65 YEARS POST GRADUATE SCHOOL 1958-2023

# Sixty First Convocation

## Significant Post Graduate Students' Research

February 20, 2023 (Monday)

# Abstracts

**Chairman**

**Dr. S L Mehta**

Former Vice Chancellor, MPUAT, Udaipur, Rajasthan

**Convenor**

**Dr. Robin Gogoi**

Head & Professor, Division of Plant Pathology

**Post Graduate School**
ICAR-Indian Agricultural Research Institute
New Delhi - 110012

भारत 2023 INDIA

INTERNATIONAL YEAR OF
MILLETS
2023

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# M.Sc.
# Thesis Abstracts

# Agricultural Chemicals


Soumyajit Ghosal

**Name of the Student** : **Soumyajit Ghosal**
**Roll No.** : **21381**
**Chairperson** : **Dr Anirban Dutta**


Dr Anirban Dutta

## *Title of the Thesis*

## Biopolymeric formulation of lutein for its application as natural food colorant

---

Growing consumer awareness about the harmful health effects of artificial food coloring agents has increased the market demand of natural food colorants in recent times. Marigold (*Tagetes* sp.) flowers are the major non-food source of lutein, a naturally occurring yellow pigment from the xanthophyll group, in its esterified forms. The additional nutraceutical values of this pigment have further augmented its growth potential. Despite the extensive commercial exploitation of this pigment from *Tagetes* sp. to incorporate in food products, aqueous insolubility, chemical instability, and poor bioavailability have limited the potential of esterified lutein. To address these challenges, the present study was carried out to develop a formulation of the pigments extracted from marigold flowers, for its use as natural food colorant. Profiling of the xanthophyll pigments extracted from florets of a hybrid genotype (DAMH-39) of *Tagetes erecta* revealed the presence of lutein in its mono- and di-esterified forms. Comparison of extraction techniques suggested that almost same amount of xanthophylls could be extracted by ultrasonic probe extraction (UPE) using minimum solvent at relatively less time as compared to ultrasonic bath extraction and conventional solid-liquid extraction. Process optimization of the UPE technique using response surface methodology (RSM) in conjunction with genetic algorithm (GA) predicted the optimized extraction conditions (31.38 solvent to solid ratio, 56.56% ultrasonication amplitude, and 30 min ultrasonication time), at which a maximum xanthophyll yield of 13099.05 $\mu g\ g^{-1}$ was obtained. Comparison of antioxidant activities of the xanthophylls extracted by different techniques exhibited no significant difference in DPPH, ABTS and CUPRAC assays. However, FRAP assay suggested a relatively higher antioxidant capacity of xanthophylls extracted by the optimized process. Further, on a quest to develop a green process of extraction of xanthophylls from marigold, hydrophobic deep eutectic solvents (HDES) were explored. HDES were prepared using two long chain saturated fatty acids ($C_8$ and $C_{10}$) at different molar ratios, and were characterized by DSC, FT-IR, and $^1H$ NMR spectroscopy. The process of ultrasound assisted extraction technique using HDES was optimized by RSM to obtain a maximum xanthophyll yield of 7570.80 $\mu g\ g^{-1}$ at the model predicted optimized conditions (1.99 molar ratio of $C_8$:$C_{10}$, 99.40 $mL\ g^{-1}$ of HDES, and 32.98 min ultrasonication time). Around 72% of the extracted xanthophylls were recovered by switching the polarity of the eutectic solvent. Water soluble powder formulations of the xanthophylls were prepared in two steps: preparation of biopolymer stabilized oil-in-water microemulsions, followed by freeze drying. Suitable biopolymer, green solvent and three different surfactants were used to prepare 27 microemulsions with variable concentration of xanthophylls. Based on thermodynamic stability, dispersibility, droplet dimensions, and color expression, three microemulsions were chosen for preparation of powder formulations by freeze drying. The powder formulations were characterized using FT-IR spectroscopy and SEM. The readily water-soluble powder formulations were analyzed for their color expression in aqueous solution, which showed an inclination towards yellow color. Accelerated storage stability study recommended safe use and storage of the powder formulations at subzero temperature, but 39-86% degradation of xanthophylls was observed at higher temperatures. The powder formulations exhibited high antioxidant activities and considerable bioavailability at simulated *in vitro* conditions. The powder formulations prepared in this study addressed the insolubility issue of lutein esters and were found to produce transparent aqueous solutions. The prepared formulations may find their potential to use as natural colorants for food and beverage industries and pharmaceutical industries as well.

# Agricultural Economics


Likhita S

**Name of the Student** : **Likhita S**
**Roll No.** : **21387**
**Chairperson** : **Dr Anbukkani P.**


Dr Anbukkani P.

*Title of the Thesis*

## Economic assessment of maize value chain and it's impact on farmers income in Davanagere district of Karnataka

Maize crop (*Zea mays* L.) has an important place in the food grain basket of our country with 10% contribution and is the third most important food grain crop in India. Maize qualifies as one of the potential crop in realizing broader vision of doubling Farmer's income by 2022. Out of all maize produced, three-fourth of it is being processed as animal feed and rest of it is used for human consumption and industrial use.It is serving as raw material in industries like poultry feed manufacturing, bio-ethanol production, starch industry, Silage and Fodder preparation. A value chain involves a set of actors and activities that add value to agricultural produce before it reaches to end-consumers. FPO's, private industries in the maize production has enlarged and diversified the maize value chain. Karnataka is contributing 14.88% and 14.8% to all India area and production of maize. Many feed industries and other maize processing industries are located at Davanagere supplying maize processed products intra-state, inter-state and abroad. Based on this, the current study is under taken with the aim of understanding prospects of maize value chain and find out more profitable ways of marketing by farmers. The main objectives of the study were to analyze the production performance of maize in India,to examine the maize value chain and price realization under different marketing channels existing in Davanagere district of Karnataka and to evaluate the impact of the value chain on farmers income, identify constraints among different stakeholders. Growth rate in area, production, productivity in India from 1990-2020 was found to be 2%, 4.6% and 2.6%. Shift in area and production of maize from northern traditional maize growing states to southern states was found over last three decades in both share and growth rate. Break in area pf under maize was found in the year 2002 and in productivity was found in the year 2006. Out of four major marketing channels existing in Davanagere specially for poultry feed, channels which do not involve merchant middlemen gave high net returns to farmers. Farmers who had undertaken FPO-led marketing realized 6307.813 rupees/ha more than farmers not following channel. Factors like distance of FPO, credit source and whether nearest FPO is marketing maize or not had influence on farmers undertaking FPO-led marketing channel. Several production, technological and marketing constraints of farmers and constraints for other stake holders and FPO exist which needs to be taken care.

# Agricultural Engineering


Karishma Kumari

**Name of the student** : **Karishma Kumari**
**Roll No.** : **21394**
**Chairperson** : **Dr. Roaf Ahmad Parray**


Dr. Roaf Ahmad Parray

*Title of the Thesis*

## Development of sensor-based device for estimation of crop disease severity

An attempt was made to develop a reliable and affordable handheld sensor based device that can provide quantified information on disease severity of a crop and estimate the same in real time at early stages. The extent of disease severity using different sensors was explored by monitoring the spectral and color characteristics of healthy and disease inoculated plants. For this, 4-5 days old tomato and cowpea plants were inoculated with Young GBNV (groundnut bud-necrosis virus) through mechanical sap transmission (Inoculation) method. This was followed by collection of spectral reflectance data in appropriate wavelength bands (RGB, NIR, IR, and Visible) for virus inoculated and mock-inoculated plants of selected crops at different growth stages. A data base of 5000 datasets was developed by recording data on spectral reflectance and color values (R, G, B) at every 24 hours. The data collected was analyzed for disease severity classification using machine learning technique The results on disease severity classification were implemented for development of hand held device for disease severity estimation. The developed device consisted of different functional components like sensor, Raspberry pi microcontroller, OLED display and battery (power bank) integrated in such a way to have compact design using advanced 3-D printing system. The device was evaluated in lab condition for its performance for in terms of efficiency for estimation of viral disease severity in real time at 6 growth stages with four DPI intervals (0, 4, 8.12, 16, 20). The highest value of the correlation coefficient (r=0.87) between spectral count and disease severity was in NIR band (700-900 nm), while it showed a negative value at F1 (415 nm) and F2 (445nm). Most effective band for disease severity detection and estimation was observed as NIR band of spectral sensor with the correlation coefficient of 0.82 for disease severity in tomato plant and 0.73 for cowpea plant. The decision tree based machine learning algorithm resulted in 93.65% accuracy for disease classification in tomato and 87.50 % for cowpea. The decision tree based machine learning algorithm resulted in 93.65% accuracy for disease classification in tomato and 87.50 % for cowpea. The accuracy of the device in classifying disease severity was observed as 100 per cent with capability to distinguish the disease severity into five major class's i.e Class-0, Class-1, Class-2, Class-3, and Class-4 respectively representing a disease severity range of <1%, (1-25) %, (26-50) %, (51-75) % and >75%. Based upon the results obtained, it was concluded that the developed device can be used under laboratory condition providing real time data on disease severity within the range of five major classes.

# Agricultural Extension


Bhaskar Ghosh

**Name of the Student** : **Bhaskar Ghosh**
**Roll No.** : **21406**
**Chairperson** : **Dr. R.R. Burman**


Dr. R.R. Burman

*Title of the Thesis*

## Role of direct benefit transfer (DBT) in enhancing livelihood of small and marginal farmers: a special reference to the PM-KISAN scheme of Government of India

The evolution of cash transfers has benefited significantly from research on the various facets of poverty and vulnerability. The performance of India's small and marginal farmers (SMFs), who make up 86 percent of the country's farmers overall, is crucial for the country's long-term agricultural growth and food and nutrition security. The PM-KISAN scheme's success at improving living conditions is seriously concerning despite the data and facts offered in numerous government reports. A research study was conducted in the states of Uttar Pradesh and Bihar selected purposively due to highest no. of SMFs. Using the simple random sampling (SRS) method, the districts of Bahraich and Bulandshahr in U.P and Bhojpur and Muzaffarpur in Bihar were chosen. Two Gram Panchayats were chosen using SRS from each of these four districts. Using *ex post facto* research design, data was collected from 240 SMFs (120 beneficiaries and 120 non-beneficiaries) through stratified disproportionate simple random sampling procedure. Additionally, 30 officials in various Agricultural development departments were also chosen randomly from the respective districts. Thurstone's Equal Appearing Interval approach was used to create a perception scale ensuring its reliability and content validity. The majority of U.P. (50 percent) and Bihar (53.33 percent) beneficiaries had a neutral perception of the programme. A four-dimensional effectiveness index was created, and it was discovered that the majority of U.P. (63.33 percent) and Bihar (50 percent) beneficiaries thought the scheme was somewhat effective in terms of the income support it offered. Eighteen indicators covering the underlying assets of livelihood *i.e.* human capital, social capital, natural capital, physical capital, and financial capital, were used to generate the Livelihood Index (LI) using Principal Component Analysis (PCA). Beneficiaries of the scheme had a mean LI score of 0.396, while non-beneficiaries had a score of 0.366. Propensity Score Matching (PSM) was used to compare beneficiaries and non-beneficiaries in order to evaluate the scheme's performance. In comparison to non-beneficiaries of the programme, there was a significant 3.34 to 4.13 percentage point improvement in the beneficiaries' Livelihood Index. SWOT analysis combined with Analytical Hierarchical Process (AHP) revealed that the major strength was Amount is transferred directly to linked bank accounts without third party and major weakness was Faulty details in Aadhaar card or Land record or Bank account no. bars from receiving benefit respectively. Land records in PM-KISAN portal reflected differently than the title deeds of land under the farmer was the major constraint as perceived by the officials.

# Agricultural Physics


Sudipta Basu


Dr. K.K. Bandyopadhyay

**Name of the Student** : **Sudipta Basu**
**Roll No.** : **21411**
**Chairperson** : **Dr. K.K. Bandyopadhyay**

*Title of the Thesis*

## Effect of tillage, residue, irrigation and nitrogen management on soil physical properties and root growth in wheat

Field experiments were conducted in an ongoing long-term tillage experiment (since 2014) during the year 2021-22, rabi season with wheat (cv HD 2967) in a sandy loam soil (Typic Haplustept) at ICAR-IARI experiment farm (MB-4C), New Delhi with the following objectives: (i) To study effects of tillage, crop residue, irrigation and nitrogen management on major soil physical properties of an Inceptisol; (ii) To analyze the response of modified soil physical condition on root growth dynamics in wheat and (iii) To evaluate tillage-residue-irrigation-nitrogen interaction effects on water- and nitrogen use efficiency of wheat. The field experiment was carried out under a Split factorial plot statistical layout with the treatments comprising of two levels of tillage (Conventional tillage (CT) and No tillage (NT)), two levels of mulching (with maize crop residue mulch @ 5t ha-1 (R+) and without residue (R0)) as main plot factors and three nitrogen doses (50, 100 and 150% of the recommended dose of N) and two levels of irrigation (full irrigation (IF) and deficit irrigation (ID)) and as subplot factors. The results showed that there was increase in MWD(Mean Weight Diameter) at 0-5, 5-15 and 15-30 cm, soil depths under NT and crop residue mulching than CT and no mulch, respectively. With increase in nitrogen, the MWD of soil increased in these depths. There was decrease in BD and increase in SHC of soil under NT and crop residue mulching. There was increase in root length density (RLD) , root mass density (RMD) and root diameter (RD) of wheat under NT than that of CT. Global meta-analysis showed that under NT there was significant increase in RLD at 0-15 cm and 15-30 cm soil depths compared to CT At milking stage, RLD at 0-15 cm soil depth, was significantly positively correlated with MWD (r= 0.79**), WSA(r=0.77**) and SHC (r= 0.70*), but showed negative correlation with BD (r= -0.60*). Grain yield, PFPN and WP of wheat was not significantly influenced by either tillage or residue management but there was significant increase in grain yield, WP and PFPN of wheat with increase in nitrogen level but no significant difference was observed due to application of 100% and 150% RDN. Under full irrigation treatment (5 irrigations), grain yield was significantly higher than under deficit irrigation (3 irrigations). Grain yield of wheat was significantly positively correlated with RLD at 0-15 cm during the flowering (r =0.47**) and milking stages (r = 0.47**). Wheat may be growth under NT with crop residue mulching and 100% RDN and five irrigations to improve soil physical health, root growth, yield and partial factor productivity of N in sandy loam soils of IGP region.

# Agricultural Statistics


Bappa Saha

| | | |
|---|---|---|
| **Name of the Student** | : | **Bappa Saha** |
| **Roll No.** | : | **21416** |
| **Chairperson** | : | **Dr. Ankur Biswas** |

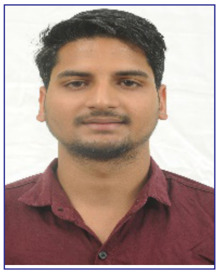

Dr. Ankur Biswas

*Title of the Thesis*

## Geographically weighted regression based model calibration approach under complex sampling design

In sample surveys, calibration approach is one of the widely used approach to incorporate the known population characteristics of auxiliary variables by modifying the original design weights. Model-calibration approach is an improvement over the usual calibration approach, where the concept of calibration approach is generalized to obtain a model-assisted estimator using more complex models. In many surveys, the relationship between the study and auxiliary variables vary across the locations and the observations tend to be similar for the nearby units than those located further apart. This phenomenon is known as spatial non-stationarity. Unlike Ordinary Least Square (OLS) model, the Geographically Weighted Regression (GWR) model takes into account spatial non-stationarity and can capture the spatially varying relationship between different variables. In the present study, several GWR based model calibration estimators of the population total were developed in the context of uni-stage Simple Random Sampling Without Replacement (SRSWOR) and two-stage sampling design when the population level complete auxiliary information is available. The proposed GWR based model calibration estimators were proved to be asymptotically design unbiased and approximately model unbiasedness under a set of regularity assumptions. Under the same set of assumptions, the approximate variances and estimators of the variances of the developed estimators were derived. The performance of the developed estimators was compared with the existing estimators like Horvitz Thompson estimator, ratio and regression estimators through a spatial simulation study considering wide range of situations. The simulation study was carried out in R software. Simulation results show that the proposed GWRbased modelcalibration estimators of the population total under SRSWOR and two stage sampling were asymptotically design unbiased on the basis of %RB. The proposed estimators were found to be more efficient than the existing estimators under consideration on the basis of %RRMSE. Finally, the developed methodology can be implemented to significantly improve the estimation of finite population parameters incorporating available complete auxiliary information under complex surveys in presence of spatial non-stationarity.

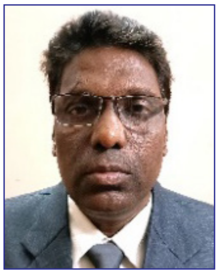
# Agronomy


Tarun Sharma

**Name of the Student : Tarun Sharma**

**Roll No. : 21427**

**Chairperson : Dr. T. K. Das**


Dr. T. K. Das

### *Title of the Thesis*

## Tillage, residue and nitrogen effects on weeds, wheat productivity, and soil properties under conversation agriculture-based pigeon pea-wheat system

Conservation agriculture (CA) with minimal mechanical soil disturbance, permanent organic mulch cover/cover crops, and diversified crop rotation including a legume crop holds a great promise for enhancing crop productivity, profitability, resource-use efficiency, improving soil health besides environmental sustainability. A field experiment on wheat grown under a long-term (12 years) conservation agriculture-based pigeon pea-wheat system was conducted in winter (*rabi*) 2021-22 at ICAR-Indian Agricultural Research Institute, New Delhi. The objectives were: to evaluate effects of tillage, crop residue and N on weed interference; to assess crop productivity, profitability and resource-use efficiency; to estimate the effects of tillage, crop residue and N management on soil properties across CA practices. Seven treatments with three replications laid out in a randomized complete block design were: Conventional tillage (CT); and 6 CA treatments i.e., permanent narrow bed with pigeon pea residue (PNBR75N and PNBR100N), broad bed with pigeon pea residue (PBBR75N and PBBR100N) and ZT flat bed with pigeon pea residue (ZTFBR75N and ZTFBR100N) along with 75% and 100% recommended doses of nitrogen. Results indicated that, compared to CT, the CA-based practices led to reduction in weed density and dry weight at 30 days after sowing and the treatment ZTFBR75N and ZTFBR100N were superior. Shannon Weiner diversity index showed higher weed diversity in CA, whereas Sorenson similarity value got reduced over a period of 12 years, which confirmed the shift in weed flora. The CA-based treatments provided significantly higher wheat root length density (15-27%), root surface area density (by 29-41%) and root volume density (by 38-56%). These practices increased wheat grain yield by 8.1-14.9%, biological yield by 4.9-10.8%, net returns by 19-23% over CT. These CA practices when supplemented with 75% or 100% N gave comparable yield implying a saving of 25% N besides having higher partial factor productivity of N and NPK in the 75% over 100%N N treatment. They also reduced total water use by 7.1-15.6% and treatments PBBR100N and PBBR75N had significantly higher water productivity (33-36% over CT). CA-based raised bed planted treatment registered 7.4-9%, 2.5-3.1% and 1.8-2.3% lower BD than in CT in 0-5 cm 5-15 and 15-30 cm soil layers, respectively. But, PBBR100N and PBBR75N had greater mean weight diameter of soil aggregates, and significantly improved total soil organic carbon and soil carbon and nitrogen fractions across soil depths. They led to 75.3% and 37.5% higher microbial biomass carbon and 56% and 36% higher dehydrogenase activity in 0-5 and 5-15 cm soil, respectively over CT. PBBR75N had 24%, 14% lower yield scale and spatial carbon footprints over CT, respectively. The PBBR75N had 27% higher carbon efficiency over CT. These two treatments (PBBR100N & PBBR75N) could save resources better, gave higher yield and improved soil properties. Therefore, PBBR supplemented with 100%N in initial years and 75%N in later years may be recommended for wheat crop production under CA-based pigeon pea-wheat system in the Indian Indo-Gangetic Plains and in similar agro-ecologies.

# Biochemistry

Rajarshi Sanyal

**Name of the Student** : **Rajarshi Sanyal**
**Roll No.** : **90001**
**Chairperson** : **Dr. Sujit K. Bishi**

Dr. Sujit K. Bishi

*Title of the Thesis*

## Identification and characterization of candidate gene(s) involved in biosynthesis of raffinose family oligosaccharides (RFOs) in peanut (*Arachis hypogaea* L.) seed

Plants adapted different strategies to cope with the ever-changing climate through evolution. Plants strategized to use carbohydrates or their derivatives as stress sensing and signaling molecules for the coordination of metabolism with growth. One of such metabolites, Raffinose Family Oligosaccharides (RFOs) plays an important role in plants but at the same time, act as antinutrients for humans and other monogastric animals. A profound understanding of genes involved in RFOs biosynthesis and their expression patterns is a prerequisite for the sustainable reduction of the RFOs content in the seeds, without compromising normal plant development and functioning. In this study, RNA-seq was performed in maturing seed stage (S1) and matured seed stage (S2) of three peanut varieties, namely, TG37A (high RFOs) and GG7 (low RFOs), from Spanish group and Girnar 2 (high RFOs), from Virginia group, to understand the expression of genes in high and low RFOs varieties, within and between groups. The results of the expression analysis suggest that different families of RFOs biosynthetic genes have tissue-specific expression patterns in peanuts. Temporal expression pattern of these genes was also found in the contrast genotypes, suggesting an alteration in preferences of high and low RFOs genotypes at S1 and S2. This is possibly the first report, explaining the Raffinose Synthase (RS) family genes to be the major players in RFOs biosynthesis in seeds. *AhRS*14 seemed to play the regulatory role in contrast genotypes, showing high specificity to seed while *AhRS*6 was found to be vital for studying variations in RFOs content between the groups. *AhRS*V is also reported for the first time as a possible marker for Virginia genotypes. Selective expression pattern of genes on the homeologous chromosome of peanut was also observed in this study. The identified candidates can further be validated in a larger population and other legumes so that they can be targeted to develop low RFOs varieties, thus improving the overall nutritional quality and solving the discomforts associated with their consumption.

# Computer Application

Vanaja V.

**Name of the Student** : **Vanaja V.**
**Roll No.** : **21441**
**Chairperson** : **Dr. Mukesh Kumar**

Dr. Mukesh Kumar

*Title of the Thesis*

## Development of decision support system for malnutrition marker assessment through energy balance techniques

Adequate nutrition is necessary for the country's human resource development. It is the foundation of human growth, particularly for women, adolescents, and children, and it also represents socioeconomic progress, national health security, and decreases in poverty. In India, one in three women had a body mass index (BMI) of less than 18.5 kg/m2 (BMI). According to UNICCEF, intergenerational malnutrition is perpetuated when an undernourished mother gives birth to an undernourished kid. Malnutrition problem can be managed by providing the desired information on time like person's intake of energy and/or nutrients based on the anthropometric measurements and energy balance techniques. In this age of the digital revolution, numerous agricultural-related mobile applications has already been developed on various aspects. In light of this, the goal of this research is to develop an Android-based mobile application that helps assess human nutritional status using a variety of anthropometric measurements and energy balance techniques that are useful for giving them a basic picture of their health status and directing them. The already-existing application "NutriGuide" has also been integrated with a mobile-based decision support system called "NutriEnergy," which helps users assess their level of physical fitness, energy expenditure, and nutritional status as well as give them a quick summary of the benefits of various food types for various age groups. This Android-based mobile application was developed using the Android Studio development environment, the Java programming language, eXtensible Markup Language for application user-end development, and a MySQL server as a backend database to store the personal information of humans and the various index values of all the humans. Additionally, it provides an option to save the data as an excel file for additional analysis and delivers personalized reports. In addition to all of this, the developed DSS offers a few brief details with recommendations for the recommended dietary allowance, recommended dietary intake, and food requirements for nutritional sufficiency.

# Entomology

Karthik Reddy M

**Name of the Student** : **Karthik Reddy M**
**Roll No.** : **21449**
**Chairperson** : **Dr. P.R. Shashank**

Dr. P.R. Shashank

*Title of the Thesis*

## Biosystematic studies on subfamily Olethreutinae (Tortricidae: Lepidoptera) of Southern Karnataka

The Tortricidae is a highly diverse and widespread family, solely representing the superfamily Tortricoidea with over 11,365 species across 1151 genera. It is divided into three subfamilies, the Chlidanotinae Meyrick, 1906; the Tortricinae Latreille, 1803; the Olethreutinae Walsingham, 1895. The Olethreutinae is the largest of the three subfamilies, with over 4417 described species in 355 genera and numerous undescribed taxa worldwide, and 300 species in 102 genera in India. Several Olethreutine moths are important agricultural pests worldwide, some of which are of quarantine importance. Contrastingly, many Olethreutine moth species are being continuously assessed for their role as biocontrol agents of weed species around the world. The present study was aimed at describing the Olethreutinae fauna of Southern Karnataka along with illustrated diagnostic keys, taxonomic treatments, and molecular diagnosis through barcodes. Over 700 specimens were collected from eleven localities across five districts of Southern Karnataka. Species were identified using morphological and molecular characters. The study revealed a total of 49 species in 34 genera and five tribes. The study contributed to the description of six new species to science, three genera and six species as new records to India, and twenty-seven species as new records to Karnataka. The highest generic and species richness were recorded from the tribe Olethreutini consisting of 11 genera and 18 species. Illustrated diagnostic keys were developed for all tribes, genera, and species in the present study for easy and authentic identification. DNA barcodes were generated for 15 species, among them, 14 species were submitted for the first time from India, and seven species for the first time from the world.

# Environmental Science

Apoorva MS

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Dr. Arti Bhatia

*Title of the Thesis*

## Interactive effect of elevated $CO_2$, temperature and N fertilizer on gaseous N fluxes and nitrogen use efficiency in Wheat

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Rising $CO_2$ and temperature level are affecting crop growth, yield and nutrient cycling processes in the soil. Wheat (*Triticum aestivum*) is one of the predominantly cultivated crop around the world and its sustainable growth is very important under the changing climatic conditions. To study the interactive effect of elevated $CO_2$, temperature and N fertilizer on emission of gaseous N fluxes and nitrogen use efficiency in wheat, a field experiment was carried out during the rabi season of the year 2021 in the temperature and carbon dioxide enrichment facility (T-FACE) at IARI, New Delhi. Wheat variety (HD 2967) was grown in the T-FACE rings under two levels of $CO_2$ i.e. ambient (402±20 ppm) and elevated (565±35 ppm) and temperature i.e. ambient and elevated (1.59-1.68°C over ambient) and their interaction with four N fertilizer treatments of neem coated urea (NCU, 120 kg N/ha), sulphur coated urea (SCU, 120 kg N/ha), liquid nano urea (NANO, equiv. to recommended) and no nitrogen (control). Elevated $CO_2$ significantly increased the growth parameters like photosynthetic rate, leaf area index, NDVI and yield parameters like biomass yield, grain yield, test weight in all the fertilizer treatments, whereas, under ET, a decrease in all the growth and yield parameters was observed as compared to ambient. However, most of the parameters were found to be at par with the ambient in the ECT treatment. The gaseous N fluxes of $NH_3$ and $N_2O$ were significantly higher under EC and ET as compared to ambient under all fertilizer treatments. The interactive effect of elevated $CO_2$ and temperature (ECT) also significantly ($p = 0.05$) increased the $N_2O$ emission and $NH_3$ volatilization over ambient. Lower cumulative emission of $N_2O$ and $NH_3$ during the crop growth period was recorded under NANO fertilizer as compared to NCU and SCU under all $CO_2$ and temperature interactions. The peak $NH_3$ volatilization loss was observed after the 1st dose of fertilizer application under all interactions. No ammonia emission could be detected after the foliar application of liquid nano urea. Microbial biomass carbon and nitrogen significantly increased under ECT. Elevated $CO_2$ significantly reduced the protein content of grain due to the nitrogen dilution effect, however, the impact was not significant under ECT. Lower soil $NO_3$- was recorded under all $CO_2$ and temperature treatments as compared to ambient. Soil NH4 reduced under ET and ECT and was at par with ambient under EC. Highest N uptake was estimated with SCU under ECT. NANO application had the highest agronomic use and recovery efficiency as compared to other N fertilizer treatments under ECT. Thus, it can be concluded that application of liquid nano urea can reduce gaseous N losses and improve N use efficiency of applied fertilizer under future climatic conditions.

# Floriculture & Landscape Architecture


Eram Arzoo

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*Title of the Thesis*

## *In vitro* gynogenesis studies in African marigold (*Tagetes erecta* L.)

The present study was carried out in petaloid type African marigold genotypes using unfertilized and *pseudo-fertilized* ovary culture and protocol for *in-vitro* mass proliferation, rooting, and acclimatization of gynogenically induced shoots was standardized. Surface sterilization of partially opened flower buds with 0.2 percent mercuric chloride ($HgCl_2$) for 5 minutes gave the lowest contamination and maximum survival percent in the cultured ovaries. The modified MS* medium enriched with 0.75 $mgl^{-1}$ TDZ and 0.2 $mgl^{-1}$NAA gave the earliest response and exhibited the highest percentage of direct regeneration from unfertilized ovaries of African marigold genotypes. The exposure to cold shock pre-treatment of 4ºC for 3 day induced the earliest callus induction and earliest direct regeneration response. However, the exposure of flower buds to 4ºC for 7 days was found to be the most effective treatment for gynogenesis as it induced the highest direct regeneration percentage. Gamma irradiation dose of 400Gy was found to be the most effective in minimizing pollen viability and germination. When partially open flower buds of African marigold were pollinated with irradiated pollen of French marigold genotype 'Pusa Deep' the resultant ovaries were showing changes in colour from white to light purple and then black, which indicated pseudo-fertilization. Irradiation treatment of 400Gy gave the highest percent direct regeneration in the pseudo fertilized ovaries of African marigold genotype. The number of developing embryos decreased as the radiation dose was increased, but these embryos were mostly of haploid origin. Among the cytokinins (BAP and KIN), BAP enriched medium was superior over the KIN in *in vitro* shoot proliferation of African marigold genotypes. Here, minimum days required for shoot emergence, maximum increase in fresh weight of cultured shoots were observed on MS medium enrich with BAP (0.5 $mgl^{-1}$). While in case of *in-vitro* root proliferation from gynogenically developed shoots the earliest rooting, highest rooting percent, better root growth character and highest no. of roots per micro shoots was recorded on the treatment comprising of ½ strength MS medium supplemented with NAA (0.5 $mgl^{-1}$). Among different *in vitro* hardening techniques, plastic pots covered with polythene cover gave the best results. Among both genotypes of African marigold, DAMH-24 performed best towards *in vitro* proliferation of gynogenically induced shoots. The developed protocol can be efficiently utilized for *in vitro* gynogenesis studies in African marigold.

# Fruit Science

Gulshan Kumar

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Dr. Manish Srivastav

*Title of the Thesis*

## Characterization of promising mango hybrids using DUS descriptor and new hyper-variable SSR markers

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The present investigation was undertaken at the Division of Fruits and Horticultural Technology, ICAR-IARI, New Delhi during 2021-22 to characterized twenty-four mango hybrids bred at ICAR- IARI, New Delhi on DUS guidelines. These mango hybrids have also been characterized using hyper-variable SSR markers designed from Amrapali genome sequences. It was observed that mango hybrids showed significant differences for leaf, inflorescence, flowering and fruit parameters. The maximum leaf area was recorded in H-4-8 (101.99 cm$^2$). Only two categories of leaf blade shapes were observed among mango hybrids and only H-3-2 had oblong leaf blade shape. Most of the hybrids (91.6%) showed presence of leaf blade twisting except H-3-2 and H-4-8. Similarly, maximum inflorescence length was recorded in H-7-1 (46.58 cm). It was evident that 45.8% of mango hybrids had medium type of coloration on rachis. However, Pusa Manohari was the only hybrid that was found to carry a strong anthocyanin coloration of rachis. It was also noted that Pusa Pratibha had earliest blooming, whereas Pusa Lalima showed earliest fruit maturity among hybrids. The maximum fruit weight and length (336.44 g, 14.56 cm) were observed in Mallika, whereas minimum fruit weight and length was recorded in NH-19-2 (94.87g, 7.56 cm). Based on morphological characterization, a barcode has been generated for all mango hybrids. The molecular characterization of 24 mango hybrids was attempted using 89 polymorphic SSRs. SSR profiling data revealed amplicons in the range of 130 to 450 bp with an average allele number of 2.60 per locus. The PIC value ranged from 0.04 (HMSSR1382) to 0.72 (HMSSR1289) with an average of 0.39. Gene diversity ranged from 0.30 to 0.62. UPGMA analysis broadly grouped mango hybrids into two major clusters. Cluster II comprises 14 hybrids followed by cluster I possessing 10 hybrids. Model based structure analysis revealed two gene pools. Analysis of molecular variance indicated that higher variation is attributed to individuals (82 %). The generated allelic profiles of polymorphic markers has been translated into DNA barcodes. SSRs analysis resulted in 11 unique and 35 rare alleles from total amplified alleles. These 11 alleles, *viz*., HMSSR965 (~150bp), HMSSR2048 (~300bp), HMSSR1382 (~300bp), HMSSR1218 (~260bp), HMSSR888 (~450bp), HMSSR1430 (~380bp), HMSSR419 (~300bp), HMSSR1226 (~290bp), HMSSR535 (~280bp), HMSSR1786 (~200bp) and HMSSR2040 (~330bp) amplified are hybrid-specific alleles and highly useful in genotyping. Attempt has been made to validate these hybrid-specific alleles in replicated tree samples grown at different places. However, only seven hybrid-specific alleles have could be validated in the present study. It was observed that the present set of HMSSRs were highly informative and serve as DNA marker resource for future molecular research in mango. It is concluded that 24 ICAR-IARI mango hybrids have been characterized based on DUS guidelines and novel hyper-variable SSRs. The information generated has significance in conservation, protection and utilization of mango hybrids.

# Genetics and Plant Breeding

Swarnadip Ghosh

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*Title of the Thesis*

## Genetic characterization and molecular mapping for γ-oryzanol and its components in rice (*Oryza sativa* L.)

γ-oryzanol, a group of steryl esters of ferulic and caffeic acid, is well documented to possess anti-oxidative properties. In the present study, a significant genetic variation (7.9-76.54 mg/100g) was observed for γ-oryzanol content in the 174 Indian rice accessions. Out of the five major steryl ferulates separated in RP-HPLC, 24-methylenecycloartanyl ferulate was found to be the major constituent of γ-oryzanol (2.4-31.78 mg/100g), followed by campesteryl ferulate (1.39-11.78 mg/100g), cycloartenyl ferulate (0.72-20.75 mg/100g), β-sitosteryl ferulate (0.6-15.61 mg/100g) and sitostanyl ferulate (0.01-6.20 mg/100g). A spatio-temporal analysis indicating significant compositional variation for γ-oryzanol in seed and non-seed (leaf blade, leaf sheath and peduncle) tissue revealed that steryl caffeates are prevalent during early reproductive stage while steryl ferulates increased towards maturity. γ-oryzanol showed differential accumulation, with maximum accumulation in bran (107.53-129.67 mg/100g) followed by embryo (46.97-59.29 mg/100g), husk (5.23-37.79 mg/100g) and endosperm (11.44-14.33 mg/100g). Furthermore, processing/milling and cooking of brown rice (in sufficient water) led to significant reduction (58.77 and 45.58% respectively). The AMMI-ANOVA showed a major portion of phenotypic variance due to genotype itself rather than environment. However, the effect of GxE interaction was also significantly high. WAASB index indicated G11 (CSR 23) as a superior and stable genotype for total γ-oryzanol content. The genome-wide association study conducted using BLINK and FarmCPU model identified 19 significant quantitative trait nucleotides (QTNs), of which 9 were previously reported and 10 were novel. These QTNs explained phenotypic variance ranging from 0.001 to 48.875%. A maximum of six QTNs were identified for sitostanyl ferulate (mapped to chromosome 1, 4, 9 and 11) followed by four QTNs each for 24-methylenecycloartanyl ferulate (chromosome 5, 7 and 12) and campesteryl ferulate (chromosome 4, 5 and 12), three for β-sitosteryl ferulate (chromosome 3, 5 and 6) and one each for cycloartenyl ferulate (chromosome 6) and total γ-oryzanol content (chromosome 5). *In-silico* analysis identified 23 putative candidate genes governing γ-oryzanol content. Among these, genes encoding cycloartenyl synthase, squalene cyclase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and sterol C-methyltransferase 1 play key role in biosynthesis of sterols which are the precursors of γ-oryzanol. The significant QTNs identified in this study hold great potential in the marker assisted breeding programs aiming the development of nutrient dense rice varieties.

# Microbiology


S. Yaadesh

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*Title of the Thesis*

## *Azospirillum-Bacillus* association for growth promotion of pearl millet under drought stress

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Bacteria belonging to *Azospirillum* and *Bacillus* spp. are considered among the most efficient plant growth-promoting rhizobacteria owing to their multifunctional PGP traits. The association of *Azospirillum* and *Bacillus* may have additive PGP effects on the host plants. In the present investigation, three strains of *A. formosense* and twelve strains of *Bacillus* spp. were first compared for *in vitro* PGP traits. The prominent PGP traits exhibited by *Azospirillum* sp. strains were IAA (upto 34.94 µg/mg protein), nitrogenase, siderophore production, ammonia production and osmotic stress tolerance. Whereas, *Bacillus* spp. strains showed IAA production (6.3 to 13.14 µg/mg protein), siderophore production, ammonia production, nutrient solubilization, osmotic stress tolerance (upto 1000mM mannitol) and antagonism against broad fungal pathogens (IMSB1, RP24, IMJ4 could inhibit all six tested fungi) as potential PGP traits indicating variation in the type and expression of PGP traits. Based on PGP traits and *in vitro* compatibility, *A. formosense* strains AIM57 and seven *Bacillus* spp. strains (IMSB1, AB4, RP24, IMBJ3, IMJ4, IMJ7, IMJ12) were further evaluated in co-culture system. Interestingly, under co-culture (*Azospirillum* + *Bacillus*) conditions significant increase in the expression of PGP traits (nitrogenase, P-solubilization, siderophore) indicating the synergistic interactions. Effect of individual and co-inoculations was also observed on seed germination, root traits and seedling vigor indices of pearl millet under 0, 10, and 20% of PEG6000 indicating better adaptation of the plants to stress. The synergistic strains, *A. formosense* strain AIM57 and *Bacillus* spp. strains (IMSB1, IMJ4 and RP24) were evaluated as individual and combined seed inoculants in pearl millet crop under limited moisture and nitrogen conditions through a pot experiment. As compared to treatment T1 (100%FC+100%RDN), the plant growth parameters were negatively affected in T2 (75%FC+75%RDN). Positive effect of inoculation on growth parameters (shoot length and biomass, leaf area index, RWC, chlorophyll content) was observed under stress conditions. The treatments with co-inoculation (T2+*Azospirillum*+*Bacillus*) showed improved growth over single strain inoculations. Significant increase in antioxidant enzymes level observed in T2 as compared to T1. The inoculated treatments at 75%FC+75%RDN showed significant increase in antioxidant enzymes as compared to un-inoculated positive control T1, however the antioxidant enzymes level was low as compared to un-inoculated stressed control T2, indicating reduced level of stress due to inoculation. Lipid peroxidation decreased and the membrane stability increased significantly upon inoculation and the

co-inoculated treatments showed better performance over individual inoculations. Variations in proline, total sugars and reducing sugar levels indicated variable response of inoculated treatments. Significant increase in the shoot N and K content was observed in treatment 75%FC+75%RDN+AIM57+IMSB1. Significant improvement in co-inoculated treatments was also observed on root traits (length, volume, area etc.) over single inoculations and T2. To conclude, the study indicated potential use of *Azospirillum* and *Bacillus* as synergistic bioformulation for combating nutrient and drought stress in pearl millet particularly in nutritionally poor dryland agricultural systems. The metabolic/molecular interplay between the two strains needs to be explored to understand and harness their synergistic potential.

# Molecular Biology and Biotechnology

Anik Basak

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Dr. Vinay Kumar

### *Title of the Thesis*

## Identification and characterization of bacterial endophytes having potential antimicrobial activities against Fusarium wilt in chickpea

Chickpea (*Cicer arietinum* L.) is one of the most important and essential legume crops for semiarid tropical area and contributes around 40% of total pulse production. India is largest producer of chickpea in the world sharing about 70% of the world production. As the demand for sustainable protein sources develop, chickpea may be the appropriate substitute for animal-sourced commodities. As a result, boosting chickpea yield is the most important factor. The vulnerability of chickpea to various biotic and abiotic stresses is major constraint for reduced yields. Among the biotic stresses, Fusarium wilt caused by soil-borne fungal pathogen, *Fusarium oxysporum* f.sp. *ciceri* is of most economic importance. For controlling this disease fungicide-based chemicals are being used, which are less effective to control this deadly disease but also have undesirable impact on environmental health. The application of bacterial endophytes as biocontrol agent have emerged as eco-friendly and complementary approach. Endophytes live inter and intra-cellularly in plant tissues and known to play a crucial role plant in growth and development ranging from providing nutrition, imparting resistance to biotic and abiotic stress and reciprocal interactions. This study was conducted to isolate and identify the bacterial endophytes (BE) which can protect chickpea plants against Fusarium. A total of 119 bacterial endophytes were isolated different tissues of chickpea. The number of bacterial endophytes isolated from the root, stem leaf, flower and nodule samples were 32, 41, 32, 8 and 4, respectively. Morpho-biochemical and molecular characterization using 16s rDNA sequencing were used reveal the identity of isolates. Gram's staining showed that (77) isolates were positive and 42 isolates were Gram's negative. Higher number of isolates from chickpea roots were found gram positive. The bacterial endophytes were tested for Plant growth-promoting (PGP) traits and found that the number of isolates were positive for phosphorus solubilisation activity (45), siderophore production (100), DNase activity (16), IAA production (72), Nitrate reduction activity (3), Urease production (7) and Citrate utilisation (5). Furthermore, 16 isolates were shown to have antagonistic activities against Fusarium in the dual culture assay with the growth inhibition ranged from 31 to 60 %. Isolates showing the antimicrobial activities were tested for the presence of lipopeptide genes and showed the presence of iturin, surfactin, fengycin and bacilliomycin D lipopetides. On the basis of *in vitro* antagonistic and PGP activities, three isolates namely *Bacillus xiamenensis* strain NIBSM_CaL1, *Pseudomonas stutzeri* strain NIBSM_CaS37 and *Bacillus inaquosorum* strain NIBSM_CaS25 were selected for in planta validation on chickpea plants. Chickpea plants bio-primed with endophyte showed better survival rate against the Fusarium pathogen with protection over control ranged from 57 to 75%. The endophyte bio-primed plants showed significant increase in plant biomass (128% to 250% over the control). Among the endophytes tested on plants, isolate NIBSM_CaS37 was found to be the best in the protection of plant against Fusarium. Tripartite interaction (Chickpea- Fusarium- Endophyte) was studied to understand differential expression of genes probably involved in imparting endophyte mediated resistance against Fusarium. An increased expression of the genes namely NAC transcription factor (NAC TF), Auxin binding protein ABP19a (AUX BP), 14-3-3 like protein (14-3-3 P), Linoleate 9S-lipoxygenase (LOX) and Leucine-rich repeat protein (LRR) was found in the endophyte bio-primed and pathogen inoculated plants in early stage of pathogen infection. These genes enhances the plant's immunity by modulating phytohormone pathways, signalling, production of secondary metabolites, regulating jasmonic acid pathway. Chickpea bacterial endophytes having antagonistic activity against Fusarium wilt may be included in an integrated disease control module and understanding the molecular mechanism of Endophyte Mediated Resistance.

# Plant Genetic Resources


Rinky Reshma Panda

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*Title of the Thesis*

## Development of cryopreservation protocol of *Artocarpus lacucha* Buch.-Ham. - An indigenous underutilized fruit species

The objectives of the present work were standardization of cryopreservation protocol for *Artocarpus lacucha* Buch. -Ham. (IC612468) and to develop taxonomic key on fruit and seed characters of *Artocarpus* species for authentic identification of germplasm for conservation. Standardization of cryopreservation protocol included selection of multiplication media using media of different concentration of hormones and PVS2 treatment duration. Murashige and Skoog media supplemented with different concentrations of hormone viz., 0.2-1.5mg BAP/l were used for shoot multiplication. PVS2 treatment duration was standardized by treating shoot tips with PVS2 for different durations like 20min, 30min, 40min and 60min. Out of these, shoot tips excised from cultures kept in BOD condition for 1 week treated with PVS2 for 30min duration was optimized. Germplasm when received as fruit/part of fruit or seed needs validation before starting of research work because species cannot be identified by fruit and seeds. A taxonomy key is the most useful technique of identification of this species before starting of any research work on it. Taxa of edible value found in India viz. *A. chama* Buchanan Hamilton (Assam), *A. hirsutus* Lam (Kerala, Karnataka)., *A. heterophyllus* Lamarck (Assam, Odisha and Bihar), *A. lacucha* Buch.-Ham. (Andhra Pradesh, Jharkhand, Odisha), and *A. gomeziana* Wall. (Assam), *A. communis* J. R. Forster and G. Forster (Andhra Pradesh, Goa, Karnataka) are less-known for fruit and seed characters. In the present study, fruit and seed characters of edible *Artocarpus* species in India have been used for identification and development of taxonomic key.

# Plant Pathology


Hamida Dudekula

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## Quantitative variation in fusaric acid production by different isolates of *Fusarium oxysporum* f. sp. *ciceris* and its correlation with pathogen virulence and post-infectional physiology of chickpea

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Fusarium wilt is the second most serious disease of chickpea with 14 – 32% disease incidence and causing 12% loss annually. Chickpea wilt caused by *Fusarium oxysporum* f. sp. *ciceris* (Foc) is known to produce fusaric acid which plays an important role during pathogenesis. In the present study, cultural and morphological variability along with the quantity of fusaric acid produced by 14 different isolates of Foc in in vitro culture filtrate was estimated through HPLC and their correlation with pathogen virulence was confirmed. Further, effects of culture filtrate of selected isolates were examined on (a) plant pigments like chlorophyll a, chlorophyll b, total chlorophyll, and carotenoids; (b) physical parameters like chickpea leaf relative water content, root-shoot length, root-shoot fresh and dry weight; and (c) plant defense-related biochemical parameters like peroxidase, polyphenol oxidase, superoxide dismutase and phenylalanine ammonia-lyase enzymes in resistant cv. WR 315 and susceptible cv. JG 62 chickpea seedlings. The quantity of fusaric acid produced by 14 different isolates of Foc in *in vitro* culture filtrate was estimated through HPLC and their correlation with pathogen virulence was confirmed. Further, effects of culture filtrate of selected isolates were examined on (a) plant pigments like chlorophyll a, chlorophyll b, total chlorophyll, and carotenoids; (b) physical parameters like chickpea leaf relative water content, root-shoot length, root-shoot fresh and dry weight; and (c) plant defense-related biochemical parameters like peroxidase, polyphenol oxidase, superoxide dismutase and phenylalanine ammonia-lyase enzymes in resistant cv. WR 315 and susceptible cv. JG 62 chickpea seedlings. These enzymes' activity was found 3-5.6 fold higher with the treatment of culture filtrate of ITCC 7682 whereas, there was a 1-2 fold increase with ITCC 7681 and pure fusaric acid treatments as compared to control. Increased activity of antioxidant enzymes (Superoxide Dismutase, Phenylalanine Ammonia Lyase) was also recorded in both resistant and susceptible cultivars upon treatment with FOC isolates and pure fusaric acid standard. But this increment was only 1-1.5 fold in all the treatments with FOC isolates and fusaric acid standard and not much difference was also noticeable between resistant and susceptible cultivars.

# Plant Physiology


Purbali Mukherjee

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*Title of the Thesis*

## Interactive role of sucrose, ROS and auxin during development of female gametophyte of wheat (*Triticum aestivum* L.) under high night temperature

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The increase in temperature is a crucial component of climate change which impairs crop production through reproductive failure of gametes or loss in seed weight. The rate of increase in minimum temperatures is twice that of maximum temperatures in rabi season. The reproductive phase of the late sown wheat in rabi season is vulnerable to both maximum and minimum high temperatures (HT) which can affect flowering and grain filling. The present study was conducted in the contrasting wheat genotypes HD 2329 (HT susceptible) and Raj 3765 (HT tolerant) to investigate the effect of two intensities of high night temperature; HNT+5°C and HNT+8°C on female gametophyte which is a pivotal organ for seed formation. The experiment was conducted in the absence and presence of the chemical trap of hydrogen peroxide ($H_2O_2$), DMTU to confirm the role of ROS in various metabolic processes. HNT caused a 1.8 to 6.8-fold increase in production of $H_2O_2$ with increasing temperature in both the genotypes although with lesser magnitude in Raj 3765 in absence of DMTU. The ROS was balanced by an increase in activity of peroxidase with increasing temperature. Cytosolic glyceraldehyde-3-phosphate dehydrogenase activity was inversely related to $H_2O_2$ production in Raj 3765 indicating its role in regulating H2O2 levels under stress. Translocation of 14C sucrose under HNT in Raj 3765 was preferentially towards stamens and pistils. Increase in sucrose invertase activity with temperature suggested its involvement in synthesis of sugars for stress tolerance. Significant raffinose accumulation under HNT+8°C in pistil of Raj 3765 is a part of the protective mechanisms to alleviate high-temperature stress. Raj 3765 maintained cooler ears until morning to facilitate optimal temperatures for the impending events of anthesis and fertilization. At the hormonal level, an increase in ABA and decrease in GA3 content with increasing temperature may be responsible for upregulating the signalling network for heat tolerance. Our study suggests that various metabolic pathways are altered in the pistil of the tolerant genotype to ameliorate the high night temperature-induced changes at the cellular level.

# Seed Science & Technology


Poomani S.

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Dr. Sangita Yadav

*Title of the Thesis*

## Effect of priming techniques on seed quality enhancement of lentil and their efficacy under heat stress

Lentil (*Lens culinaris*) is the second most important rabi season pulse crop in India. Abiotic stress negatively impacts the crop resulting in decline in production. Due to the increase in the global average temperature year over year, the effect of heat stress needs to be addressed. Lentil is found to be susceptible to heat stress and thus, early seedling growth of lentil is severely affected resulting in poor plant growth and yield. Seed priming is the simple quality enhancement technique for mitigating abiotic stresses in several crops. Keeping above facts in view, humic acid was used as a seed priming agent to enhance seed quality parameters under stress. Among the various concentration and duration used, seeds primed with humic acid @ 600 ppm for 18 h showed highest germination (100%), seed vigour index I (1891) and seed vigour index II (1.10). Similarly, thermo priming at 32oC for 24 h also improved germination and vigour of lentil seed. Heat stress (30oC/20oC) significantly affected the seed germination as well as biochemical traits at seedling stage in all three lentil varieties (IPL 316, PDL 1 and L 4147) taken under this study. Seed priming with humic acid was found to increase germination percentage (20-23%), seed vigour index I (31-34%), seed vigour index II (29-32%), membrane stability index (14-18%), chlorophyll content (32-68%), proline content (55-68%), phenolic content (30- 31%), catalase activity (49-61%), peroxidase activity (54-64%), superoxide dismutase content (40%), total soluble sugar content (11-12%), soluble protein (3-8%), free amino acid content (5- 10%) and significant reduction was recorded with mean germination time (8-10%), malondialdehyde (20-24%), hydrogen peroxide (18-28%), carbohydrate content (3-5%) in IPL 316 and PDL 1 varieties under heat stress condition. However, thermo priming was found to be effective in L 4147 variety with increase in germination (50%), seed vigour index I (29%), seed vigour index II (55%) and bio-chemical parameters. In this study, it was observed that seed priming not only enhanced the stress tolerance potential of sensitive varieties but also imparted enhanced stress tolerance to the tolerant varieties in lentil. Priming triggered the antioxidant machinery and osmotic adjustment which reduces the accumulation of reactive oxygen species and lipid peroxidation thereby minimizing the negative consequences of heat stress.

# Soil Science & Agricultural Chemistry

Saloni Tripathy

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Dr. Sunanda Biswas

*Title of the Thesis*

## Assessment of resistance and resilience of soils under rice-based cropping system

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Climate is the main factor affecting agricultural productivity. The productivity of crops will be impacted by changes in land and water regimes brought on by temperature and precipitation changes resulting from climate change. Particularly, the stability of the soil community has an impact on its turnover rate, which in turn has an impact on the ecological activities that the soil biota drives. As a result, the ideas of resistance and resilience, or an ecological system's capacity to withstand and recover from perturbations in order to retain its structure and function, have emerged as a key area of ecological research. Concerned about possible long-term climatic change implications on agriculture, the current study entitled *"Assessment of resistance and resilience of soils under rice-based cropping system"* was taken up. Soil samples were collected from 0-15cm depth from a 11 years old experiment of conservation agriculture (CA) based rice-wheat-mungbean cropping system, conducted at the Research Farm of the Division of Agronomy, Indian Council of Agricultural Research-Indian Agricultural Research Institute (ICAR-IARI), New Delhi with eight treatments viz. (ZTDSR-ZTW, ZTDSR + WR – ZTW + RR, ZTDSR + WR + CBM – ZTW + RR ,ZTDSR + WR + SBM – ZTW + RR, ZTDSR-ZTW – ZTMB, ZTDSR + MR – ZTW + RR – ZTMB + WR, TPR-ZTW-ZTMB,TPR – CTW- CTMB) and from 32 years old long term conventional tillage (CT) based rice-rice cropping system situated at Regional Rice Research Station of Assam Agricultural University (AAU), Titabar, Assam with eight treatments viz. control, 100%N, 100%NPKZn with S,100%NPKZn without S, 50%NPK+50%GM-N, 50%NPK+50%FYM-N, 50%NPK+25%GM-N+25%FYM-N, FYM@10ton/ha. Enzymatic activities, microbial populations, and carbon mineralization following heat and moisture stress were examined in the soil samples. Soil resilience index (SRI) was validated with soil health index (SHI), soil organic carbon (SOC) and yield attributes. Results revealed that enzyme activity and microbial population are significantly reduced by heat and moisture stress. The recovery rate of microbial population ranged from 63% to 89% and the recovery rate of enzyme activity ranged from 57% to 88% at 45 days after stress (DAS). Zero-tilled plots outperformed conventional plots in terms of resistance and resilience of enzyme activity and microbial population. The triple zero tillage with triple residue retention treatment demonstrated the highest resilience and resistance to heat and moisture stress among all the zero tilled treatments. The treatments in heat-stressed samples with and without glucose as well as between normal samples with and without glucose significantly affected the carbon mineralization up to 23 days of incubation. C mineralization was highest in normal soil with glucose on 3rd, 6th, 13th, and 23rd days of incubation, while heat-stressed soil without glucose had the lowest values. The FYM@ 10 t ha-1 treatment had the maximum C mineralization in all 4 sets of soils, followed by 50%NPK+25%GM-N+25%FYM-N treatment whereas the control treatment had the lowest C mineralization. With an SRI value of 0.84, the 50%NPK+25%GM-N+25%FYM-N treatment was the most resilient to heat stress, whereas control soil was the least resilient. Under a rice-rice cropping system in the acidic Alfisol of Assam, available Zn, available K, acid phosphatase activity, and bulk density were chosen as the key indicators of soil health. Integrated treatments that were 50% NPK+25% GM-N+25%FYM-N and FYM@10 t ha-1had highest SHI than rest of the treatments. The SHI and SRI had a strong agreement (73%) with each other. Under a CA-based rice-wheat system in the Indo-Gangetic plain, triple zero tillage with triple residue retention may be advised, and CT based rice growing farmers in Assam may get benefit from integrated nutrient management practices.

# Vegetable Science

Neha Kumari Mandal

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Dr. Anilabha Das Munshi

*Title of the Thesis*

## Understanding the regulatory role of important growth hormones in relation to parthenocarpy in cucumber

Cucumber is a model plant for studying parthenocarpy with abundant slicing- and pickling-type germplasm. This study was undertaken to understand the role of the important cytokines (CKs), auxin (AUX) and gibberellin (GA) biosynthesis and degradation genes for the induction of parthenocarpy in slicing and pickling germplasm. Two genotypes of gynoecious parthenocarpic cucumber, PPC-6 and DG-8, along with an MABC-derived gynoecious non-parthenocarpic line, IMPU-1, were evaluated in this study. The slicing and pickling cucumber genotypes PPC-6 and DG-8 were strongly parthenocarpic in nature and set fruit normally without pollination. Endogenous auxin and gibberellin were significantly higher in parthenocarpic than non-parthenocarpic genotypes, whereas the concentration of cytokinins varied among the genotypes at different developmental stages. However, the exogenous application of Zeatin and IAA + Zeatin was effective in inducing parthenocarpic fruit in IMPU-1. Expression analysis with important CK, AUX, and GA biosynthesis-related genes was conducted in IMPU-1, PPC-6, and DG-8. The expression of the CK synthase, IPT, IPT3, PaO, LOG1, LOG2, CYP735A1, and CYP735A2 was up-regulated in the parthenocarpic genotypes. Among the transcription factor response regulators (RRs), positive regulation of CSRR8/9b, CSRR8/9d, CSRR8/9e, and CSRR16/17 and negative feedback of the CK signalling genes, such as CsRR3/4a, CsRR3/4b, CsRR8/9a, and CsRR8/9c, were recorded in the parthenocarpic lines. Homeostasis between cytokinin biosynthesis and degradation genes such as CK oxidases (CKXs) and CK dehydrogenase resulted in a non-significant difference in the endogenous CK concentration in the parthenocarpic and non-parthenocarpic genotypes. In addition, up-regulation of the key auxin-inducing proteins and GA biosynthesis genes indicated their crucial role in the parthenocarpic fruit set of cucumber. This study establishes the critical role of the CKs, AUX, and GA regulatory networks and their cross-talk in determining parthenocarpy in slicing and pickling cucumber genotypes.

# Ph.D.
# Thesis Abstracts

# Agricultural Chemicals

Rohan Sarkar

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*Title of the Thesis*

## Isolation, characterization and valorisation of functional carbohydrates from tubers of *Pachyrhizus erosus* and peels of *Citrus sinensis*

Prebiotic compounds are one kind of functional carbohydrates that help to improve natural population of gut friendly microbes within our digestive system. Being a less explored source of prebiotic substance, inulin; tubers of yam bean (*Pachyrhyzus erosus*) are not explored to its full potential as prebiotic. Similarly citrus peels are a prominent source of pectin or pectic polysaccharides along with different bioactive compounds. In this study, yam bean tubers and citrus peels were explored for prebiotic substances and other functional components. Extraction of inulin from yam bean tubers were carried out using ultrasound and microwave assisted extraction techniques. Extraction parameters (energy, time and solid/solvent ratio) were optimized using response surface methodology as well as artificial intelligence based genetic algorithm approach. Under optimised condition, inulin yield was higher for ultrasound (11.97-12.15 %) and microwave assisted extraction (11.21-11.38 %) compared to conventional heating (9.34 %). Characterisation of inulin was done using FTIR and XRD analysis. Prebiotic activity was assessed against *Lactobacillus fermentum* showing 58.75 % higher effect over bacterial population compared to glucose. Enzymatic hydrolysis of inulin polysaccharide was done to study the effect of short chain oligosaccharides for their prebiotic activity. Molecular docking study predicted higher affinity of inulin residue with monomer units of 3 and 7 towards exoinulinase enzyme. Under laboratory condition, prebiotic activity of inulin residue with monomer units of 3 was maximum followed by 7 unit and it was better than whole inulin molecule. Extracted inulin was valorised with β-carotene using encapsulation technique with the help of pumpkin seed oil. Prepared formulation was characterised by confocal microscopy and XRD analysis that clearly indicated proper encapsulation of β-carotene within inulin molecule. Release profile of β-carotene from encapsulated product was 44.12 % and 31.06 % under simulated gastric and simulated intestinal condition. Different functional components (essential oil, carotenoid, phenolics and pectin) were extracted from three different citrus peels (mosambi, kinnow and orange) in a sequential manner. Nanoemulsion was prepared from extracted essential oil using three different techniques *i.e.,* ultrasonic bath sonication, ultrasonic probe sonication and high-speed homogenisation. Mean droplet size were found as 33.42-48.83 nm, 34.56-47.32 nm and 33.87-48.25 nm for mosambi, kinnow and orange peel oil respectively depending upon different techniques used. Out of nine prepared nanoemulsions, seven passed the thermodynamic stability and dispersibility test. Bioefficacy study was conducted against *Candida albicans* (a human pathogen).

*In-silico* analysis revealed that three major constituents of essential oil (d-limonene, β-myrecene and α-pinene) were active in the inhibition of the all the three putative *Candida albicans* protein targets *i.e.,* Glucosamine-6-phosphate synthase, Endo-1,3(4)-β-glucanase and δ (14)-sterol reductase). *In-vitro* study showed that the nanoemulsions provided 3-4 times higher activity compared to respective coarse emulsions. Carotenoid and phenolic fractions were also extracted and quantified. Antioxidant activity was higher for orange peel carotenoid fractions compared to other peels, whereas, for phenolic fractions mosambi peel exhibited highest activity. Functional carbohydrate, pectin was extracted and characterised that showed >6 % of methoxyl content, >65 % of anhydrouronic acid content with >50 % of degree of acetyl value. Prebiotic activity of three different pectin was done using method similar to that of inulin, showing 55.23 % higher activity over bacterial population compared to glucose. Cellulose and hemicellulose content was determined after extracting all functional components from the peels. Using these resistant carbohydrates, bioethanol production potential was evaluated by fermentation process using suitable yeast culture. All three citrus peels produced ethanol with >70 % fermentation efficiency. Orange peel showed better result (8.77 g $L^{-1}$ ethanol with 84.21 % efficiency) compared to kinnow (7.56 g $L^{-1}$, 82.07 %) and mosambi peel (5.34 g $L^{-1}$, 74.62 %). These materials could effectively be utilized as potential nutraceutical product as well as feedstock for bioethanol production.

# Agricultural Economics

Praveen K.V.

**Name of the Student** : **Praveen K.V.**
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Dr. Alka Singh

*Title of the Thesis*

## Estimating the effects of fertilizer use in agriculture: implications for crop response and environmental sustainability

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Fertilizer is an indispensable input in Indian agriculture. However, the indiscriminate, use of fertilizers also affects the environmental health posing sustainability issues. At present, the country is at the juncture, where, we need to carefully plan the future trajectory to embrace both food security and environmental sustainability. Against this backdrop this study targets to estimate the effects of fertilizer use on crop response and environmental sustainability. Secondary data from various published sources as well as primary data of 400 farmers from theIndo-Gangetic Plains region were used in the analysis. The trends in fertilizer use, the role of policies on fertilizer consumption, spatial variation in crop response, environmental costs of fertilizer use, biofertilzer adoption and its potential and constraints are the topics dealt. Findingsfrom the study reveal that the national level growth in fertilizer consumption has slowed in the current decade. The policies like Retention Price Scheme, and the DBT pilot scheme have had a significant effect on fertilizer consumption. Wide variation in yield response to fertilizer use existed among the states and responses were lower in states where the share of farmers overusingnitrogen was higher. Further, the trend in the Nitrogen budget indicated increasing Nitrogen surplus and decreasing Nitrogen use efficiency. The meta-analysis found an average yield improvement of 0.05 tonnes per hectare due to biofertilizer application. The adoption of biofertilizers by farmers were very poor. Farmers preferred liquid-form biofertilizers, from government sources, and with a definite effect on crop yields. In general young, educated farmers, with membership in farmer organizations, who got the opportunity to undergo trainingon biofertilizers, and have a positive perception towards biofertilizers were found to adopt this technology more. Overall, this study finds that policies are effective means of regulating fertilizer use in the country, hence they should be utilized to correct imbalances in the nutrient application. The low crop response to fertilizers at least in some parts of the country is connectedto the overuse of fertilizers, which have environmental costs. The surplus nitrogen in Indian agriculture is growing steadily, and the nitrogen fertilizer application, as well as manufacture, contribute equally to nitrous oxide emissions. Greener forms of fertilizers like biofertilizers havethe potential to enhance crop yields, but more efforts are required for increasing their adoption. Our findings on the farmers' preference for biofertilizer characteristics and the factors determining biofertilizer adoption by farmers could act as a kick-off point for this.

# Agricultural Engineering


Pramod S. Shelake

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Dr. D. Mohapatra

### *Title of the Thesis*

## Dynamics of ozone in bulk storage system for onion (*Allium cepa* L.) and its effect on shelf-life

In this study, the efficacy of gaseous ozone for the elimination of *A. niger* and *E. carotovora* inoculated on onion bulbs was investigated. Ozone concentrations of 100, 200, and 300 ppm were applied to the inoculated bulbs in pulsed mode (*i.e.,* frequency of exposures 1, 2, 3). The reduction in microbial load of *A. niger* and *E. carotovora* varied from 0.47 – 2.31 log CFU/g and 0.72 – 2.99 log CFU/g, respectively. The efficacy of ozone on microorganisms increased with an increase in concentration and number of exposures. Scanning electron microscopy (SEM) revealed the structural disintegration of bacterial cells and fungal spores with the severity of ozone application. The effect of gaseous ozone on quality-related attributes of onion bulbs was also examined. The pungency imparting pyruvic acid and ascorbic acid content decreased with an increase in the concentration of ozone and the number of exposures. In contrast, total phenol and flavonoid content increased to an effective ozone concentration (concentration × exposure) of 400 ppm. Higher concentrations inadvertently decreased the antioxidant properties. Ozone treatment resulted in a non-significant decrease in firmness, anthocyanin content, and onion colour.

Ozone decomposition kinetics varied significantly in the presence of biological commodities. Ozone decomposition kinetics in onion bulbs at temperatures (2, 10, 18 °C) and relative humidity (85, 35 %) for different ozone concentrations (100, 200, 300 ppm) and number of exposures (1, 2, 3) were investigated. Zero-order, first-order, and second-order kinetic models were fitted to the temporal ozone decomposition data. The ozone decomposition kinetics followed first-order reaction and decomposition constant () varied from $1.712 \times 10^{-3}$ 1/s - $5.181 \times 10^{-3}$ 1/s. The spatiotemporal ozone distribution inside the ozone storage structure was investigated using Computational Fluid Dynamics (CFD) technique. An ozone dispenser was designed to increase fumigation efficiency and uniformity of gas distribution in the structure domain. The full dispenser with an aperture of 0.002 m in the headspace (0.21 m), 0.004 m in the upper section (0.525 m) and 0.010 m in the lower section (0.525 m) yielded better ozone gas distribution in the domain.

During bulk storage of onion (500 kg), the fungal and bacterial counts in ozone-treated bulbs remained significantly lower than in the untreated samples. The rotting percentage was higher in control (untreated) bulbs than in the single-treated ones, followed by periodically treated ones. For a storage period of 120 days, the rotting percentage was observed to be 15.46%, 24.10% and 34.76% for the periodically-treated, single-treated and untreated bulbs, respectively. With storage, sprouting, physiological loss in weight and dry matter content increased; however, the effect of ozonation on these physiological parameters was non-significant.

# Agricultural Extension


Bhagya Vijayan

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Dr. Manjeet Singh Nain

*Title of the Thesis*

## An analysis of access, status and impact of selected agricultural development programmes

Following its independence, India chose the route of planned development, in which the federal and state governments must work together to promote growth. India's post-independence problems included poverty and underdevelopment. The government launched numerous development programmes to combat poverty, the biggest barrier to progress. Although there have been many programmes for agricultural development, the major shift in agriculture development came in the late 1990s. But since the middle of the 2000s, the government has redoubled its efforts to encourage agricultural growth through a plethora of agricultural development initiatives, including the National Food Security Mission and the National Agriculture Development Program alias *Rashtriya Krishi Vikas Yojana*. The National Development Council decided that agricultural development plans needed to be revised to better serve farmers' interests, and it urged the federal and state governments to adopt a plan to revive agriculture. For the 11th plan, the NDC reaffirmed its goal of 4% yearly growth in the agriculture sector. It is challenging to fully profit from the numerous agricultural development programmes in the areas of food grain production, vegetables, fruits, eggs, meat, fish, flowers, wool, oilseed, and pulses, as well as the standard operating procedures associated with each programme. It is important to consider the opportunities these programmes provide for Indian farmers at a time when the government aimed to double farmers' income by 2022. Due to their bigger stakes in the agricultural GDP, two states Uttar Pradesh and Karnataka were purposively chosen for study. Two districts and two blocks from each district from the designated states were chosen further. 140 respondents were chosen from each district, including 80 farmers who were beneficiaries, 40 farmers who were non-beneficiaries, and 20 extension personnel making the total sample size 560. The research investigation revealed satisfactory grass root institution involvement, participatory planning and funding in Uttar Pradesh and Karnataka for both NFSM and RKVY. Beneficiaries of both states opined that the programme effectiveness augmented after the revamp of both programmes, and so does the operational efficiency. The level of awareness of beneficiaries had marked an upward trajectory after the revamp of NFSM and RKVY and had drastic differences with non-beneficiaries in agricultural practices. It was also seen that Karnataka beneficiaries of NFSM and RKVY had a higher notch in the level of awareness than Uttar Pradesh NFSM and RKVY beneficiaries. There was a phenomenal positive shift in the pattern of access of beneficiary farmers to agricultural development programmes after the implementation of NFSM and RKVY, which further improved after the revamp. Delineating the access pattern, it was observed that except for social relation and empathy, the rest of all access variables were found to be significant in the case of Uttar Pradesh and Karnataka beneficiary farmers of NFSM. In the case of Karnataka-RKVY beneficiary farmers social relation, empathy and reliability were found to be non-significant, while for Uttar Pradesh-RKVY beneficiaries, social relation and empathy were found to be non-significant. Analysis of the socio-economic transformation brought about by pre and post-revamped NFSM revealed credible and pertinent changes in the lives of beneficiaries than non-beneficiaries of both states. Socio-economic variables: education and social participation registered a reverse trend for beneficiaries of both states. Correlational analysis of nine socio-economic variables to overall socio-economic transformation also reiterated the trend set by social participation and education for NFSM beneficiaries. Following the trail of socio-economic transformation of RKVY beneficiary farmers culminated in revealing significant differences and positive transformation of all the ten socio-economic variables considered for both states' beneficiaries. Correlation analysis of the contribution of access variables to overall socio-economic transformation revealed that for Karnataka beneficiary farmers, among the socio-economic variables, education had set a reverse trend while for Uttar Pradesh beneficiary farmers' social participation and education marked a reverse trend. Analysis of the knowledge level of department personnel of NFSM revealed that more than half of the department personnel were in the high knowledge category in both States. The results were similar for department personnel implementing RKVY in both states. Albeit the excellence in implementation, several lacunae impede NFSM and RKVY. The research study calls for policy interventions to plug the loopholes in the implementation of these agricultural development programmes: NFSM and RKVY to reach a larger farming population. Increased sensitization of the farming community, timely action plans, and augmented capacity development programmes of the department personnel can be a slew of measures that can be roped into for sustaining these programmes for the larger good.

# Agricultural Statistics


Sayantani Karmakar

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Dr. Cini Varghese

*Title of the Thesis*

## Multi-Balanced experimental designs for agricultural research

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Designing the experiments appropriately can prove to be profoundly beneficial in any type of agricultural research. Though conventional designs are appropriate for most agricultural trials, they may become inadequate in specific situations. In this study, some new series of partially balanced t-designs (a generalized class of Incomplete Block Designs (IBDs)) have been developed. These generalized IBDs are of particular interest when there is a requirement of selecting t-components out of v ($v > t$). The characterization properties of the designs have been studied and the association of the proposed designs with t-packing designs has also been demonstrated. Amalgamating various compatible IBDs in a systematic manner led to the development of some new series of Incomplete Row-Column (IRC) designs. General expressions of the information matrices have been derived to study the properties of these designs. An algorithmic method of construction and an R package "iRoCoDe" for easy generation of IRC designs are developed. Further, for situations where certain experimental units are not available for the application of treatments, structurally incomplete (SI) designs viz., 2-part SI row-column designs and 2-part SI block designs have been developed through appropriate fusion of IBDs. The canonical efficiency factors of all the proposed designs are computed using developed SAS codes and the designs are found to be quite efficient.

# Agronomy

Rishi Raj

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Dr. T. K. Das

*Title of the Thesis*

## Weed seed bank dynamics and productivity in a long-term conservation agriculture-based rice-wheat cropping system

Conservation agriculture (CA)-based rice-wheat system (RWS) can be a resource-efficient and environmentally sustainable alternative to conventional transplanted puddled rice (TPR)-conventional till wheat (CTW) system. But, the DSR faces severe problems of weeds and nematodes. Therefore, the present study was conducted over a period of two years 2018-19 & 2019-20 under an on-going long-term CA-based RWS at ICAR-IARI, New Delhi to evaluate tillage, residue and weed management effects on weeds and weed seed bank dynamics, productivity, profitably and resource use–efficiency, soil physical and chemical parameters, greenhouse gases emissions. Five CA practices, namely, ZTDSR- ZTW (CA1), wheat residue (WR)+ZTDSR -rice residue (RR)+ZTW (CA2), WR+ZTDSR+ brown manuring (BM)-RR+ZTW (CA3), ZTDSR-ZTW-ZTMB (CA4), mungbean residue (MR)+ZTDSR-RR+ZTW-WR+ZTMB (CA5) were compared with transplanted puddled rice (TPR)-conventional till wheat (CTW) (CT) in main plots. Four sub-plot weed control treatments were un-weeded control (W1), pendimethalin at 1.5 kg/ha applied as pre-emergence (PE) followed by (fb) bispyribac-Na at 0.025 kg/ha as post-emergence (PoE) in rice and sulfosulfuron + metsulfuron (ready mix) 0.040kg/ha as PoE in wheat (W2), pyrazosulfuron-ethyl at 0.025 kg/ha as PE fb cyhalofop-butyl at 0.100 kg/ha + bispyribac-Na at 0.025 kg/ha at PoE in rice and tank-mix clodinafop-propargyl 0.060 kg/ha+metsulfuron-methyl 0.004 kg/ha as PoE in wheat (W3), and pyrazosulfuron-ethyl at 0.025 kg/ha as PE fb cyhalofop-butyl at 0.100 kg/ha fb bispyribac-Na at 0.025 kg/ha as PoE in rice and tank-mix clodinafop-propargyl 0.060 kg/ha+carfentrazone-ethyl 0.02 kg/ha as PoE in wheat (W4). The experiment was laid out in a split plot design with three replications. All CA-based treatments encountered higher weeds and plant parasitic nematodes (PPNs) than TPR-CTW system in rice. Root-knot nematodes (RKN) galls were found in four grassy weeds (*Echinochloa colona, Echinochloa crusgalli, Dinebra retroflexa, Eleusine indica*) and one broad-leaved weed (*Eclipta alba*) among 14 weeds present in rice and was found for the first time in *D. retroflexa.* A CA-based rice-wheat-mungbean system with residue (CA5) reduced root knot nematode galls in weeds and rice plants by 75-81%. The pyrazo. fb cyhalo. fb bispyri. led to a reduction in RKN galls by 74% in rice plants through reducing weed density by 83%. At the upper 0-7.5 cm soil layer, weed seed bank density was higher under all CA-based treatments over CT, whereas in lower 7.5-15.0 cm soil layer, CT had higher weed seeds. Weed seed density under CA5 was reduced by 22% at 0-7.5 cm soil layer after fourth cropping cycle. The application of pyrazo. fb cyhalo. fb bispyri. in rice and clodi.+carfen. in wheat led to 72% reduction in weed seed bank at 0-7.5 cm soil layers. The CT resulted in 13% higher rice yield than CA5, which, on the contrary, led to 15 % higher wheat yield than CT. Similarly, the system productivity (REY) and system net returns in CA5 treatment were 37 and 51% higher than CT, respectively. The CA5 had lower bulk density at 0-5 cm soil depth and soil penetration resistance but higher proportion of large macroaggregates (>2 mm) than TPR-CTW system. The total organic carbon (1.47%), active C (0.93%) and passive C (0.53%) pool were significantly higher under CA5 than CT at 0-5 cm soil depth. The UWC resulted in significantly higher active C pool than herbicide treatments. Higher microbial biomass carbon and soil enzyme activity were observed under CA5 compared to CT. The methane emission was considerably lower in CA-based treatments than CT, whereas $N_2O$ emission was higher in CA-based treatments. Residues of all four herbicides (pyrazosulfuron, cyhalofop, pendimethalin, bispyribac) in soil and rice grains and straw were below detectable level. Thus, this study indicates that the CA-based triple ZT system, involving ZT direct-seeded rice (DSR) with mungbean residue - ZT wheat with rice residue - ZT mungbean with wheat residue combined with the application of pyrazosulfuron *fb* cyhalofop *fb* bispyribac in rice and clodinafop + carfentrazone in wheat would reduce weed seed bank and nematodes effectively and provide higher RW system productivity and net returns. This may be recommended for adoption in the Indo-Gangetic Plains of India.

# Agronomy


Hari Sankar Nayak

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Dr. C. M. Parihar

*Title of the Thesis*

## Machine learning evidence-based agronomic practices for higher yield and lower emission in rice-wheat system

The increasing availability of complex, geo-referenced on-farm data demands analytical frameworks to guide crop management recommendations. Recent developments in interpretable machine learning techniques offer opportunities to use these methods in agronomic studies. The objectives of studies were three-fold: (1) to identify the most appropriate machine learning algorithms (ML) to appropriately model the rice and wheat yields in north-western IGP, (2) Examine patterns in yield gaps and resource use efficiency and identify potential trade-off between yields and GHG emissions, and (3) Document the ways in which ML and 'big-data' analytics can be used to deliver evidence-based climate smart agronomic recommendations. A suite of fine-tuned machine learning models was statistically compared and fine-tuned for the bias-variance trade-off. *Post-hoc* model agnostic techniques, i.e., variable importance, interaction strength, and two-way interaction were used for model interpretation. Random forest was the best performing method in terms of goodness-of-fit and model precision and accuracy, with RMSE, MAE, and $R^2$ ranging between 367-470 kg ha$^{1}$, 276-345 kg ha$^{-1}$, and 0.44-0.63, respectively. The most important management variables explaining rice yield variability were crop duration, cumulative precipitation, average seasonal minimum and maximum temperature, and irrigation number, whereas nitrogen application rate, crop residue management, monthly cumulative solar radiation during February and March were important for wheat. The effect size of the important variables on rice yield were to the tune of 800 kg ha$^{-1}$ for small fraction of the farmers to less than 300 kg ha$^{-1}$ response among a large group of farmers. The effect size of wheat yield ranged between 227 kg ha$^{-1}$ for nitrogen application rate to 372 kg ha$^{-1}$ for cumulative solar radiation in February and March. Further, the data of rice and wheat production in the Northwestern Indo-Gangetic Plains of India was used to decompose rice yield gaps and to investigate the scope to reduce nitrogen (N) inputs without compromising yields. Stochastic frontier analysis was used to disentangle efficiency and resource yield gaps. Rice yield gaps were small (ca. 2.7 t ha$^{-1}$ or 20% of Yp) and mostly attributed to the technology yield gap (ca. 1.8 t ha$^{-1}$ or ca. 15% of Yp). Efficiency and resource yield gaps were negligible (less than 5% of Yp in most districts). The small yield gaps were associated with high use of irrigation water and N with small yield responses. The PFP-N can be improved through better matching N rates to the variety types cultivated Alike rice, the wheat yield gaps were also small, i.e., 12% of the yield gap was explained by efficiency and resource use. The sustainable resource use assessment was done for energy use efficiency. A two-step analysis comprising bootstrapped data envelopment analysis with a metafrontier approach and truncated regression was applied to investigate the scope to reduce energy inputs for the same level of energy output. Irrigation and fertilizers were the two most important energy inputs, accounts for slightly larger than 75% of the cumulative energy input. The district-specific technical efficiency scores ranged between 0.68-0.99, with a mean value of 0.86-0.90. On average, the energy-use efficient farms had 42% or higher energy-use efficiency in the districts of Ambala, Fatehgarh Sahib, and Karnal, whereas in other districts the efficient farms had 5-19% higher energy-use efficiency. The evidence and methodology provided from this study can help to identify sustainable intensification pathway and framing district specific policy actions.

# Entomology


Mogili Ramaiah

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Dr. Debjani Dey

### *Title of the Thesis*

## Biosystematic studies on leafhopper (Hemiptera: Cicadellidae) species associated with bamboo from India

Leafhopper family Cicadellidae (Order: Hemiptera) is one of the largest insect family with over 22,000 described species. They are economically important as most species cause considerable damage by directly feeding on the plants and a few others by being vectors of plant pathogens. Since information of these species on bamboo from India is fragmentary, therefore a comprehensive attempt was made to study them. The current study aimed at identification, compilation of an annotated checklist, description/redescription of various taxa with formulations of keys for the taxa at all levels associated with bamboo and molecular characterization of important species. Explorations conducted at 35 locations of 12 states of India led to the collection and study of around 8000 specimens. For the descriptions, emphasis was given to male genitalia variations. The annotated checklist compiled included details of valid name, synonyms, type locality, location of depository and geographical distribution along with new records from India. This checklist included 11 tribes, 35 genera and 59 species from India and also included details of 12 first records for India along with 13 new locality records established during the current studies. Diagnostic keys were also prepared for identification at all taxonomic levels. 43 species belonging to 30 genera from 11 tribes under 5 subfamilies resulted in the discovery of 4 new genera viz., *Bambuphaga* gen. nov.; *Niranjana* gen. nov., *Shanaya* gen. nov., unknown gen. nov. and 10 species viz., *Bambuphaga balajii* sp. nov., *Mukariella viraktamathi* sp. nov., *Mohunia* sp. nov., *Myittana* (*Myittana*) *bidentata* sp. nov., *Niranjana bicaudospina* sp. nov., *Niranjana curvielongata* sp. nov., *Niranjana* sp. nov., *Shanaya spatulata* sp. nov., *Shanaya* sp. nov. and Unknown sp. nov. to science. Phylogenetic analysis based on morphological and molecular data 28S (D2 & D9-D10) and Histone (H3) revealed the paraphyletic nature of tribes. Attempt was also made to solve problems of misidentification due to existence of colour polymorphism among the species.

# Environment Science

G K Dinesh

**Name of the Student** : **G K Dinesh**
**Roll No.** : **11027**
**Chairperson** : **Dr. Dinesh Kumar Sharma**

Dr. DK Sharma

*Title of the Thesis*

## Quantification of ecosystem services in conservation agriculture under maize-wheat-mungbean cropping system

Ecosystem services are becoming critical for evaluating the sustainability of any ecosystem. However, agricultural intensification, excess resource usage, and heavy mechanization are often considered for their negative impact rather than positive ecosystem services. Keeping this in mind, the study was conducted from 2018 to 2020 to evaluate and quantify the food, fodder services, C-stock accumulation, nutrients cycling, earthworms' population, and GHG emissions in the maize-wheat-mungbean cropping system under conservation agriculture practices. The study was performed at the long-term experimental site (since 2012) at a research farm (block 9B) of ICAR-Indian Agricultural Research Institute, New Delhi, India. Summer mung beChaian (cv. Pusa Vishal), Kharif maize (cv. PMH 1), and wheat (cv. HD 2967) were grown at the experimental site having sandy loam soil (Typic haplustept). The experiment was carried out with zero tillage with residue retention (ZTWR) and zero tillage without residue retention (ZTWoR), along with precision nitrogen management. This study revealed that cumulative total ecosystem services were highest in ZTWR 50%BN+GS (Rs. 6,44,423) and lowest in ZTWoR 70%BN+GS (Rs. 5,26,906) among the treatments. ZTWR was observed to have the greatest values (Rs.6,10,892) among the main plot treatments, and ZTWoR plots have the lowest values (Rs. 5,49,632). The result of precision nitrogen management, particularly the application of 50%BN+GS, had the greatest values (Rs. 6,08,095), followed by 33%BN+GS (Rs. 5,85,591) and RDN (Rs.5,75,833), while the lowest value was recorded in treatment 70%BN+GS. The result also indicates that ZTWR performed better than ZTWoR plots. Value of ecosystem services under ZTWR plots, through food production (Rs. 318979), fodder production (Rs. 84306), C-stock (Rs. 186744), GHG emissions (Rs. -43911), nutrient cycling (Rs. 16432), and earthworms (Rs.114), are from the maize-wheat-mungbean cropping system under conservation agriculture practices. This study provides the best understanding of the economic worth of agricultural ecosystem services, particularly in maize-based no-tillage farming systems. This study would help to make a policy framework for farmers to provide the payment for ecosystem services and aid in ensuring the long-term sustainability of farms and farmers' income.

# Floriculture and Landscape Architecture


Parvathi Bennurmath

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**Roll No.** : **11031**
**Chairperson** : **Dr. Rajiv Kumar**


Dr. Rajiv Kumar

*Title of the Thesis*

## Evaluation of Chrysanthemum (*Dendranthema x grandiflora* Tzvelev) for photo-insensitivity

The present investigation was undertaken in a naturally ventilated polyhouse at ICAR-IIHR, Bengaluru during 2018 to 2021. 20 genotypes were evaluated under 3 photoperiod treatment combinations in factorial CRD. Pooled data of two years revealed that photoperiod T9 (Photoperiod 16/8 hrs + No Black in) significantly recorded maximum plant height (46.86 cm) and leaves/plant (115.78), however, V10 (Roopanjali) (70.46 cm) and interaction T9 x V10 (72.68 cm) recorded maximum plant height. Photoperiod T5 (Photoperiod of 15/9 hrs + Black in for 10/14 hrs) significantly recorded early flower bud appearance (22.32 days), T2 (Photoperiod of 14/10 hrs + Black in for 10/14 hrs) recorded early first flower opening (58.88 days) and early optimum flowering (77.23 days). Arka Pink Star recorded early flower bud appearance (13.09 days), first flower opening (33.30 days) and optimum flowering (55.57 days). Photoperiod T5 recorded significantly maximum flower diameter (4.18 cm), number of flowers per plant (52.94) and flowering duration (31.75 days) while genotype V12 (Kargil) recorded maximum number of flowers per plant (96.43) and longer flowering duration (38.52 days). Based on response groups, eightgenotypes *viz*., Arka Pink Star, Pusa Anmol, Ajay, Marigold, Arka Kirti, Winter Queen, Kargil and Punjab Gold showed uniform flowering across different photoperiods.

High heritability coupled with high genetic gain as *per cent* of mean was recorded for plant height, branches/plant, leaves/plant, days to bud initiation, first flower opening, optimum flowering, flower diameter, flowers/plant and flowering duration. Number of flowers/plant exhibited positive and significant correlation with number of branches and leaves/plant, days to bud initiation and optimum flowering. Photoperiod T2 (photoperiod of 15/9 hrs + black in for 8/16 hrs) recorded maximum starch content (50.73 mg/g) compared to T1 (natural condition) (39.84 mg/g), however, genotype V3 (Ajay) recorded maximum starch (55.88 mg/g) which was at par with V4 (Marigold) (51.15 mg/g) and V2 (Pusa Anmol) (50.93 mg/g), whereas, V8 (Punjab Gold) recorded minimum starch (34.33 mg/g). Interaction effect of photoperiod and genotypes (T2 x V6) recorded maximum starch content (60.34 mg/g) which was at par with T2 x V3 and T2 xV7. Screening of 180 genotypes for white rust resistance based on disease severity (*per cent* disease index) under natural condition revealed that 79 genotypes were identified as highly resistant, 27 as resistant, 38 as moderately susceptible, 20 as susceptible and 16 were categorized as highly susceptible. Among 20 genotypes screened *in vitro,* 17 genotypes showed resistance while 3 were susceptible.

# Food Science and Post Harvest Technology

Chander Bhan

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Dr. Ram Ashrey

*Title of the Thesis*

## Postharvest disease management and shelf life extension of Kinnow mandarin

Kinnow mandarin is a high value citrus crop among fruit industry, widely grown in tropical and subtropical regions of the world. Being rich in high moisture content, soft and debilitation nature, the fruits undergo a significant quantitative and qualitative losses. To address this problem, we carried out an integrated research work consisting of edible coatings, plant extracts and bioagents to prolong the shelf life and decreasing the postharvest fungal diseases of Kinnow mandarin fruits. To execute this study, three objectives were proposed. In the first objective, bio-efficacy of bioagents and plant extracts against major postharvest pathogens of 'Kinnow' mandarin were assessed under *in vitro* conditions. The results exhibited that the yeast *Rhodotorula minuta* var. *minuta* ($1\times10^8$ CFU $ml^{-1}$) was the most promising antagonist against postharvest green mold, blue mold and sour rot of Kinnow mandarin over bioagents such as *Debaryomyces hansenii*, *Lactobacillus plantarum*, *Metschnikowia pulcherima*, *Pichia guilliermondi.* Ethanolic plant extracts of moringa leaves exhibited the highest antimicrobial activity against postharvest green mold, blue mold and sour rot of Kinnow mandarin under *in vitro* conditions. However, ethanolic mixed plant extracts (moringa, marigold and periwinkle at 1:1:1) had better antimicrobial efficacy than using solo plant extracts. Mixed plant extracts at 2000 ppm were found the best concentration for the inhibition of target pathogens (*P. digitatum*, *P. italicum* and *G. candidum*). In the second objective, we elucidated the effects of chitosan (CH) and guar gum (GG) based composite edible coating incorporated with tamarind (TAM) seed starch and jackfruit (JACK) seed starch on physicochemical quality and storability of Kinnow fruit under ambient conditions. The results indicated that GG + TAM coated fruits maintained significantly ($P \leq 0.01$) lower physiological losses in weight (PLW) (3.12 %), decay incidence (0.83 %), and respiration rate (13.57 ml $CO_2$ $kg^{-1}$ $h^{-1}$) compared to control. The reduced activity of pectin methylesterase (PME) (0.97 µmol $min^{-1}$ $g^{-1}$ FW) and lipoxygenase (LOX) (1.97 µmol $min^{-1}$ $g^{-1}$ FW) were noted in GG + TAM coated fruits. Also, the GG + TAM coated fruits retained higher fruit firmness (6.77 N), titratable acidity (TA) (0.94 %), ascorbic acid (AA) (27.83 mg 100 $g^{-1}$), total phenols (213.05 mg GAE 100 $g^{-1}$ FW), antioxidants activity (23.57 µmol TE $g^{-1}$) along with higher sensory score (1.89-fold) over the control. In the third objective, shelf life and quality attributes of Kinnow mandarin fruits treated with the guar gum-based composite coating (GG+TAM), plant extracts, alone and in combination and stored under ambient conditions were evaluated. Our results revealed that GG+TAM coating was compatible with bio-agent *R.*

*minuta var. minuta* without any marked influence on the growth of bioagent (*R. minuta* var. *minuta*) under *in vitro*. A layer-by-layer E+MPE+B coating treatment was the most effective and safer approach among all the applied coatings compared to control for extension of shelf life of harvested Kinnow mandarin fruit up to 30 days during storage at ambient conditions. Layer-by-layer E+MPE+B coating remarkably decreased PLW (2.20%), decay incidence (0.06%) and respiration rate (12.25 ml $CO_2$ $kg^{-1}$ $h^{-1}$) and the activity of fruit softening enzymes like PME (0.93 µmol $min^{-1}$ $g^{-1}$ FW) and LOX (1.90 µ moles $min^{-1}$ $g^{-1}$ FW). In addition, such fruits have also conserved substantially higher fruit firmness (7.00 N), titratable acidity (1.03%), ascorbic acid (33.43 mg 100 $g^{-1}$), total phenols content (248.94 mg GAE 100$g^{-1}$ FW), total antioxidants activity (25.84 µmol TE $g^{-1}$) and lesser TSS (10.89 $^{o}$B) and marked higher score for sensory quality (1.96-fold) over the control. Overall, these results suggest that layer-by-layer E+MPE+B coating (an integrated eco-friendly strategy) could be used successfully as an advantageous alternative to prevalent commercial waxes for maintaining quality and extending the shelf life of stored Kinnow mandarin fruits under ambient conditions.

# Fruit Science


Nusrat Perveen

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Dr. M.R. Dinesh

*Title of the Thesis*

## Variability enhancement in polyembryonic genotypes of mango (*Mangifera indica* L.)

Variability Enhancement in Polyembryonic Genotypes of Mango (Mangifera indica L.) Abstract Polyembryonic mango genotypes are the best resources for development of rootstocks owing to the production of uniform, true-to-type nucellar seedlings with deep tap root system. However, the use of these genotypes in breeding programmes is often limited by their narrow genetic base due to maternal inheritance. Hence, widening of genetic base of the polyembryonic genotypes for different rootstock traits might make them more desirable to be used as rootstock. The study was planned for widening the genetic base of three polyembryonic mango genotypes viz. 'Bappakkai, Nekkare and Kurukkan', for traits like dwarf stature and salinity tolerance using mutation breeding approach by treating kernels with different doses of gamma rays ranging from 15 to 35 Gy. The generated putative mutants were validated using volatile profiling and characterized by 12 SSR markers to determine the genetic diversity in them. Three years old selected putative mutants were also subjected to three levels of salt stress viz., 25 mM, 50 mM and 75 mM NaCl+CaCl2 (1:1) to select progenies tolerant to salt stress. Further, transcriptome analysis of two polyembryonic mango genotypes (salt tolerant Turpentine and salt susceptible Mylepelian) was done to understand the molecular basis of salinity tolerance and to identify genes responsible for salinity tolerance in mango. Irradiation created significant variation in the studied morphological and endomorphic traits and resulted in delayed germination and decrease in germination percentage, number of seedlings emerging per kernel, plant height, inter-nodal length and number of leaves with increasing dosage of irradiation. LD50 determined using probit analysis based on mortality percentage of kernels was found to be 22.39Gy, 19.95 Gy and 19.95 Gy for Bappakkai, Nekkare and Kurukkan, respectively. Monoterpenes and sesquiterpenes were the major volatile compounds present in all the samples under study and a clear distinction between treated and untreated plants could be made based on their volatile profiles. Molecular characterization revealed high heterogeneity in the putative mutant populations and the high allelic richness and mean Shannon's Information observed in the putative mutant population suggests that mutation created variability in the treated population. Imposed salt stress resulted in increase in Na+, Cl-, Malondialdehyde content (MDA), total phenols, SOD, POD and CAT and decrease in K+, Ca2+, chlorophyll content, membrane stability index, relative water content, leaf water potential, photosynthetic rate, stomatal conductance and transpiration rate in all the genotypes. The putative mutant 202 population of Bappakkai was found to

contain higher concentration of calcium and potassium ion, lower Na+/K+ ratio along with highest fold increase of ABA, SA, asparagine, presence of higher concentration of chlorogenic acid and ferulic acid along with the lower reduction in the levels of caffeic and sinapic acid at higher level of salt stress suggesting that these are better at tolerating salt stress as compared to the putative mutant populations of Nekkare and Kurukkan. RNA sequencing by Novaseq6000 platform resulted in a total of 2795088, 17535948, 7813704 and 5544894 clean reads in Mylepelian treated (MT), Mylepelian control (MC), Turpentine treated (TT) and Turpentine control (TC) respectively. In total, 7169 unigenes annotated against all the five public databases, including NR, NT, PFAM, KOG, Swissport, KEGG and GO. A total of 7697 SSRs defined as di- to hexanucleotide motifs were also identified, the most abundant being mono-nucleotide repeats. Further, Between MT and MC, 2106 genes exhibited significant changes in gene expression where 987 genes were up-regulated and 1119 genes were down-regulated while between TT and TC a total of 587 genes had significantly different gene expression wherein 260 genes showed up-regulation while 327 genes were down-regulated and between MT vs TT, 1158 genes showed significant changes in gene expression and among these, 510 and 648 genes were up-regulated and down-regulated, respectively. The differentially expressed genes under different treatment levels included transcription factors (bZIP, NAC, bhLh), genes involved in signal transduction (CDPK), ABA biosynthesis, Photosynthesis etc. Expression of few of these genes was experimentally validated through quantitative real-time PCR (qRT-PCR) and contrasting expression pattern of ARF2, LEA and CDPK genes were observed between Turpentine and Mylepelian. The results suggest effectiveness of induced mutation in bringing about variability in traits like plant height and salt tolerance for developing dwarf and salt tolerant rootstocks to be used in high density planting. The findings also indicate that volatile profiling could be used as a tool to detect variation in a mutated population and validate putative mutants in polyembryonic mango genotypes. Further, the information generated by transcriptome analysis will be useful in understanding the possible molecular mechanism underlying salt tolerance in mango and the genes identified could prove to be a potential source for development of SSR markers which can serve as valuable baseline information to generate new targets for mango breeding for salt tolerance.

# Genetics and Plant Breeding


Rahul Kumar

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Dr. Akshay Talukdar

### *Title of the Thesis*

## Inheritance and molecular mapping of seed traits in soybean [ *Glycine max* (L.) Merr.]

Seed size, shape and seed coat color are important traits in soybean [*Glycine max* L. (Merrill)] as they are desirable for specialty soy foods like *tofu*, *natto*, *miso*, and *edamame*. Inheritance and mapping of seed coat color and 100-seed weight was studied in direct and reciprocal cross combinations between a large seeded ( 100-seed weight 30g), brown seed coated vegetable soybean variety AGS457 and small seeded (e 100-seed weight 7g) and yellow seed coated genotype SKAF148 . In both the combinations, the seed coat of the $F_{1:2}$ seeds were green while the same in the $F_{2:3}$ generation segregated in the ratio of 9:3:4 for green, yellow and brown respectively indicating that the inheritance of seed coat color was controlled by two genes in supplementary interaction. Inheritance of the seed shape and 100-seed weight in the $F_2$ generations indicated it to be governed by polygenes. In order to map quantitative trait loci (QTLs) and find candidate genes for seed shape and 100-seed weight, the $F_2$ and $F_{2:3}$ mapping populations derived from the above-mentioned cross were used. 42 QTLs were mapped over 13 chromosomes. Out of these, seven were stable QTLs and of which five were major QTLs namely *qSL-10-1, qSW-4-1, qSV-4-1, qSLW-10-1*and *qSLH-10-1*. Thirteen of the 42 QTLs were mapped at known loci, while the remaining 29 were novel of which 17 were major QTLs. 66 genes within seven stable QTLs were predicted, based on Protein Analysis Through Evolutionary Relationships (PANTHER) gene annotation information and literature search, to be possible candidate genes that might regulate 100-seed weight and seed shape in soybean. Thus, Genetics of seed coat color and mapping of QTLs and identification of underlying key candidate genes for seed shape and 100-seed weight in soybean has been successfully carried out in the present work These findings of the study would be very helpful in marker-assisted breeding for developiFng soybean varieties with improved seed weight and desired seed shape.

# Microbiology


Nishanth S.

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Dr. Radha Prasanna

*Title of the Thesis*

## Prospecting the potential of cyanobacterial biofilms as options for Fe and Zn mobilization in maize (*Zea mays* L.)

The inoculation of cyanobacteria, and/or cyanobacterium-based biofilms is known to improve the nutrient availability in soil, stimulate plant growth, and biofortify the produce. Hence, the proposed research program involved firstly, the biochemical and metabolite characterization of Anabaena torulosa (An), Trichoderma viride ITCC 2211 (Tr), Providencia sp. (PW5), cyanobacterial biofilms -An-Tr & An-PW5. Further research focused on exploring the interaction of microbial inoculants, with an elite maize hybrid, Pusa Vivek QPM9 Improved, and its parents, PMI PV1, and PMI PV2 on iron and zinc micronutrient translocation and related expression of zinc, and iron-related transporter genes (ZmZIP). Co-culturing of cyanobacterium, A. torulosa with T. viride / Providencia sp. as a partner brought about a significant 4.3-fold increase in exopolysaccharides, in An-PW5 and total chlorophyll by 21.42, and 3.30% in An-Tr and An-PW5 respectively, over An alone. Untargeted gas chromatography and mass spectroscopic analyses illustrated a significant modulation of the metabolite profiles in the cyanobacterial biofilms vis-à-vis partners. Both the partners- PW5 and Tr, elicited a notable influence on the metabolite profiles of An. The An-Tr biofilm recorded a distinct cluster of metabolites, as revealed by heat map and cluster analysis, as also highest percentage of sugars (66.85%) with maltose, lactose, and D-mannitol being the most abundant. Mesocosm experiment with maize crop and field experiments conducted during Kharif 2019-20, and 2020-21, with the individual cultures and biofilm formulations, showed that the application of An-Tr biofilm formulation, led to an increase by 14- and 3.3- fold respectively, in the soil nitrogenase activity and chlorophyll over RDF, at the mid-vegetative stage. As compared to the parent genotypes, Pusa Vivek QPM9 Improved showed 1.2 1.5- fold increase in nitrogenase activity. Among all the microbial formulations, cyanobacterial biofilms - An-Tr, and An-PW5 improved Fe and/or Zn mobilization and their translocation to maize kernels. The kernel iron content increased by 0.31 0.43-fold in treatments with An- Tr, and 0.18 0.28-fold in An-PW5, attributed to the increased ferric chelate reductase activity in maize roots; whereas the kernel zinc content showed 0.46 0.66, and 0.37 0.55- fold increase in An-Tr, and An-PW5 biofilms respectively, over RDF. In addition to Fe/Zn fortification, increased assimilation of carbon was also evident, in terms of the activity of carbonic anhydrase and phosphoenol pyruvate carboxylase. Inoculation led to the exceptionally higher relative expression of zinc and iron-related transporter genes - ZmZIP6 and ZmZIP8 in the kernels of Pusa

Vivek QPM9 Improved. Albeit, ZmZIP1 was found to be important, as it showed a positive and significant correlation with kernel iron (r=0.54*), and kernel zinc content (r=0.82***) at harvest, soil iron content (r=0.81***), leaf iron (r=0.68**), leaf zinc (r=0.52*) in the mid-vegetative stage, and leaf iron (r=0.75**), root iron (r=0.53*), leaf zinc (r=0.54*), and soil iron (r=0.81***) content in the pre-flowering stage. This comprehensive study illustrated that cyanobacterial biofilms- An-Tr, and An- PW5 are promising priming options, which can save approximately 25% N fertilizers, besides improving the iron and zinc mobilization to maize kernels. Long-term use of such cyanobacterial formulations can also enhance soil fertility and plant growth.

# Molecular Biology and Biotechnology


Suhas Gorakh Karkute

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Dr. Amolkumar U Solanke

*Title of the Thesis*

## Cloning and characterization of *Magnaporthe oryzae* responsive von Willebrand Factor type A domain (vWA) containing genes in rice

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Blast disease severely hampers rice production across the world. Blast disease resistance in rice is mediated mainly by resistance (R) and defense regulator (DR) genes. There is frequent breakdown of R gene mediated resistance whereas DR genes provide broad-spectrum durable resistance. To identify novel R and DR genes, comparative transcriptome analysis of blast infected panicle tissues of resistant cultivar Tetep and susceptible cultivar HP2216 was carried out and two novel *von Willebrand factor domain A* (*vWA*) containing genes have been identified as important blast responsive genes. Considering the novelty of vWA genes in plants, the vWA family in rice has been characterized. This superfamily in rice consisted of 40 vWA genes and named as *OsvWA1* to *OsvWA40* based on their position on chromosomes 1 to 12. Transposon insertion polymorphism analysis in vWA genes in 3000 rice genotypes showed the negligible frequency of transposon elements indicating their important role in growth and development. SNP analysis showed that vWA genes in susceptible cultivars HP2216 and Nipponbare are highly conserved, whereas there are large number of SNPs in Tetep. Evolutionary relationship through phylogenetic tree showed two major clades which further divided into 6 groups. The 20 vWA genes are evolved independently whereas rest are evolved from single gene. Expression analysis of vWA genes in blast infected rice tissues revealed that *OsvWA9, OsvWA18, OsvWA36,* and *OsvWA37* are highly upregulated in blast disease. Transgenic plants overexpressing *OsvWA36* gene by constitutive ubiquitin promoter have been developed in a susceptible TP309 cultivar. All the putative transgenic plants were confirmed by PCR. Southern hybridization revealed three independent transgenic events with one, two and multiple copies of transgene. The *OsvWA36* gene was highly expressed in transgenic plants compared to non-transgenic plants. The transgenic plants exhibited strong resistance against highly virulent Mo-ni-025 strain of *M. oryzae* in detached leaf, panicle inoculation and seedling spray inoculation assays. In all the assays, non-transgenic plants showed prominent lesions whereas transgenic plants showed immune response. *In silico* analysis predicted the interaction of OsvWA36 protein with Pi21, OsvWA37, OsSPL2, NB-ARC domain containing protein and receptor like kinase protein which are all functionally associated with disease resistance. Overall, the study has identified and functionally validated the novel and crucial *OsvWA36* gene as a potential candidate for panicle and leaf blast resistance in rice.

# Nematology


Chaitra Ganapati Bhat

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**Chairperson** : **Dr. Uma Rao**

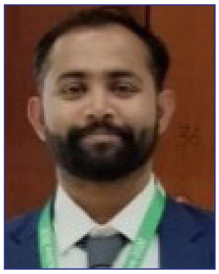

Dr. Uma Rao

### *Title of the Thesis*

## A molecular investigation of *Heterorhabditis* nematode factors involved in symbiosis with *Photorhabdus* bacteria

The specific association between the entomopathogenic nematode (EPN) *Heterorhabditis* and entomopathogenic bacteria (EPB) *Photorhabdus* offers a powerful model to study animal-bacterial symbiosis. Several molecular determinants of bacteria involved in the symbiotic association have been identified. However, information on nematode factors that govern the symbiosis is lacking. Additionally, genomic information of *Heterorhabditis* nematodes available in the public domain is very scant. Here, we present the first draft genome sequence of *H. indica*, which is widely present in the warmer and tropical climatic regions and is one of the most commercialized EPNs. The draft genome of the *H. indica* Hms1-i20 was sequenced using three genomic libraries of 300 bp, 600 bp and 5 kb sizes by Illumina HiSeq platform. The size of the draft genome assembly was 91.26 Mb, comprising 3,538 scaffolds. 10,494 protein-coding genes were predicted in the present genome. Comparative analysis of *H. indica* genome in comparison to four other nematode genomes revealed that *H. indica* shared 6,574 orthologous groups with *H. bacteriophora*, 6,635 with *C. elegans*, 6,228 with *S. carpocapsae* and 6,669 with *O. tipulae*. Protein domain and secretome characterization identified 2,525 transmembrane domain proteins and 370 putative secreted proteins. Subsequent analyses identified 56 GPCRs, 38 peptidases, 31 peptidase inhibitors and 2 Fatty-acid retinol binding proteins in *H. indica* proteome and such proteins may facilitate nematode interactions with insect hosts or bacterial symbionts. Additionally, 2,549 microsatellite loci, 1,548 transposable elements, 631 non-coding RNA loci, 21 likely cases of horizontal gene transfer (HGT) were identified. The mitochondrial genome of *H. indica* was assembled separately which is 17,393 bp in size and 46 genes were detected in mitochondrial genome. RNA-sequencing was employed to investigate nematode factors involved in symbiosis at the early adult stage of *H. bacteriophora*. A total of 754 differentially expressed transcripts were identified in symbiotic nematodes. Additionally, 12,151 transcripts were unique to symbiotic nematodes. Endocytosis, cAMP signalling and focal adhesion were the top enriched pathways in symbiotic nematodes, and a large number of transcripts involved in nematode immune/defence responses against bacteria were identified. Subject to functional validation of the identified transcripts, our findings suggest that the nematode immune system plays a pivotal role in maintenance of symbiosis with its bacterial partner. To the best of our knowledge, this is the first global investigation of animal factors involved in the modulation of microbial symbiosis. Moreover, screening for dsRNA uptake in different developmental stages of *Heterorhabditis* and subsequent RNAi experiments provided the proof of concept for successful RNAi by soaking post-IJ recovery stage in dsRNA solution. This method can be adopted for gene function validation in *Heterorhabditis* nematodes in future.

# Plant Pathology


Rahul Kumar Tiwari

**Name of the Student** : **Rahul Kumar Tiwari**
**Roll No.** : **10652**
**Chairperson** : **Dr. Rashmi Aggarwal**


Dr. Rashmi Aggarwal

*Title of the Thesis*

## Identification, pathophysiology and management of potato dry rot caused by *Fusarium* spp.

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Globally, *Fusarium* is a notable genus of phytopathogenic fungi which cause dry rot of potato tubers during storage. Dry rot infection causes prominent quantitative and qualitative damage to harvested potatoes, resulting in significant losses for processing industries and consumers. The objectives of this study were to identify *Fusarium* species involved with potato dry rot disease in various potato growing regions of India and to determine their pathogenicity, pathophysiology and formulating suitable management strategy. A total of 106 *Fusarium isolates* were identified in potato tubers collected from ten important potato production regions of India, out of which six different *Fusarium* species, *Fusarium sambucinum*, *Fusarium solani*, *Fusarium oxysporum*, *Fusarium verticillioides*, *Fusarium proliferatum* and *Fusarium flocciferum*, were isolated. The identification of each species was confirmed by sequencing analysis of~700 bp DNA fragment derived from the translation elongation factor-1 alpha gene and ~550 bp DNA fragment derived from internal transcribed spacer region. Three different species *viz., Fusarium sambucinum, Fusarium solani and Fusarium oxysporum* were found to be the predominant species among the collected isolates. *Fusarium proliferatum, Fusarium verticillioides* and *Fusarium flocciferum* were reported for the first time In India. Twenty-one popular Indian potato cultivars were screened against three predominant species and observed to be moderately to highly susceptible for this disease except Kufri Chipsona I, II and III which had shown some level of tolerance. We assessed the susceptibility parameters and quality aspects of two contrasting cultivars, Kufri Pukhraj (table purpose) and Kufri Chipsona 3 (processing purpose) during infection. 'Kufri Pukhraj' was shown to be more susceptible than 'Kufri Chipsona 3' in terms of lesion diameter, fungus penetration, and rot volume after 20, 40, and 60 days of storage. In comparison to *Fusarium oxysporum*, *Fusarium sambucinum* was highly aggressive. However, regardless of cultivar, a mixed inoculum of *Fusarium* species resulted in greater damage. After 60 days of storage, fungal infection (individual or mixed inoculum) results in a decrease in starch and amylose content in both cultivars. Additionally, both cultivars had shown increased amylopectin, lowered sugars, sucrose, and total soluble sugar content in response to fungal infection. The glycemic index and glycemic load were also significantly ($p<0.005$) elevated in the diseased tubers as compared to control which indicated the unsuitability of dry rot infected tubers for human consumption. The altered antioxidant metabolites such as ascorbic acid, total phenols, carotenoids and total amino acids demarcated the pathogen's ability to dissipate the necessary metabolites of the tubers. Among the suitable management approaches to mitigate this disease, the sodium metabisulfite (0.3M), melatonin (15mM) and *Chaetomium globosum*-derived silver nanoparticles (150mg/L) were observed to be highly efficacious. This study will pave a path for future research highlighting the effect of storage fungal infection on the nutritional quality parameters of potato tubers, which is a major concern for consumers and the potato processing industry.

# Plant Physiology


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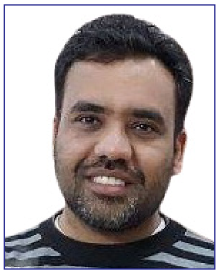
## Analysis of glycemic index and associated attributes in potato tubers

People leading a sedentary lifestyle and consuming high amounts of carbohydrate-rich food leads to develop obesity and type-II diabetes. Upon digestion of starchy food, postprandial blood glucose level rises rapidly and sharply, which reflects a high glycemic index (GI) value. Our study showed a significant negative correlation (R=-0.88) between GI and RS, whereas a negative correlation (R=-0.79) was found between GI and amylose content. Further, starch storage of cooked potato tubers at 4ºC for various periods (up to 48h) resulted in a significant reduction in GI and an increase in RS. Moreover, adding pulses to potato resulted in lowering GI and enhancement of RS. The retrogradation (4°C for 48 h) of potato-pulse combination showed GI lowering effect compared to control. The addition of oils to potato during cooking reduced GI and glycemic load (GL), with an increase in RS. Further, storage of cooked potato-oil combination at 4°C for 48 h resulted in the reduction of GI and increase in RS. In another study, the effect of the combination of potato with eight different types of vegetables was studied for predicted glycemic response and related traits. Out of eight vegetables taken for combination, fenugreek leaf, cauliflower and fenugreek seed were found to be effective in lowering the average GI of both cultivars to about 71, 70 and 68, respectively, compared to control (79). Concomitantly, our results suggest that adding pulse, vegetable and cooking oil to potato, followed by retrogradation/ cooling, might be an effective approach to managing the postprandial rise in blood glucose levels. The study will be helpful for the diabetic person for deciding the type of mixed meal and effective management of postprandial rise in blood glucose level and for food technologists to design food materials for health-conscious people.

# Vegetable Science



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## Molecular identification of cytoplasm types, Ms locus and development of genomic resources in short day Indian Onion (*Allium cepa* L.)

This study was carried out for molecular identification of cytoplasm and genotype of fertility restorer Ms locus in the selected 24 individual plants of 35 short-day commercially adopted varieties. It was found that there was no correlation of anther and pollen colour for the identification of fertility status of onion plants. Indian onion population have only S and N type of cytoplasm and no T-cytoplasm. In case of Ms locus, more than 90 percent plants possessed homozygous recessive. Among the tested cultivars, plants of eight varieties possessed S-type cytoplasm which was validated through two cytoplasm specific (accD and MKFR) and four (OPT, AcSKP1, AcPMS1 and jnurf-13) Ms locus specific. For cytoplasm, accD and for Ms locus AcPMS1 exhibited the complete linkage disequilibrium. The genotypes namely Pusa Red, Arka Bheem and KRR were determined to have S-type male sterile cytoplasm. Besides this, forty-five commercial short-day onion varieties were selected for the molecular, morphological and biochemical diversity analysis. For molecular diversity analysis, 137 microsatellite markers were developed where forty-three primer pairs were amplified and among these eleven were identified polymorphic along with 12 already available SSR markers in the public domain among the tested onion genotypes and relative species. Forty-three alleles, ranging from 2-5, were detected with an average of 2.867 alleles per SSR locus. PIC value ranged from 0.203- 0.715 with an average of 0.431. Highest PIC value was detected in ACM091 (0.715) and lowest in ACM463 (0.203). Genetic dissimilarity ranged from 0.067 to 0.933 with a mean of 0.476. Forty-eight genotypes clustered into three 3 groups where locals and exotic genotypes clustered distinctly with minor admixture in each cluster. The results of morphological characterization of the studied accession showed no correlation with molecular data. Grouping of studied accessions was independent of any morphological traits. Among morphological parameters, plant height, number of leaves, leaf width and length, pseudo stem diameter and length, average bulb weight, number of rings, average thickness of rings, root disc diameter, polar and equatorial diameter, neck thickness, neck fall, and so on. All the parameters exhibited significant variation. They displayed enough genetic diversity among the cultivars selected on the basis of bulb colour and growing geographical region of the country. Dry matter content, total soluble solids, pyruvic acid, total phenol content, total flavonoid content, ascorbic acid, mineral profile, amino acid profiling etc were estimated in all the selected forty-five commercial short-day onion cultivars.

# Water Science & Technology


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## Sensor based automatic basin irrigation system for enhancing irrigation efficiency

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A soil moisture sensor-based automatic basin irrigation system was developed which consists of three main units i.e., a sensing unit, a communication unit and a control unit. The sensing unit is comprised of capacitance-based soil moisture sensor, PVC pipe, solar panel, microcontroller, and LoRa module. The communication unit is equipped with LoRa and a GSM module, and the control unit with solar powered check gate. Wireless communication between soil moisture sensors and check gate was established via LoRa and GSM module. The testing and evaluation of the system were done under both bare soil and wheat crop at the research farm, Indian Agricultural Research Institute, New Delhi for the years 2019-20 and 2020-21, respectively. The size of the experimental field was 60 x14 m with 0.0005 m/m slope. A check gate was installed in the irrigation channel at the inlet of the field. The location and depth placement of three soil moisture sensors (SMSs) were at 25% of field length from the inlet & 37.5 cm depth for SMS-1, 50% field length from the inlet & 15 cm depth for SMS-2, and 75% field length from inlet & 7.5 cm depth for SMS-3. Three operational schedules of check gate for opening and closing were designed to identify the best location and depth of the SMSs in the field based on different irrigation performance indicators. The results revealed that two separate SMSs are required to open and close the check gate automatically. For opening the check gate the placement of SMS-2 was found suitable, whereas for closing, the placement of SMS-1 at soil moisture depletion ≥ 40% and SMS-3 at soil moisture depletion ≥ 20% was found suitable. The infiltration parameters and Manning's surface roughness coefficients *'n'* were estimated using the event analysis tool of WinSRFR 5.1.1 for thirteen irrigation events under bare soil and wheat crop. Kostiakov's infiltration parameters *'a'* and *'k'* varied from 0.24-0.69 and 11.84-38.84 mm/hr$^a$, respectively in bare soil and from 0.24-0.73 and 26.84-39.84 mm/hr$^a$ under wheat crop conditions, respectively. The values of *'n'* varied from 0.041-0.1 and 0.056-0.13 in bare soil and wheat crop conditions respectively. A new approach to estimate *'n'* using water front advance data was successfully validated with wheat field data and compared with the WinSRFR 5.1.1 estimated *'n'* value. This automatic irrigation system achieved irrigation application efficiency of >85%, distribution uniformity > 0.85 and water requirement efficiency of > 95% in wheat crop. The results revealed that approximately 24.3% of irrigation water was saved under this automatic irrigation system than the manually controlled irrigation system in wheat crop. Operational schedules were also developed which will provide a quite useful and handy information to the irrigators. The solar powered sensor-based automatic surface irrigation system was found a robust, easy and an effective tool to the farmers for enhancing surface irrigation efficiency.

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