67 YEARS
THE GRADUATE SCHOOL
1958-2025

# Sixty-third Convocation

## Significant Post Graduate Students' Research

March 17-18, 2025

# Abstracts

Chairperson
**Dr. B.M. Prasanna**
CIMMYT Distinguished Scientist
and Regional Director, CIMMYT-Asia, New Delhi

Convenor
**Dr. Anil Dahuja**
Professor, Division of Biochemistry

Co-Convenor
**Dr. Atul Kumar**
Associate Dean (PG), ICAR-IARI

The Graduate School
ICAR-Indian Agricultural Research Institute
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# M.Sc.
# Thesis Abstracts

# Agricultural Chemicals

Mr. Subhajit Rakshit

**Name of the Student** : **Mr. Subhajit Rakshit**
**Roll No.** : **21805**
**Chairperson** : **Dr. Tirthankar Banerjee**

Dr. Tirthankar Banerjee

*Title of the Thesis*

## Status of glyphosate residues in waters of NCR region and its sorption behavior in soil

Glyphosate, a widely used herbicide, has become a significant environmental concern due to its presence in water, alongside its toxic metabolite amino methyl phosphonic acid (AMPA). The International Agency for Research on Cancer (IARC) classified glyphosate as a ‘Type IIA’ carcinogen linked to liver cancer, diabetes, and cardiovascular diseases. However, detecting low levels of glyphosate and AMPA residues 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 utilizes multiple reaction monitoring (MRM) transitions to quantify glyphosate and AMPA, with a total run time of 10 minutes and specific retention times for both compounds. The method involved extracting glyphosate from water by derivatizing with 9-FMOC-Cl, partitioning with dichloromethane, filtering, and analyzing via 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 77.3–81.3% for glyphosate-FMOC and 74.0–80.4% for AMPA-FMOC, with repeatability confirmed through SANTE/11312/2021 guidelines. The matrix effect was negligible, and expanded uncertainties were reported for both analytes. Real-world water samples from the NCR region and other parts of India were analyzed, revealing glyphosate residues up to 0.346 µg/mL in drinking water. Sorption, desorption, and leaching experiments were conducted in various soils of India, and it was found that glyphosate sorption was highest in soils with higher organic carbon content. In sandy soils, leaching was significant, while in clay-rich soils, no leachate was observed.

# Agricultural Economics

Ms. Athulya S.

**Name of the Student** : **Ms. Athulya S.**
**Roll No.** : **21834**
**Chairperson** : **Dr. Praveen K. V.**

Dr. Praveen K. V.

*Title of the Thesis*

## 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, a significant 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.

# Agricultural Engineering


Mr. Sajja Poojith

**Name of the student** : **Mr. Sajja Poojith**
**Roll No.** : **21965**
**Chairperson** : **Dr. Adarsh Kumar**


Dr. Adarsh Kumar

*Title of the Thesis*

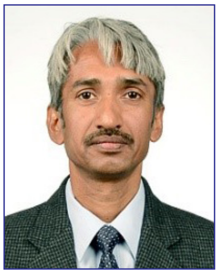
## Ergonomic assessment of powered cylindrical lawn mower for enhanced operator's comfort

Landscaping is one of the allied sectors in agriculture that focuses on planning and maintaining lawns and gardens. Lawn mowers are used for cutting grass on lawns to a predetermined height and are usually powered by diesel engines, causing discomfort to operators due to noise and vibration. Therefore, a study was conducted to assess noise and vibration from lawn mowers. A lawn mower with a 5 hp engine and 524 mm width of cut was selected for the study. Based on feasibility, three engine speeds and two operational modes were selected for the study. Noise and hand-arm vibration (HAV) were measured using a sound level meter and a vibration meter respectively. Human parameters like heart rate, RULA, REBA, BPDS and ODS were assessed in the lawn mower operation. The noise and vibration levels exceeded their permissible limits. Therefore, noise and vibration interventions i.e., acoustic enclosure for the engine, and polyurethane sheets and bushes were developed and retrofitted to the lawn mower. The noise levels were reduced with a maximum reduction of 10.13%, with a major reduction beyond 2500 Hz. The minimum daily safe noise exposure duration increased from 0.71 h to 6.65 h. The HAV levels achieved a reduction of 56.74%, with the major decrement of amplitude at 20–40 Hz. It increased the minimum years for the prevalence of finger blanching up to 2.5 times. Heart rate and energy consumption slightly increased due to the addition of weight on the lawn mower. BPDS slightly decreased to 46.8, whereas ODS remained the same i.e., 4. RULA and REBA scores did not change as the posture remains the same. The making cost of the interventions was approximately 8% of the machine cost. These simple, low-cost retrofits can enhance lawn mower operator safety. It is recommended to use ear protection aids and anti-vibration gloves for additional safety.

# Agricultural Extension Education

Ms. Simran Pundir

**Name of the Student** : **Ms. Simran Pundir**
**Roll No.** : **21969**
**Chairperson** : **Dr. R. N. Padaria**



Dr. R. N. Padaria

*Title of the Thesis*

## Rural women leadership in climate change adaptation and sustainable livelihood

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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 and 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.

# Agricultural Physics

Mr. Supriyo Dhara

**Name of the Student** : **Mr. Supriyo Dhara**
**Roll No.** : **21804**
**Chairperson** : **Dr. Rajeev Ranjan**

Dr. Rajeev Ranjan

### *Title of the Thesis*

## 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 the 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) 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 ($R^2 = 0.92$). 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, $R^2 = 0.73$), stomatal conductance (GS, $R^2 = 0.63$), transpiration rate (Tr, $R^2 = 0.73$), and moderate correlation with surface soil moisture ($R^2 = 0.56$) 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. 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.

# Agronomy


Ms. Sneha Bharadwaj

**Name of the Student** : **Ms. Sneha Bharadwaj**

**Roll No.** : **50096**

**Chairperson** : **Dr. C. M. Parihar**


Dr. C. M. Parihar

*Title of the Thesis*

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

The northeastern hill regions of India suffer from significant yield gaps, primarily due to inefficient resource use. However, research-based evidence has shown that optimizing management practices can bridge these yield gaps and enhance climate resilience. Therefore, two field experiments were conducted for 2-rice varieties, i.e., Shahsarang and Mendri, at ICAR-RC-NEH, Umiam. Results of the present study revealed that the application of 100% recommended dose of nitrogen-100% RDN, resulted in superior crop performance, with higher grain yield and marginal returns. In addition to field experiments, the study hinges on identifying the yield gaps using the APSIM-based long-term simulation and evaluating diverse nutrient management, supplemental irrigation, plant density, etc. to bridge these gaps in combination with varying SOC dynamics and transplanting windows. In this study, nitrogen limitation caused yield gaps of 2.80 t/ha in Shahsarang and 1.63 t/ha in Mendri under rainfed conditions. Integrating 5.0 t/ha FYM with 75% RDN maintained or even improved yields compared to 100% RDN while increasing SOC by 2.72–6.17%. Compared to conventional farmers' practices, INM enhanced grain yield by 14.7–134% and SOC by 7–32.1%. Further, APSIM-based simulation showed that early transplanting (before 5th July) minimizes yield losses by ~28% under current conditions and by 29–52% under future climate scenarios. In contrast, late transplanting (beyond 3rd August) results yield a reduction of ~25–30 kg/ha/day. Moreover, under future climate scenarios, optimal flowering periods shift earlier, with rapid development before flowering in early transplanting and shorter flowering-to-maturity phases in late transplanting. Among management practices supplemental irrigation (50mm) and high plant density increased rice grain yield by 7–22% and 6.7–12.7% under delayed transplanting, respectively. These findings offer a transformative reference for NEH region farmers, promoting resilient rice production and supporting sustainable intensification to enhance food security in this resource-rich yet underutilized region.

# Biochemistry

Mr. Mohammed salman C. K.

**Name of the Student** : **Mr. Mohammed Salman C.K.**
**Roll No.** : **21754**
**Chairperson** : **Dr. Veda Krishnan**

Dr. Veda Krishnan

*Title of the Thesis*

## 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 labour-intensive nature and high costs, impeding widespread implementation in clinical and industrial settings. This study developed and validated an optimized, 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.

# Bioinformatics

Ms. Surapuram Aswini

**Name of the Student** : **Ms. Surapuram Aswini**
**Roll No.** : **21915**
**Chairperson** : **Dr. Sanjeev Kumar**

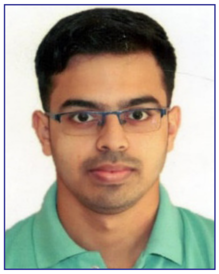
Dr. Sanjeev Kumar

*Title of the Thesis*

## Integrating Genome Wide Association Studies-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 important for understanding the genetic basis of complex traits. This project seamlessly integrates a GWAS analysis tool with the existing phenomics data analysis software platform High Throughput Phenomics-Data Analysis Platform (HtP-DAP) aimed at enhancing and streamlining GWAS analysis workflows. HtP-DAP has been specifically designed in-house project to facilitate the analysis of extensive image datasets of crop plants, captured through various camera systems. The integrated tool addresses key challenges in GWAS by offering robust preprocessing capabilities. 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. Result visualization is also one of the key components 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. 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.

# Entomology


Mr. Sourav Chakrabarty

**Name of the Student** : **Mr. Sourav Chakrabarty**
**Roll No.** : **21816**
**Chairperson** : **Dr. P. R. Shashank**


Dr. P. R. Shashank

*Title of the Thesis*

## 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 the present study, we have identified 20 insect species associated with crucifer crops. We have provided brief morphological descriptions for 14 insect species with illustrations, and comparative diagnostic characters with the related species. We have also prepared a comprehensive checklist of agriculturally important insects associated with crucifers, comprising 289 species, with special reference to their functional roles and analysed species diversity and functional diversity. Further, for the identification of insects and their damage symptoms in crucifer crops, a YOLOv5l-based single-stage object detection model has been developed. A total of 2,730 images are captured from different fields and poly houses using different smartphones and an SLR camera. The images are curated, annotated, resized, augmented, split, 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 0.87%, 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 the AI DISC mobile application. In conclusion, this study is a novel approach wherein taxonomic identification of insects on crucifers is linked with developing an artificial intelligence-based detection model.

# Environmental Sciences


Ms. Ashwaini Yadav

**Name of the Student** : **Ms. Ashwini Yadav**

**Roll No.** : **60124**

**Chairperson** : **Dr. Ashish Khandelwal**


Dr. Ashish Khandelwal

### *Title of the Thesis*

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

Surface-tension reducing compound (37.4 mN/m , yield 2.65 g/L) was isolated from Lysinibacillus sp. MW444883 and its putative nature were identified using CTAB/methylene blue agar test, bromothymol blue test, biuret test, FTIR (3284/cm and 1646/cm corresponds to the N-H and CO-N stretching vibrations), GC-FID [abundance of 26.6% Palmitic (C16:0) and 25.4% Oleic acid (C18:1 9c)] and LC-HRMS [Palmitelaidic acid methyl ester (m/z 268.2401), N~2~-Acetyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-alaninamide (m/z 1041.728, ($C_{47}H_{92}N_{16}O_{10}$)] as lipopeptide. 56.4–86.6% reduction in oil area (using ArC GIS software) 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. Rheology showed decrease in viscosity with the addition of biosurfactant in oil-water emulsion, leads 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 concentrations (0.5, 1, 3 and 5%) and pH (3, 5, 7, 9, 11). Degradation and half-life of PAHs in acidic and alkaline Inceptisol soils (collected from Delhi and Jharkhand agricultural field) under different environment (28 and 37 °C) varied for naphthalene (20.8–100%; 1.16–9.86 d), fluorene (5.8–93.8%; 5.6–14.4 d), phenanthrene (6.0–94.1%; 5.4–22.5 d) and pyrene (5.8–78.7%; 10.3–27.0 d), respectively. Three biosurfactant-based products, bead (PB), water dispersible granules (PWDG) and soluble liquid (PSL) were developed and tested in two different soils. In addition, effect of different doses of biosurfactant was also assessed (@ 425, 850, and 1700 µg/g) and the degradation effect in biosurfactant (free from) and formulated form was assessed. 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 not much effect of the double dose of biosurfactant on degradation. Among different formulations, soluble liquid (PSL2) based formulation was found to be effective for the degradation of PAHs in soil. $CO_2$ release varied from 189-430 mg/kg/d in Delhi soil as compared to Jharkhand soil (146–401 mg/kg/d). Isolated biosurfactant was also found effective against whitefly (LC50 0.044%).

# Floriculture and Landscaping

Mr. Shorya Sharma

**Name of the Student** : **Mr. Shorya Sharma**
**Roll No.** : **21963**
**Chairperson** : **Dr. Reeta Bhatia Dey**

Dr. Reeta Bhatia Dey

*Title of the Thesis*

## 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 the form of leaf spot and 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 the 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.

# Fruit Science


Mr. Sahil

**Name of the Student** : **Mr. Sahil**
**Roll No.** : **21875**
**Chairperson** : **Dr. R.M. Sharma**


Dr. R. M. Sharma

*Title of the Thesis*

## 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) (641–4762.07 mg 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 nutrient concentrations (K, P, Ca, Mg, Fe, Zn, Mn, and Cu), which were higher in the 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.

# Genetics and Plant Breeding

Mr. K. Victor Paul

**Name of the Student** : **Mr. K. Victor Paul**
**Roll No.** : **21775**
**Chairperson** : **Dr. Rajkumar Uttamrao Zunjare**

Dr. Rajkumar Uttamrao Zunjare

## *Title of the Thesis*

## Genetic variability and molecular analysis of folate accumulation in maize kernels

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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. Significant effects of genotype, DAP stage and genotype × DAP stage interactions were observed for 5-MTHF, 5-FTHF and total folate content. 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 of 0.36, ranging from 0.19 to 0.59. A neighbor-joining tree grouped 48 genotypes into three distinct clusters. The lack of significance of folate mean between different clusters implies the dispersion of high and low inbreds across the cluster. High folate lines such as PMI-SWT016, PMI-PV7 and MGU213wx can be used as donors for future biofortification programmes. The high folate-QTLs/genes can be mapped using mapping populations developed by crossing the contrasting inbreds (ex. PMI-PC101 × MGU213wx and MGU205R × PMI-PV7). Expression analysis of three candidate genes including 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. This is the first research effort in the country dealing with the characterization of the maize genotypes for folate accumulation.

# Microbiology

Ms. Kamali R.

Dr. Minakshi Grover

**Name of the Student** : **Ms. Kamali R.**
**Roll No.** : **21904**
**Chairperson** : **Dr. Minakshi Grover**

*Title of the Thesis*

## Prospecting bacterial exopolysaccharides for plant growth stimulation

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Microbial metabolites play a crucial role in sustainable agriculture by enhancing soil health, promoting plant growth, and improving crop resilience. Among these, exopolysaccharides (EPS) facilitate plant-microbe interactions and can serve as biostimulants, reducing reliance on chemical fertilizers. This study explored the potential of EPS from pearl millet seed endophytic bacteria (PMSEB) for plant growth stimulation. Initially, 86 PMSEB strains along with three characterized PGPB Mezorhizobium ciceri (Ref 1), *Azospirillum formosense* AIM57 (Ref 2), and *Bacillus subtilis* RP24 (Ref 3) were screened for EPS production on nutrient agar and ATCC No. 14 media. EPS was extracted using the ethanol precipitation method from selected strains and quantified using the anthrone method, with strain PC7N47 producing the highest EPS. A pot study revealed that inoculation with strains PC7T5, PC7N47, and MPT77 significantly enhanced early-stage wheat growth. The agar plate bioassay confirmed EPS's biostimulatory effect on wheat germination, seed vigor indices and dry weight, suggesting its potential to improve wheat seedling growth. EPS exhibited strain-specific and dose-dependent biostimulatory effects (0.25%, 0.5%, 1%). Based on biostimulatory effects, three PMSEB strains (MPT27, PC7N47, and PC7T5) along with Ref 1 were selected for EPS production optimization. Optimal conditions were 30°C, pH 7, and sucrose as the carbon source, except for PC7T5, which preferred 45°C and pH 6. Nitrogen sources varied, with MPT27 favoring $KNO_3$, PC7N47 urea, and PC7T5 utilizing both. EPS characterization revealed differences in water absorption capacity and antioxidant activity. FTIR analysis confirmed polysaccharide structures, while HPLC-based compositional analysis identified MPT27 and PC7N47 EPS as heteropolysaccharides and PC7T5 EPS as homopolysaccharides. SEM showed compact fibrous matrices, enhancing water retention. The selected strains were identified as *Atlantibacter hermannii* MPT27 (PQ182223), *Bacillus subtilis* sub sp. subtilis PC7N47 (PQ182224), and *Bacillus subtilis* subsp. subtilis PC7T5 (PQ182225). These findings highlight PMSEB as promising EPS producers and potential biostimulants in agriculture.

# Molecular Biology and Biotechnology


Mr. Akshay Bharat Ghodake

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| **Name of the Student** | : | **Mr. Akshay Bharat Ghodake** |
| **Roll No.** | : | **21761** |
| **Chairperson** | : | **Dr. Sarvjeet Kaur** |


Dr. Sarvjeet Kaur

## *Title of the Thesis*

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

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*Fusarium oxysporum* and *F. graminearum*, two of the top five 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 agroclimatic zones in India. Thirty-four Bt isolates were selected from our collection of native isolates, based on best gene profiles studied previously in our laboratory. The genetic diversity of selected isolates was identified through Amplified Ribosomal DNA Restriction Analysis (ARDRA), which produced 22 distinct band patterns and helped us to include most diverse isolates for further screening. Out of a total 34 isolates, PCR screening revealed the 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 the involvement of other bioactive factors. Chitinolytic activity confirmed using Chitinase-Detection Agar in isolates SK-957 and SK-966, correlated with the results of bioassay and observation of fungal mycelial degradation and cell wall thinning, indicating chitin breakdown. Considering the importance of chitinases, cloning and sequencing of chi genes from the 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 *in-silico* 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 in Integrated disease management (IDM) systems, offering an environmentally friendly alternative to chemical fungicides and promoting sustainable agriculture.

# Plant Genetic Resources


Mr. Suhail Ansari

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| **Name of the Student** | : | **Mr. Suhail Ansari** |
| **Roll No.** | : | **21928** |
| **Chairperson** | : | **Dr. Manjusha Verma** |


Dr. Manjusha Verma

*Title of the Thesis*

## 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 its diverse uses in culinary and medicinal applications. This study, provides an in-depth analysis of 96 accessions to assess their genetic and nutritional variability. Utilizing 16 novel genomic Simple Sequence Repeat (SSR) markers, the molecular characterization uncovered substantial genetic diversity, 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 6.31–17.61 g/100 g, calcium levels varied from 113.01–408.02 mg/100 g, iron from 2.09–14.32 mg/100 g, potassium from 652.45–1913.22 mg/100 g, and magnesium from 133.86–289.18 mg/100 g. Additionally, moisture content ranged from 7.85–25.12%, influencing post-harvest handling and storage. These findings present the 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.

# Plant Pathology

Mr. Prantik Mazumdaer

**Name of the Student** : **Mr. Prantik Mazumder**
**Roll No.** : **21789**
**Chairperson** : **Dr. Anirban Roy**

Dr. Anirban Roy

*Title of the Thesis*

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

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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.

# Plant Pathology

Ms. Sangale Smita Bhausaheb

**Name of the Student** : **Ms. Sangale Smita Bhausaheb**
**Roll No.** : **21902**
**Chairperson** : **Dr. Malkhan S. Gurjar**

Dr. Malkhan S. Gurjar

*Title of the Thesis*

## 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 0.05–0.60, 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.

# Plant Physiology


Mr. Krutika S.

**Name of the Student** : **Ms. Kruthika S.**
**Roll No.** : **70018**
**Chairperson** : **Dr. Gurumurthy S.**


Dr. Gurumurthy S.

## *Title of the Thesis*

## 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 under varying water stress levels in five genotypes. 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.

# Seed Science & Technology


Ms. Ayushi Yadav

**Name of the Student** : **Ms. Ayushi Yadav**
**Roll No.** : **21907**
**Chairperson** : **Dr. Sangita Yadav**


Dr. Sangita Yadav

*Title of the Thesis*

## 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* sub *sp. chinensis*, *B. rapa* var. toria, *B. napus*, *B. rapa* var. *yellow sarson*, and *B. nigra*, were analysed for seed germination, seed vigour indices, oil content, and fatty acid composition. Seed germination percentages varied from 2–100%, with a mean of 75%, and significant variation was observed in seed vigour indices (I and II). Biochemical analysis revealed oil content ranging from 18.03–47.48% 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 R-squared (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, brings forth a novel approach for effective and practical seed viability and vigour prediction.

# Soil Science

Mr. Arijit Chowdhuri

**Name of the Student** : **Mr. Arijit Chowdhuri**
**Roll No.** : **60123**
**Chairperson** : **Dr. Manoj Chaudhary**

Dr. Manoj Chaudhary

*Title of the Thesis*

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

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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 present study 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. The 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.

# Vegetable Science


Ms. Ananya P. Kumar

**Name of the Student** : **Ms. Ananya P. Kumar**
**Roll No.** : **21862**
**Chairperson** : **Dr. Jeetendra Kumar Ranjan**


Dr. Jeetendra Kumar Ranjan

*Title of the Thesis*

## 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 as 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 hydroponic phenotyping approach. This underscores its applicability for efficient and rapid screening against *Fusarium* wilt. Furthermore, molecular marker analyses using SCAR and SSR markers validated the observed resistant reactions. With good polymorphism and phenotypic variation rates, the reported three SSR markers hold significant potential for marker-assisted selection within the germplasm. Phenol estimation also indicated differential responses among resistant and susceptible accessions upon infection. The identified resistant genotypes, along with the phenotypic, anatomical, molecular and biochemical insights, will contribute to advancing brinjal improvement programs aimed at enhancing resistance to Fusarium wilt.

# Ph.D.
# Thesis Abstracts

# Agricultural Chemicals

Ms. Rajni Godara

**Name of the Student** : **Ms. Rajni Godara**
**Roll No.** : **11665**
**Chairperson** : **Dr. N.A. Shakil**

Dr. N.A. Shakil

*Title of the Thesis*

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

A series of 32 prenylated chalcones were synthesized by microwave-assisted green synthesis with higher yield (86–95%) and lower reaction time (1–4 min) as compared to the conventional method. 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 compound 5B to be the most active with LC50 of 30.40, 20.11, and 14.47 µg/mL after 24, 48 and 72 h, respectively. Among (6A-6P) series, compound 6F was found most active with LC50 17.19, 9.22 and 4.69 µg/mL after 24, 48 and 72 h, respectively. Compounds 6B, 6D, 6E , and 6F were taken for pot study, which revealed the highest activity of 6F @ 1000 µg/mL at 30 DAI and 60 DAI with enhanced plant growth parameters. Among (5A-5P) series, 5E and 5B having ED50 23.28 and 25.70 µg/mL possessed highest activity against *S. rolfsii* and *F. oxysporum*, respectively. Among (6A-6P) series, 6P, showed the highest antifungal activity against *S. rolfsii* (ED50 25.02 µg/mL) and *F. oxysporum* (ED50 31.87 µg/mL). Compound 5E and 5M were chosen for pot experiments against *S. rolfsii*, revealing significant increase in shoot length for 5E followed by 5M @ 1000 µg/mL at 60 DAI. Minimum percent disease incidence was observed for 5E @ 1000 µg/mL. Recoveries using modified QuEChERS from fortified soil and tomato samples were in the range 70–120% at 0.05 and 0.1 µg/g fortification levels. The dissipation studies were conducted and half-lives of the compounds 5E, 5M, 6B, 6D, 6E, 6F, hexaconazole and fluopyram in soil were found to be 1.31, 1.47, 1.60, 1.52, 1.07, 1.51, 18.57 and 26.86 days, respectively.

# Agricultural Economics

Mr. Omprakash Naik

**Name of the Student** : **Mr. Omprakash Naik**
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**Chairperson** : **Dr. Venkatesh P.**

Dr. Venkatesh P.

*Title of the Thesis*

## 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. Land use change is the primary force driving changes in agro-ecosystem service. 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, a research 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% 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 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). The soil loss prevented by cropland was 21.4 tonnes/ha/year during 2019–20. The economic value of carbon sequestration and soil loss prevention were 442 and 20 $/ha/year 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) has the highest carbon stock (51.86 Mg C/ha), followed by Conservative Agriculture (CA). The CA offers opportunities for increasing farmers' income by linking to carbon credit markets. Around 98% of farmers showed a willingness to enroll in conservative agriculture. Single-bound contingent valuation analysis found a mean compensation of ₹ 5,645/ha is required for practicing conservative agriculture by the farmers. The consumers are willing to pay an extra ₹ 10.45/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.

# Agricultural Engineering

Mr. Manojit Chowdhury

**Name of the Student** : **Mr. Manojit Chowdhury**
**Roll No.** : **11684**
**Chairperson** : **Dr. Tapan Kumar Khura**

Dr. Tapan Kumar Khura

*Title of the Thesis*

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

Rice, a staple for over 60% of India's population, is essential for food security, with production needing to meet a projected demand of 140 million tonnes by 2050. However, low nitrogen use efficiency (NUE) in rice results in excessive nitrogen fertilizer application, leading to environmental and economic challenges. This study developed a nitrogen assessment and prescription device using vegetation indices (NDVI, NDRE, and RVI) for real-time, site-specific nitrogen management. The research involved analysing rice canopy spectral characteristics, optimizing nitrogen levels, and developing a soil slit-cutting mechanism and aqueous urea metering system. The device's performance was compared to GreenSeeker and Spectroradiometer in assessing vegetation indices, and correlations between these indices and leaf nitrogen concentrations (LNC) at different growth stages and nitrogen levels were established. The results showed strong correlations with commercial devices, and the paired t-test revealed no significant difference ($p < 0.05$) between the Spectroradiometer, GreenSeeker, and the developed device in assessing NDVI, NDRE, and RVI. Optimal data collection was achieved at a sensing height of 30 cm with a field of view of 36.86 degrees, with precision and accuracy exceeding 98% and 94%, respectively. NDVI and NDRE were reliable indicators of nitrogen status, while RVI improved at later growth stages. The device's development cost was ₹5218, making it economically viable. Aqueous urea solutions above 12% nitrogen concentration were lethal to rice, while the N10 treatment achieved the highest benefit-cost ratio of 2.37. Three NAP devices on a high-clearance vehicle allowed variable-rate subsurface application of aqueous urea, covering three rows simultaneously. Operating at 1.83 km/h and a sensing height of 31.44 cm, the system achieved a precision rate of 90.6%. It reduced fertilizer use by 22.4% and 28.4% during the first and second top-dressing stages, respectively, increased yield by 12.3%, improved NUE by 53.7%, and reduced fertilizer costs by 25.4%, providing significant economic and environmental benefits.

# Agricultural Extension Education

Mr. Sujay Basappa

**Name of the Student** : **Mr. Sujay Basappa Kademani**

**Roll No.** : **11426**

**Chairperson** : **Dr. M. S. Nain**

Dr. M.S. Nain

*Title of the Thesis*

## A study on institutional interventions for agri-entrepreneurship development

Agricultural sector has undergone a remarkable transformation in the country evolving from reliance on food aid to becoming a powerhouse in food production. Despite this progress, farmers continue to grapple with economic challenges. Dalwai Committee, advocates for agri-entrepreneurship to enhance farmers' economic sustainability and drive innovation. This study was conducted on such a backdrop, with specific objectives including the analysis of entrepreneurship promoting institutions, assessment of the extent of support and its effect, identifying factors for effective intervention, and exploring constraints and suggestions. The study focused on selected institutions from Telangana and Rajasthan states, chosen purposively with a total of 200 entrepreneurs and 43 professionals as the respondents. Majority of the institutions established in the past 5–10 years, were majorly (56.3%) affiliated with academic or research institutions, emphasizing entrepreneurship development and most of them (56.25%) operated with national coverage. Among the strategic areas of support, there was a unanimous emphasis on training & workshops with experts, certification support (68%), and business and financial model development (56.3%). An analysis of institutional support using Institutional Support for Agripreneurship Development Scale (ISAD-S) revealed satisfactory support in production and marketing and technical dimensions, albeit with room for improvement in legal, bureaucratic and financial dimension. A robust Index for Perceived Effect of Institutional Support for Agripreneurs (I-PEISA) was constructed to measure the effectiveness of institutional interventions. Further, determinants of effective intervention were explored considering the psycho-personal, socio-economic and institutional factors. Support for project formulation, vocation-oriented syllabi, long term strategic involvement, and Training Institute-Industry-Market-Entrepreneur (T-I-M-E) connect were emphasized. Constraints such as lack of priority lending, delays and bias in grants, and a lack of prototype testing facilities were reported. Recommendations included transparent evaluation processes, post-programme loan & subsidy, streamlining administrative processes, and fostering an entrepreneurial culture among farmers. Both entrepreneurs and experts desired better financial support.

# Agricultural Physics


Ms. Nandita Mondal

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| **Name of the Student** | : | **Ms. Nandita Mondal** |
| **Roll No.** | : | **11706** |
| **Chairperson** | : | **Dr. Pragati Pramanik Maity** |


Dr. Pragati Pramanik Maity

*Title of the Thesis*

## 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 2021–22 and 2022–23, 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-products 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. The result showed that a significantly higher wheat yield was recorded in PBB+R (6.12 t/ha) compared to CT (4.88 t/ha). Overall, the retention of crop residues has significantly improved the grain yield by ~13%. Approximately, a 15.7% increase in grain yield was reported under CA in the 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 the value of SOC stock over CT. Grain yield (t/ha) was strongly (positive) correlated with soil available N ($R^2 = 0.84$), soil available P (R2= 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 ₹ 122,733/ha (CT) to ₹ 152,452/ha (PBB+R) with a mean value of ₹ 137,171/ha. 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.

# Agricultural Statistics

Mr. Harish Nayak G. H.

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**Roll No.** : **11999**
**Chairperson** : **Dr. Md Wasi Alam**

Dr. Md Wasi Alam

## *Title of the Thesis*

## Modeling agricultural price through deep learning techniques

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.

# Agronomy


Mr. K. Srikanth Reddy

**Name of the Student** : **Mr. K. Srikanth Reddy**
**Roll No.** : **12001**
**Chairperson** : **Dr. C.M. Parihar**


Dr. C.M. Parihar

*Title of the Thesis*

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

The rice-wheat system in eastern India faces persistent challenges of lower productivity and resource exploitation. Achieving a balance between economic viability, environmental sustainability, and system resiliency requires all-inclusive efforts. Our research combines field experiments (conducted during 2022–23 and 2023–24, at IRRI-SARC, Varanasi) with the use of the DNDC model, and meta-analysis to assess the impacts of conservation agriculture, irrigation methods, and nitrogen levels on crop productivity, economics, and greenhouse gas emissions in rice-based cropping systems. The results showed higher productivity under sub-surface drip (SSD)-based methods, which consistently matched or exceeded PTR-based plots, bridging the 15% yield gap observed in flood-irrigated DSR plots. Nitrogen uptake under SSD treatments was 14–20% higher, reflecting the higher nitrogen use efficiency of these plots. The SSD plots also saved water by ~70%, resulting in 3–4 times higher water productivity compared to traditional flood-irrigated plots. Economic analysis revealed that SSD-DSR-based plots had 24–29% higher net returns than PTR-based plots. Further, a meta-analysis confirmed the environmental benefits of DSR, showing a 69.9% reduction in methane emissions, a 36.7% reduction in global warming potential, and a 34.4% lower carbon footprint. However, nitrous oxide emissions increased by 84.6%, with a ~11% yield penalty in dry DSR. The DNDC model also validated these findings, showing a 75–83% reduction in methane emissions and improved water and nitrogen balance in SSD-based plots by minimizing evaporation, leaching, and volatilization losses. Furthermore, the TOPSIS analysis ranked 75% RDN + SSD as the most eco-optimized treatment in terms of yield-emissions relationship and profitability of rice-based systems. The findings of our study offer key insights into trade-offs of DSR for sustainable intensification with lower environmental footprints in the rice-based production systems for a region identified as a priority for agricultural expansion by the Government of India under the Bringing Green Revolution to Eastern India (BGREI) initiative.

# Biochemistry


Ms. Minkshi Dutta

**Name of the Student** : **Ms. Minakshi Dutta**
**Roll No.** : **11734**
**Chairperson** : **Dr. Vinutha T.**


Dr. Vinutha T.

## *Title of the Thesis*

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

Pigeonpea (*Cajanus cajan* L.), an important legume crop presents a valuable source of plant-based protein, particularly in regions facing protein malnutrition. However, anti-nutritional 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 and protein quality of two pigeonpea 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 pigeonpea protein isolates (PpPIs) from them. Total polyphenol levels in 30 genotypes ranged from 215.3–1250.2 mg GAE/100g, 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, increasing essential amino acids (0.78–7.0%) and *in vitro* protein digestibility, reaching 84.3% in Pusa Arhar 2018-4 and 90.4% in ICP 1452. Autoclaving was most effective, reducing total polyphenols (36.5%) and trypsin inhibitor activity (68.6% in Pusa Arhar 2018-4, 65.0% in ICP 1452) and enhancing the 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 and emulsifying stability. Cytotoxicity assays confirmed no adverse effects and autoclaved hydrolysates exhibited improved amino acid bioavailability and upregulated PepT1 and downregulation of SREBF2 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.

# Bioinformatics


Ms. Parinita Das

**Name of the Student** : **Ms. Parinita Das**
**Roll No.** : **11740**
**Chairperson** : **Dr. Sarika**


Dr. Sarika

*Title of the Thesis*

## A study on development of artificial intelligence-based methodology for identification of copy number variation in crops

Copy number variations (CNVs), including DNA duplications and deletions, have profound effects on gene expression, adaptation, and phenotypic diversity. Structural variations play a central role in the genome evolution and environmental adaptability of plants. This work presents MLDeCNV, a new machine-learning framework for accurate CNV detection from next-generation sequencing (NGS) data. Existing CNV detection algorithms frequently fail to detect small CNVs or areas with low read depth, resulting in incomplete detection. MLDeCNV overcomes these limitations by incorporating 32 NGS-derived features and fusion of predictions from several CNV detection tools, which are confirmed by PCR and aCGH. A novel aspect is the application of Smote-TomekLinks, a data-balancing algorithm that enhances model performance by addressing class imbalances during CNV prediction. MLDeCNV performs better than current tools like Delly, CNVnator, and Manta, with an AUC of 0.96 across a wide range of species such as rice, Arabidopsis, and pomegranate. To facilitate easier access, a web-based application was created, enabling researchers to upload typical genomic inputs and categorize CNVs as deletions, duplications, or no CNV through an easy-to-use interface. A genome-wide CNV analysis in black pepper and bitter gourd also revealed thousands of CNVs associated with important agronomic traits, including stress tolerance and pathogen resistance. These results illustrate the promise of CNVs in crop breeding, marker-assisted selection, and species adaptation research. By combining CNV information with genome-wide association studies (GWAS), MLDeCNV enables the identification of significant loci related to desirable traits. This study presents an effective tool for agricultural genomics, allowing precision breeding and evolutionary biology innovation.

# Entomology


Mr. Rudra Gouda M.N.

**Name of the Student** : **Mr. Rudra Gouda M.N.**
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Dr. S. Subramanian

## *Title of the Thesis*

## 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. Behavioural 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 signalling, insecticide resistance, and reproduction. These findings offer potential avenues for developing innovative pest management strategies targeting host recognition and reproductive processes.

# Floriculture and Landscaping

Ms. Chandana S.

**Name of the Student** : **Ms. Chandana S.**
**Roll No.** : **11778**
**Chairperson** : **Dr. Sujatha A. Nair**

Dr. Sujatha A. Nair

*Title of the Thesis*

## 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 (175.3 days), maximum spikes/plant (8.9), florets/spike (7.67), longest spikes (49.4 cm), increased spike longevity (62.3 days) and extended vase life (42 days) along with superior physiological parameters. Spacing plants at 30 cm × 30 cm in a quincunx planting system on vertical frames resulted in superior vegetative, physiological and flowering traits, including earlier spike initiation (171.5 days) and maximum spikes/plant (8.9). 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 178.7 days.

In conclusion, cultivating *Dendrobium* using charcoal in netted pots spaced at 30 cm × 30 cm on vertical frames in a quincunx system is sustainable and profitable, boosting yield and plant density by 142.8% over the conventional system with a 3.77 benefit-cost ratio. Value-added products can contribute to further enhancing income and generating employment opportunities. Aligning with UN Sustainable Development Goals (SDG 8, 11, and 15), promoting economic growth, sustainability and environmental conservation.

# Fruit Science


Mr. Narendra Singh

**Name of the Student** : **Mr. Narendra Singh**
**Roll No.** : **11261**
**Chairperson** : **Dr. R. M. Sharma**


Dr. R.M. Sharma

*Title of the Thesis*

## 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 282.0–584.77 g, 4.29–9.28 mm, and 22.9–48.2%, 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 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 (60.8–251.1 mg/L), K (574.7–1195.5 mg/L), Ca (153.6–736.0 mg/L), Mg (23.7–101.8 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 (18.4–45.9 mg/L) and Cl (17.0–289.7 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.

# Genetics and Plant Breeding

Mr. Hriipolou Duo

**Name of the Student** : **Mr. Hriipolou Duo**
**Roll No.** : **11520**
**Chairperson** : **Dr. Firoz Hossain**

Dr. Firoz Hossain

*Title of the Thesis*

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

Traditional maize endosperm protein lacks sulphur containing essential amino acid - methionine. Multi-location evaluation of 48 inbreds revealed significant variation for methionine (0.031-0.305%). Analysis using a 7 × 7 half-diallel mating design revealed the predominance of additive gene action for methionine accumulation. Sequence characterization of *aspartate kinase-2 (ask2), floury-2 (fl2), delta zein structural-10 (dzs10) and delta zein structural-18 (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 favourable 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 0.26%, 0.35% and 0.34%, respectively while the original hybrid had 0.19% methionine. Expression analysis of *ask2*, *fl2* and *TIDP2802* (putative gene in *dzr1* locus) genes across 20-, 30- and 40-days after pollination (DAP) revealed the 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 the original genotypes. Methionine-rich maize hybrid developed in the doctoral research programme has been nominated to the AICRP trial. This is the first report on the development of high methionine biofortified maize hybrids.

# Microbiology


Mr. Devashish Pathak

**Name of the Student : Mr. Devashish Pathak**
**Roll No. : 11812**
**Chairperson : Dr. Archna Suman**


Dr. Archna Suman

*Title of the Thesis*

## 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/h), 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. The SMs 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 the 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, ear head length, plant dry matter, and chlorophyll content. SM3+HA consistently showed the greatest improvements, leading to a 56.8% 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.

# Molecular Biology and Biotechnology


Mr. Gopal

**Name of the Student** : **Mr. Gopal**
**Roll No.** : **11552**
**Chairperson** : **Dr. Pradeep Kumar Jain**


Dr. Prdeep Kumar Jain

### *Title of the Thesis*

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

Chickpea, a legume crop, important source of dietary protein, particularly in countries where plant-based nutrition is prevalent. The present study explores the genes, microRNAs and circular RNAs affecting seed storage protein accumulation in six chickpea genotypes, with contrasting seed protein content, namely high protein content genotypes (HPC, ICC8397, ICC13461, ICC13523) and low protein content genotypes (LPC, FG212, BG3054, BG3043). Using RNA-seq analysis, we identified 2,810 differentially expressed genes (DEGs). From small RNA analysis total of 42 conserved miRNAs belonging to 17 families were identified. The target genes were predicted using the psRNATarget server, and it was found that *ATP-binding cassette* (ABC) transporter gene and *ABA-Insensitive 5* (ABI) gene targeted by miR156 and miR319, respectively showed negative correlation and are involved in seed protein accumulation in chickpea. Importantly, the role of miR156 was also elucidated in protein content regulation in chickpea, as we observed that over-expression of CamiR156 in *Arabidopsis* led to the extension of the vegetative phase and reduction of the reproductive phase of development. Elevated miR156 levels in the HPC genotype (ICC8397) suggest its role in seed development by regulating amino acid transporters *(AATs)*. A comprehensive analysis of the AAT gene family was carried out in chickpea leading to the identification of 109 *AAT* genes, representing 10 subfamilies with random distribution across the chickpea genome. Tissues specific expression pattern of many *CaAAT* genes was observed like *CaAAP7* and *CaAVT18* in nodules, *CaAAP17*, *CaAVT5* and *CaCAT9* in vegetative tissues while *CaCAT10* and *CaAAP23* in seed related tissues. Developing seed transcriptome data revealed that genotypes having HPC (ICC8397 and ICC13461) showed low expression of *CaAATs* as compared to the genotypes having LPC (FG212 and BG3054). To have a better insight into this complex trait and identified some more negative regulators (sugars, fatty acids, flavonoid encoding genes) of SPC accumulation, we worked on the 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. Detailed analysis underscored the relevance of circRNAs for the regulation of seed protein content. Integration and a better understanding of differentially expressed genes, circRNAs and miRNAs data hold promise for chickpea crop improvement, offering avenues for targeted manipulation to enhance traits crucial for yield and quality.

# Nematology


Mr. Manish Kumar

**Name of the Student** : **Mr. Manish Kumar**
**Roll No.** : **11555**
**Chairperson** : **Dr. Anil Sirohi**


Dr. Anil Sirohi

*Title of the Thesis*

## 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 30–70%. Nematode's unique characteristics like, feeding in wheat stem and floral primordia along with survival in the 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 the nematode's life cycle was affected by wheat sowing time and the external environment, especially temperature. After calculating Growing degree days, it was found that the 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 the 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 shows the presence of a large number of glycolases, lyases, hydrolases and 14-3-3, SNARE like effect or 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 nematode which are associated with stress resistance. 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.

# Plant Pathology

Ms. Charishma K.

**Name of the Student** : **Ms. Charishma K.**
**Roll No.** : **11568**
**Chairperson** : **Dr. A. Kumar**

Dr. A. Kumar

### *Title of the Thesis*

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

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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 55.1–78.3%, 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 23.7–54.4%. 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.

# Plant Phsyiology

Mr. Sukumar Taria

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| **Name of the Student** | : | **Mr. Sukumar Taria** |
| **Roll No.** | : | **11851** |
| **Chairperson** | : | **Dr. Ajay Arora** |

Dr. Ajay Arora

*Title of the Thesis*

## Stem reserve mobilization and stay-green traits for yield stability in wheat under combined heat and drought stress

Stay-green (SG) and stem reserve mobilisation (SRM) are two mutually exclusive traits, which can contribute to grain filling during abiotic stress. However, when current leaf photosynthesis is inhibited by abiotic stress, water-soluble carbohydrates (WSCs) stored in stems serve as a potential buffer for grain filling. 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 as well to pyramid these traits to enhance resource availability using 220 RILs population developed by crossing 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 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). Genes like K+ transporter-9, glycine decarboxylase-1-like (GDC), aspartyl protease family protein-2-like were found to be linked with LSR. Genes like endoglucanase-8-like, 9-cis epoxy carotenoid dioxygenase (NCED1), serine-threonine (ST) protein kinase OSR1-like and pentatricopeptide repeat containing protein (PPR5) were found be linked with SRE. The mapped QTLs were also validated by employing a physiological and gene expression approach during the rabi season 2022–23. Using multi-trait genotype-ideotype distance index (MGIDI), HDHI 113 and HDH I87 were selected as superior lines with combined SG and SRM traits. From the QTLs analysis of SRM from different components of the main culm, 44 major QTLs were also mapped and can be transferred to elite wheat cultivars after validation.

# Post Harvest Management


Mr. Harish T.

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*Title of the Thesis*

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

Kamalam (*Hylocereus sp.*) or dragon fruit, is an exotic fruit largely imported. During the last decade, domestic cultivation has been on the rise in several states, which may result in a glut in the near future. It is highly perishable having 5–7 days shelf life and extendable up to 2–3 weeks at low temperature. Dragon fruit powder in the market is expensive due to the spray or freeze-drying technology employed. The present study conducted at ICAR-Indian Institute of Horticultural Research, Bengaluru, aimed to standardize a cost-effective tray drying process using additives for producing free-flowing dragon fruit pulp powder and to evaluate its quality, packaging and storage potential. Red pulp dragon fruit (*Hylocereus ployrhizus*) was blended with three different types of hydrocolloids, (maltodextrin, corn starch and carboxymethyl cellulose) in various combinations and levels ranging from 2–64%. These pulp mixtures were uniformly spread on SS 304 grade trays and dried in a hot air tray dryer at 60±1°C temperature for 6-7 hours, till the sheet became brittle. The dried sheets were removed and powdered using a pulveriser. The free-flowing dragon fruit powder produced with 4% of additive combination-3 exhibited superior nutritional quality compared to other levels of additives. Packaging and storage trials of the powder revealed that powder packed in aluminium laminate pouches and stored at 13±1°C retained higher nutritional and microbiological quality over six months period, in terms of higher betalain content (323.15 mg BCE/100 g), phenols (140.7 mg GAE/100 g) and antioxidants (226.6 mg AEAC/100 g) compared to those at ambient temperature. Value-added products like cookies, milkshake, and tea infusion made using the powder developed and they had higher sensory scores (7.84–8.22/9.0) and nutritional quality. The significant achievement of this study was a development of a low-cost tray drying process to produce free-flowing red pulp dragon fruit powder, appropriate packaging material, and storage method. The cost of production was reduced by more than 50% making it a cost-competitive process with enhanced nutritional quality compared to the commercially available red pulp dragon fruit powder.

# Soil Science


Mr. Md. Basit Raza

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Dr. S.P. Datta

*Title of the Thesis*

## 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), followed by sugarcane bagasse (264 mg/kg), vermicompost (246 mg/kg), and fly ash (242 mg/kg). A novel bentonite-supported nano zero-valent iron (nZVI-Bento) (at 0.5 g/L) exhibited significant As adsorption, reducing water As levels below permissible drinking water limits (10 µg/L). The adsorption maxima (qmax) predicted by the Langmuir adsorption isotherm were 354 and 198 mg/g 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.

# Vegetable Science

Mr PradeepKumara N.

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Dr Chander Parkash

## *Title of the Thesis*

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

One hundred twenty-five $F_2$ 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 colour, 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 QTL IciMappingV4.0 software, 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 (q*NFFF2.1, 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 13.1%, while the other (*qNFFF2.1*) was minor, with a PVE of 6.95% during the summer season of 2022.


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