantly to the field of agricultural genomics, showing how CNVs can be leveraged for crop improvement, marker-assisted breeding, and understanding species adaptation. The study's findings underscore the value of integrating CNV data with genome-wide association studies (GWAS) to identify important loci linked to key traits, positioning MLDeCNV as a valuable resource for advancing genomic research in agriculture and evolutionary biology.

Development of computational tool for mining intron length polymorphism markers and designing primers

Intron Length Polymorphism (ILP) markers are molecular markers that identify differences in intron lengths between different genotypes. ILP markers are widely distributed across the genome and can exhibit polymorphism, making them robust, co-dominant markers in eukaryotes. They are locus specific, convenient, reliable, and uniquely capable of representing genetic variation within genes. These characteristics make ILP markers suitable for various applications, including genetic diversity analysis, linkage map construction, QTL mapping, comparative genomics studies, and association mapping. Polymorphism can also be used in functional studies of genes for physical mapping and linkage analysis. However, the in vitro detection of ILP markers is costly and time-consuming, necessitating an in-silico approach. ILP markers can be detected using genomic sequence data, making the process easier. ILP-MP is a web server developed using HTML, CSS and JavaScript available at http://backlin.cabgrid.res.in/ilpmp which identifies ILP markers from genomic sequence data. The user friendly interface is developed using HTML, CSS and PHP for server-side scripting, with C++ handling the backend processing. The primary advantage of the ILP-MP web server is its requirement for minimal input files, allowing it to be applicable to any crop. The ILP-MP tool successfully identified a total of 14 ILP markers from the 1st chromosome of the pomegranate genome. This user-friendly, cost-effective web-based tool is valuable for applications in QTL mapping, population evolutionary genetic studies, and molecular marker-assisted breeding

Standardizing workflow for identifying stress-tolerance contributing non-coding RNAs in Vigna and developing a comprehensive Ncrna database for legumes

This investigation led to the development of a comprehensive pan-transcriptome for the *Vigna* genus, which serves as a valuable resource for comparative analysis and the identification of stress-responsive genes, crucial for genome editing and crop improvement. The pan-transcriptome revealed core, dispensable, and unique species-specific genes, with the long non-coding RNAs (lncRNAs) showing significant variability across the seven species analyzed, while microRNAs (miRNAs) exhibited greater conservation. A total of 676 lncRNAs were discovered within the pan-core dataset. Among these, 58 and 64 lncRNAs were identified in MYMV-resistant accessions, while 61 and 70 lncRNAs were found in MYMV-susceptible accessions. Further comparative genome analysis identified 35 genes, 11 lncRNAs, and four miRNAs, including two novel miRNAs. In MYMV-resistant V. mungo accessions, 35 genes were upregulated and 11 lncRNAs were downregulated, suggesting that these lncRNAs may act as target mimics, with upregulated miRNAs contributing to the resistance mechanism. These genes were mapped in *V. radiata* and identified in other related species through comparative analysis conducted in the present investigation. Orthologous protein cluster count analysis revealed significant variations in genomic complexity across the seven Vigna species. *G. max* and *V. unguiculata* displayed lower genetic diversity, while *V. radiata* and *L. angustifolius* exhibited higher diversity. Detailed analysis of genome-wide proteins in *V. radiata* and *V. mungo* indicated significant genomic complexity and relatedness, with less than 2% variation at the genome level. Phylogenetic analysis and heatmap visualization provided insights into the genetic relationships and divergence within the Vigna genus. Differential expression analysis identified key genes involved in MYMV resistance, highlighting potential targets for breeding programs aimed at developing stress-resistant and nutritionally rich legume varieties. Additionally, the development of the FabELM_ncRNAdb database for ncRNA research in Fabaceae, along with the identification and mapping of genes contributing to MYMV resistance, offers a valuable resource for crop improvement. This investigation contributes to global food security and sustainability by enhancing crop resilience and productivity, aligning with the goals of sustainable development.

Theme 2: Data Integration and Visualization for Genomic Research

Development of HapMap database and visualization tool for tea

Conventional breeding methods are inadequate to address complex crop challenges, but genomics-assisted breeding (GAB) and next-generation sequencing (NGS) offer high-density markers and improved accuracy, enabling development of high-yielding, resilient, and nutritious crops. Advances in genomics utilize millions of DNA polymorphisms, improving genomic selection and gene mapping, and powering haplotype-based breeding for precise trait identification. Whole-genome haplotype analysis is crucial for understanding crop traits, particularly in commercially important crops like tea, which requires comprehensive haplotype mapping and visualization to uncover trait associations and drive informed breeding decisions. Hence, in the current study, based on the SNP information of 369 tea genotypes along with Linkage Disequilibrium measures, Haplotypes were generated using Sliding window approach. Haplotype database has been developed using My SQL. For visualizing the haplotype information, a web tool has been developed namely “HapTea: Haplotype Database of Tea”. This Visualization tool has the ability to visualize the haplotype of 369 tea genotypes. In this webtool user can choose the chromosome no, set the window size and visualize the pattern of haplotype of tea genome.

Integrating GWAS module with HtP-DAP for SNP-trait associations mining

Genome-wide association studies (GWAS) provide a crucial methodology for identifying genetic variants associated with traits in organisms. These studies are essential for understanding the genetic basis of complex traits, which can aid in improving crop performance, human health, and livestock breeding. This thesis seamlessly integrates a GWAS analysis tool with the existing phenomics data analysis platform, HtP-DAP, aimed at enhancing and streamlining GWAS analysis workflows. The tool addresses key challenges in GWAS by offering robust preprocessing capabilities, including data filtering based on allelic frequency thresholds, imputation of missing genotypic data, and file conversion to ensure compatibility with various analysis pipelines. A major feature of the tool is its comprehensive set of relatedness analysis functions, which include kinship estimation, principal component analysis (PCA), and multi-dimensional scaling (MDS). These analyses provide critical insights into the underlying genetic architecture of populations, facilitating more accurate GWAS results. The GWAS analysis itself is highly flexible, supporting both single-locus models, which test individual markers for trait associations, and multi-locus models, which examine interactions between multiple markers. Result visualization is a key component of the tool, offering users the ability to generate clear and informative graphical outputs, such as Manhattan plots to highlight significant associations, circular Manhattan plots for a more compact genome-wide view, and Q-Q plots to assess the quality of the GWAS results and also provide a platform for presenting results in a meaningful way for publication or further research. The tool's backend leverages the power of the GAPIT R package, known for its efficiency and scalability in handling large genomic datasets. GAPIT enables the seamless execution of GWAS analyses by managing the computational load, thus ensuring that the tool performs optimally even with large-scale datasets. By incorporating this GWAS tool within the HtP-DAP platform, this study bridges the gap between phenotypic data from high-throughput phenotyping and genotypic data from modern genomic studies. The integration facilitates a holistic approach to genetic research, allowing users to move from data collection to meaningful biological insights within a single platform.

Integrating a module with HtP-DAP for QTL mining using high throughput phenomics and genomics

The High-Throughput Phenomics Data Analysis Platform (HtP-DAP) is GUI (Graphical User Interface) based software which was developed in ICAR-IASRI for pre-processing, statistical analysis, genetic analysis, data modeling and interpreting of high throughput phenomics data, which is generated from Nana-ji Deshmukh plant phenomics centre at ICAR-IARI. This platform plays a pivotal role in the analysis of phenomics traits related to abiotic and biotic stress in crop plants. HtP-DAP efficiently handle high-throughput phenomics data but lack of the capability to process genomics data for QTL mapping. Existing QTL analysis tools lack of the capability to handle both high-throughput genomics and phenomics data together in graphical user interface because, most of these tools operate through a command-line interface and require programming skills. To address this issue, we developed a tool that integrates QTL analysis capabilities with HtP-DAP, enabling the combination of genomics and phenomics data for QTL mining in graphical user interface based. Initially, we created a data handling and pre-processing module designed to manage high-throughput phenomics and SNP data, streamlining the preparation and integration of data for analysis. Subsequently, we incorporated the R/qtl package and developed a GUI-based framework within HtP-DAP, providing users with an intuitive interface for performing QTL mapping. Finally, we built a result visualization module within HtP-DAP to facilitate the easy interpretation of QTL mapping results. The developed tool utilized to identify QTLs for phenotypic traits in recombinant inbred lines (RILs) from four-way cross populations of wheat. When two input files in CSV format are uploaded to HtP-DAP, the tool generated a merged file, which is then used for QTL analysis within the platform. The analysis produced an output file containing an LOD table in .csv format and a LOD curve in .jpg format. The highest LOD (logarithm of the odds) value for a specific SNP reflects the strength of the association between that SNP and a quantitative trait. If the LOD value for specific SNP surpasses a predefined threshold, it indicates a statistically significant likelihood that the SNP is associated with the QTL affecting the trait of interest. KEYWORDS: Genomics, High throughput phenomics, QTLs, Quantitative traits, SNPs, Recombinant inbred lines, Simple interval mapping, Composite interval mapping, HtP-DAP

List of the students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Dipankar Mandal (21859)	M.Sc.	Development of Hapmap database and visualization tool for tea	Dr. U.B. Angadi	*ICAR-IASRI, New Delhi
2.	Surapuram Aswini (21915)	M.Sc.	Integrating GWAS module with HtP-DAP for SNP-Trait associations mining	Mr. Sanjeev Kumar	*ICAR-IASRI, New Delhi
3.	Soumya Shivamurti (21934)	M.Sc.	Development of computational tool for mining intron length polymorphism markers and designing primers	Dr. U.B. Angadi	*ICAR-IASRI, New Delhi
4.	Ashok S (21935)	M.Sc.	Standardizing workflow for identifying stress-tolerance contributing non-coding RNAs in Vigna and developing a comprehensive NCRNA database for legumes	Dr. Yasin Jeshima K.	*ICAR-IASRI, New Delhi
5.	Satendra Shivam (21959)	M.Sc.	Integrating a module with HtP-DAP for QTL mining using high throughput phenomics and genomics	Mr. Sanjeev Kumar	*ICAR-IASRI, New Delhi
6.	Jutan Das (11468)	Ph.D.	Development of artificial intelligence based fish specific long non-coding RNA biomarkers discovery tool and web genomic resource	Dr. Sarika	*ICAR-IASRI, New Delhi
7.	Parinita Das (11740)	Ph.D.	A study on development of artificial intelligence-based methodology for identification of copy number variation in crops	Dr. Sarika	*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. The abstracts under theme areas are detailed as under:

Theme 1: Decision Support System/ Machine Learning/Web/Mobile Based Application in Agriculture

Development of mobile application for the shelf life of pearl millet flour using rancidity

Millets, known as "God's Grain" for their nutrient density, face challenges like rancidity, off-odors in flour which limits the global appeal of pearl millet. To address this, the "SHLP" mobile application was developed to aid breeders in assessing pearl millet genotypes and their susceptibility to rancidity. The app leverages data from previous research by Goswami et al. (2020), which identified CA and CP values as key factors influencing rancidity.The app employs a three-tier architecture with database, web server, and presentation layers, built using Java, XML, and Android Studio. It uses SQLite to store genotype data, matrices, and related values. Java connects the database to the user interface, enabling seamless data retrieval based on user inputs. Users must register to access the app. "SHLP" provides students, researchers, and breeders with vital insights into genotype shelf life, delivering CA and CP values for specific genotypes. It enhances work efficiency, reduces costs, saves time, and offers a user-friendly experience.

Development of mobile App for energy audit surveys in india in the context of SDG 7.0

The "Survey App for AICRP on EAAI" has been designed for agricultural data management. Developed in Kotlin for its concise syntax and robust security, the app aligns with ICAR-AICRP on EAAI sampling methodologies. Key features include the Volley library integrated with Network Callback for seamless asynchronous network operations, enabling real-time data transfer even with intermittent internet access. Offline data collection is supported via SQLite, allowing users to record crop data, farm profiles, soil types, and energy usage without requiring constant connectivity. Once online, the app synchronizes stored data with a central server to maintain up-to-date information. The app also employs the Fused Location Provider API for accurate background location tracking, aiding informed agricultural decision-making. By enhancing data collection and synchronization, the app significantly contributes to achieving the objectives of SDG 7.0, promoting sustainable energy use in agriculture. This robust integration of technology supports efficient, reliable data management, benefiting both researchers and farmers.

Web application on causal analysis for identification of best production practices for maximizing crop yield

Agriculture is the backbone of India's economy, with over 70% of the rural population depending on it for livelihood. As challenges like climate change and resource scarcity intensify, sustainable food production has become crucial. Causal inference models are essential for optimizing cultivation practices, as they identify cause-and-effect relationships between interventions and outcomes such as crop yield and soil health usingtechnique like Generalized Random Forest thatenables data-driven decision-making for sustainable farming.The Landscape Diagnostic Survey (LDS), conducted under Cereal Systems Initiative for South Asia (CSISA)byICAR, provided valuable data on cropping systems in Haryana, focusing on cotton-wheat, pearl millet-mustard, and rice-wheat systems. Leveraging LDS data, a web application was developed using ASP.NET and C# to perform causal analysis and integrate with the existing CSISA LDS Dashboard. The application allows users to select crops, variables, and covariatesand provides recommended practices tailored for improving yield and sustainability. With its intuitive interface, the tool empowers extension personneland researchers to make informed decisions, fostering sustainable agricultural practices and addressing critical challenges in food production.

Web-based personalized recommender system through bibliometric measures and collaborative filtering approaches in agriculture

The rapid growth of scientific publications, driven by internet advancements and global digitalization, has made it increasingly challenging for researchers to find relevant materials. Recommender Systems (RS) have gained prominence in addressing this issue across education, research, and industry. However, existing systems often rely on single criteria, limiting their effectiveness. To overcome this, a multi-criteria-based recommender system (MCP-RS) has been developed, leveraging collaborative filtering with Singular Value Decomposition (SVD) to recommend research papers in agriculture.The system, built using the Django framework, offers a user-friendly interface and efficient database interaction through Django's ORM model, ensuring scalability and ease of use. It sources publication data from ICAR's KRISHI repository, supplemented by student evaluations based on seven implicit criteria: "Contribution," "Originality," "Literature Review," "Readability and Organization," "Technical Quality," "Testing Procedure," and "Quality of References."By incorporating overall and individual criteria, as well as their combinations, MCP-RS predicts and recommends research papers tailored to users' specific needs.

Decision support system for equine disease diagnosis and management

In equines, accurate disease diagnosis and effective management are essential for maintaining their health and utility across sectors such as agriculture, transportation, and sports. An Android-based mobile application, "EquineHealth" has been designed to facilitate real-time diagnosis of equine diseases. The application analyzes user-input symptoms, cross-referencing them with an extensive disease database to deliver management strategies. Developed using Android Studio, Java, XML for the user interface, and SQLite as the backend database, the app serves as a Decision Support System (DSS) for both veterinarians and equine caretakers.Users can input symptoms such as coughing, nasal discharge, or breathing difficulties, which the system processes to generate probable diagnoses and suggest corresponding management practices. The application features an intuitive interface that simplifies symptom selection, enabling efficient use by a wide range of users. By integrating a robust database and offering real-time guidance, the app enhances equine health management, contributing to disease prevention and control. The DSS aims to strengthen equine health security, minimize economic losses stemming from inadequate health management, and foster sustainable practices within the equine care industry.

Theme 2: Artificial Intelligence/Deep Learning/ Natural Language Processing/Machine Learning Application in Agriculture

Development of deep learning based application for real-time wheat ear detection

Wheat, a globally significant cereal crop, is critical for food security, with phenotyping playing a key role in improving yield and management. Accurate detection and counting of wheat ears, which directly correlate with grain yield, are vital but traditionally labor-intensive and inefficient for large-scale operations. This study introduces an Android application integrating the YOLOv5 deep learning model for real-time wheat ear detection and pot association. Development involved dataset collection from The Nanaji Deshmukh Plant Phenomics Centre at IARI, model training and system integration. The model achieved 82.3% precision, 75.2% recall, and 80.7% mAP@0.5 for wheat ear detection, and 97.7% precision, 98.3% recall, and 98.6% mAP@0.5 for pot identification. Statistical analysis showed moderate accuracy for wheat ear counting (RMSE: 2.39, MAE: 1.28, R^2: 0.66) and perfect performance for pot identification (RMSE: 0.0, MAE: 0.0, R^2: 1.0). Overall wheat ear counting accuracy was 79.8%, while pot identification achieved 100%.The counting algorithm processes each frame, accurately associating wheat ears with the correct pots. Additional app features include data visualization and export to CSV for further analysis.

Image analysis based plant phenotyping for yield estimation using artificial intelligence techniques

Rice is a vital staple crop with immense cultural, economic, and food security significance. This study focuses on analyzing rice phenotypic parameters using image-based techniques at the Nanaji Deshmukh Plant Phenomics Centre, ICAR-IARI, New Delhi, to develop advanced methodologies for panicle detection, yield estimation, and phenotyping through AI.The proposed PanicleDet model, an ensemble of base YOLOv5 and an extended YOLOv5, detects key paddy panicle stages—boot leaf, heading, anthesis, grain filling, and grain maturity. It outperformed state-of-the-art models, achieving a mean Average Precision (mAP) of 93% and 77.9% at Intersection over Union (IoU) thresholds of 0.5 and 0.5:0.95, respectively. A novel segmentation approach, PanicleSegNet, based on DeepLabV3 with ResNet50, was developed to delineate panicles during grain filling and maturity stages. Training on 512x512 pixel images yielded 93.67% pixel classification accuracy and a Dice Similarity Coefficient of 0.9799, demonstrating precise segmentation performance.Yield prediction was conducted using RGB images from paddy grown in pots for phenotypic research. Support Vector Regression (SVR) delivered the best results, with R^2 of 0.611, RMSE of 4.019, MAE of 2.859, and MAPE of 4.338%.These models collectively provide robust solutions for rice research, integrated into the web-based Artificial Intelligence-based Image Phenotyping Platform for Rice (AI2PP-Rice). This tool facilitates non-destructive yield estimation and growth stage analysis, translating research into practical applications. AI2PP-Rice advances sustainable and efficient rice cultivation practices, marking a significant step forward in agricultural innovation.

List of contributing students and Chairpersons of their advisory committee

S. No.	Name of the student & roll no.	Degree	Title of the thesis	Chairperson	Institute
1.	Mohammed Safwan (21858)	M.Sc.	Development of mobile application for the shelf life of pearl millet flour using rancidity	Dr. (Md.) Samir Farooqi	*ICAR-IASRI, New Delhi
2.	Krantibira Swain (21954)	M.Sc.	Development of mobile app for energy audit surveys in india in the context of SDG 7.0	Dr. S.B. Lal	*ICAR-IASRI, New Delhi

3.	Anwan Alam (21955)	M.Sc.	Web application on causal analysis for identification of best production practices for maximizing crop yield	Dr. Soumen Pal	*ICAR-IASRI, New Delhi
4.	Jatindra Nath De (21957)	M.Sc.	Web-based personalized recommender system through bibliometric measures and collaborative filtering approaches in agriculture	Dr. Anu Sharma	*ICAR-IASRI, New Delhi
5.	Ms. Kamaladharani S (21958)	M.Sc.	Decision support system for equine disease diagnosis and management	Dr. Soumen Pal	*ICAR-IASRI, New Delhi
6.	Pradyuman Thakur (21933)	M.Sc.	Development of deep learning based application for real-time wheat ear detection	Dr. Anshu Bhardwaj	*ICAR-IASRI, New Delhi
7.	Himanshushekhar Chaurasia (11012)	Ph.D.	Image analysis based plant phenotyping for yield estimation using artificial intelligence techniques	Dr. Alka Arora	*ICAR-IASRI, New Delhi

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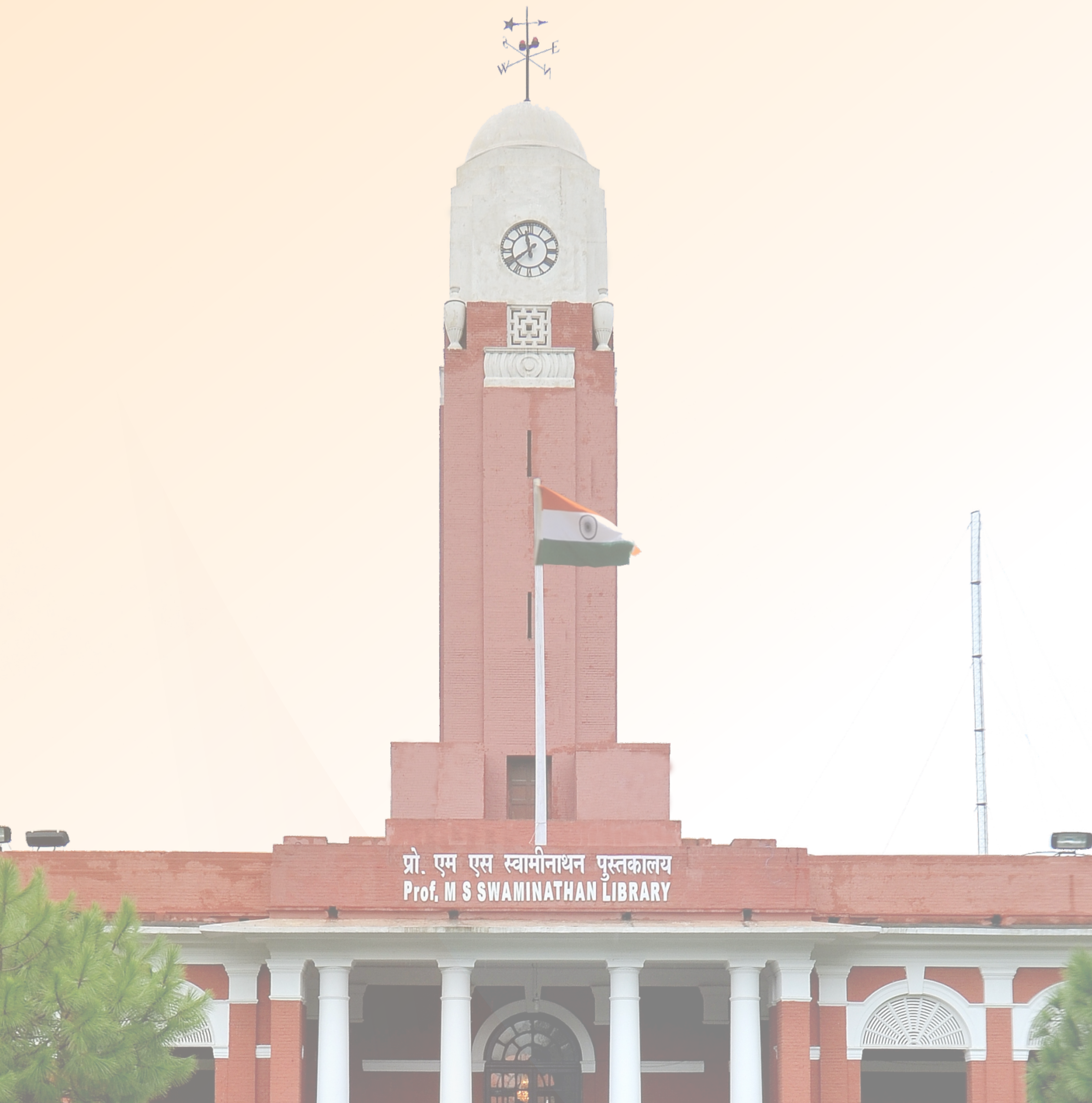
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