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POST GRADUATE SCHOOL
1958-2022

Sixtieth Convocation

Significant Post Graduate Students' Research

February 6-7, 2022

Abstracts

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Dr. B.S. Dhillon
Former Vice Chancellor, PAU, Ludhiana

Convenor
Dr. Anil Dahuja
Professor, Division of Biochemistry

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

Agricultural Chemicals

Anirban Sil

Name of the Student : **Anirban Sil**
Roll No. : **21201**
Chairperson : **Dr. Suman Gupta**

Dr. Suman Gupta

Title of the Thesis

Synthesis and Assessment of Pesticide Removal Potential of Magnetite Based Composites from Water

Globally, rampant use of pesticide has become an evil issue and so is the persistence of its residues in the surface and groundwater bodies. To eliminate these micro pollutants from water, magnetite was combined with biopolymers (MAG 1-7), Graphene oxide (MAG 8-10), nano and non-nanoclays (MAG 11-15), and other combinations (MAG 16-18), using co-precipitation and hydrothermal methods. The prepared composites were applied for removal of twelve commonly used pesticides namely chlorantraniliprole, clothianidine, azoxystrobin, acetamiprid, fipronil, imidacloprid, thiamethoxam, dinotefuran, thiacloprid, tricyclazole and nitenpyram). Based on the preliminary screening four composites were selected for further evaluation. These were characterized using FT-IR, SEM and TEM. Sorption experiments suggested that at 25^{o}C, 10 mg of prepared material with 4 hours of contact time in a 5 mL of neutral to alkaline (pH 7-9.2) pesticide mixture solution at a fortification level of 1 μg/mL gives the optimum adsorption. The kinetic studies revealed that 2000-2500 μg/g was the maximum adsorption capacity of the composites and multiple steps including the intraparticle diffusion was involved in adsorption. Further, agreement of data with Freundlich sorption model signifies that adsorption involves a heterogeneous multilayer phenomena. The regeneration and re-usability using methanol followed by ultrasonication and centrifugation, was valid up to three cycles with over 80% retention of adsorption capacity. For the validation purpose, two natural water samples from IARI and Yamuna River were collected and analysed for the presence of the selected pesticides. After application of our two best performing composites, MAG 15 and MAG 18, nearly ~60-100% removal was found for all the selected pesticides. Thus, such organic-inorganic hybrid materials will find huge applicability in future water remediation processes.

Agricultural Economics


Miyir Loyi

Name of the Student : **Miyir Loyi**
Roll No. : **21211**
Chairperson : **Dr. Shiv Kumar**


Dr. Shiv Kumar

Title of the Thesis

An Econometric Analysis of Import Demand of Selected Edible Oils in India

---

India is the world's fourth largest edible oil economy in the world after US, China, and Brazil. India accounts for over 7 percent share of production and 12 percent share of consumption making it the second largest consumer of the world edible oil. Owing to the low productivity, production of oilseeds in India has remained almost stagnant. The consumption side nonetheless is galloping where the annual demand of the country is increasing at the rate of 6 per cent while the domestic output has been increasing at just about 2 per cent. To abridge the huge gap in the demand-supply of edible oil production in the country, government has resorted to imports which met 60 percent of the country's demand; only 40 percent of the demand could be fulfilled through domestic sources. The import bill for vegetable oil close to 70000 crores in 2018-19 accounting for 50 per cent of India's total agricultural imports bill. Out of the total quantity of oils imported, palm oils (crude and refined) account for over 60 per cent of total oil imports and are primarily imported from Indonesia and Malaysia, while soybean oil accounts for roughly 20 per cent of total imports and is primarily imported from Argentina and Brazil. Sunflower oil accounts for about 15 per cent of the total and is primarily imported from Ukraine. The study is based on secondary data and analytical tools like standard deviation, regression and GARCH models were used to study price instability, transmission in price, and price volatility, respectively. Simple tools like compound annual growth rate (CAGR) were used for analyzing trend and Cuddy-Della Valle index (CDVI) for instability in import demand, slightly more complex model like autoregressive distributed lag (ARDL) and error correction model (ECM) were used to investigate the import demand and compute the long run and short run import elasticities. An ARDL model is a more appropriate method over Johansen co-integration, when the sample size is small. It was found that there is transmission of prices from international to domestic markets however no transmission of volatility is observed. Examination of growth deciphered the highest growth of 15.89 percent per annum (1994- 2019) in case of sunflower oil. The highest instability was seen in soybean oil with CDVI value of 69.58 percent. The import function analysis using ARDL test found GDP and domestic production to be most significant in the long run. Deeper understanding of the relation among import variables, its influence and price volatility helps policymakers to devise proper policy initiatives and strategies to boost edible oil economy.

Agricultural Extension


Arun Kumar G.S.

Name of the Student : **Arun Kumar G.S.**
Roll No. : **21227**
Chairperson : **Dr. Manjeet Singh Nain**


Dr. Manjeet Singh Nain

Title of the Thesis

Assessment of Financial Inclusion and Skill Development in Agricultural Sector through Aspirational District Programme

Aspirational districts programme was launched by Government of India in 2018 to raise the living standards of citizens by focusing on five major thematical areas viz. health and nutrition, education, agriculture and water resources, financial inclusion and skill development and basic infrastructure in the poor performing 115 districts. Among the five broad thematical areas financial inclusion and skill development play a major role in tackling the problem of unemployment and poverty in rural areas. Financial inclusion aids in providing the basic financial products and services to the most vulnerable section of the society. Whereas, skill development through appropriate trainings improves the capabilities of an individual to perform better and efficient for his/her overall growth. The present study was aimed to explore the extent of financial inclusion and skill development in agriculture sector through aspirational district programmes. Three training institutes per district which were actively providing skill-based trainings in agriculture sector were purposively selected from two aspirational districts (Raichur and Yadgir) of Karnataka state for the purpose of acquiring list of trainees from the inception of aspirational district program. From the list of trainees, 30 farmers and 30 agricultural labourers were selected from each district making a total of 120 samples through stratified random sampling method. It was found that overall extent of financial inclusion was moderate. Half of the respondents were in the medium level of financial inclusion. Awareness on financial products and services was ranged from moderate to high. Due to lack of financial institutes in the rural areas 37.5 per cent of the respondents reported difficulty in the accessing financial products and services as such the level of usage was low. Around 50 per cent of the respondents were having low level of use of financial products and services. Whereas, overall satisfaction on the financial products and services was moderate. Multiple regression analysis revealed that age, distance to financial institute and lower level of education showed negative and significant contribution towards extent of financial inclusion. Operational land holding, annual income and frequency of visit to financial institutes showed positive and significant contribution to the extent of financial inclusion. The overall effectiveness of skill development trainings was found to be 51 per cent which came under medium effectiveness category. Among the eight different aspects of training programme 'coverage' was found to be more effective. But trainings were least effective in ‘need assessment’ of trainees. A majority of trainees perceived that training improved their knowledge and skills but less useful in the improvement of entrepreneurial ability and income. The multiple regression analysis revealed that number of training programmes attended, learning motivation, innovativeness, motivation to transfer learning, self-efficacy and achievement motivation were positive and significantly affecting the training effectiveness. Lack of literacy on financial products and services, low income and cumbersome procedures were most raked constraints to financial inclusion. Lack of hands-on training and lack of access to government benefits were most rated constrains related to training effectiveness. It can be concluded that financial inclusion and skill development in terms of training effectiveness was moderate in aspirational districts. As such it calls for necessary action to increase the accessibility to financial products and services. In case of training attention has to be given to the need assessment, which may further help in scaling up of financial inclusion and skill development in aspirational districts.

Agricultural Physics


Abhradip Sarkar

Name of the Student	:	**Abhradip Sarkar**
Roll No.	:	**21234**
Chairperson	:	**Dr. Pragati Pramanik Maity**


Dr. Pragati Pramanik Maity

Title of the Thesis

Evaluation and Prediction of Structural Stability and Hydraulic Conductivity in Saline Soils using Machine Learning

---

The inability to maintain proper soil structure, soil hydraulic properties and soil organic carbon levels can seriously hamper soil health and crop production. Soil salinity can degrade soil quality and decrease crop yields. To evaluate the effect of soil salinity on structural stability and hydraulic properties, and to predict those properties, total 121 soil samples were collected from 0-15 and 15-30 cm of soil depths from eighteen villages of Nilokheri, Nissang and Assandh block of Karnal district, Haryana. Result showed that in 0-15 cm soil depths, soil pH varied from 8.24 to 10.08 and EC of 0-15 cm soil layer varied from 2.46 to 16.4 dS/m. The range of MWD varied from 0.18 to 1.21 mm and showed high variability. The results of fractal dimension (D) showed that D is positively related with the clay and silt % but negatively related with sand %. Total organic carbon (TOC) in class 2 (pH>9.5) soils were 0.02% more than class 1 (pH= 8-9.5) soil, though the difference was not statistically significant. Average MWD was 0.11 mm more in class 2 soils as compared to class 1 soils. Glomalin content had positive correlation with HC and sand content and negative correlation with BD, clay and silt %, but the correlations were not significant. No significant correlation was obtained with MBC and other soil parameters. The soil pH had significant negative correlation with sand content whereas, it showed significant positive correlation with sand content. Soil EC showed a strong positive correlation with soil pH. Labile pool of 0-15 cm soil was 3.13 gC/kg soil and was 15.49% more than 15-30 cm. Recalcitrant pool of 0-15 cm soil layer was 2.85 gC/kg soil and was 21.79% more than 15-30 cm. Inclusion of D in prediction of HC by MLR model did not show any improvement, rather it performed poor both for training and testing dataset. In case of ANN, for both the input sets, ANN with three hidden layers performed better. Inclusion of D in input set (i.e., ANN-HCD). Inclusion of fractal dimension in input dataset (CART-HCD) has no improvement in both training and testing dataset. RF performed better both in RF-HC and RF-HCD models in prediction of HC as compared to CART. The results showed that among all the models, SVM-HCD performed best based on the statistical evaluation criteria.SVM models predicted the HC and MWD with more satisfactory performance as compared to the other models owing to their more flexibility and capability to model non-linear relationships. Evaluation of effects of soil salinity on different soil parameters are very much required for improving soil structure and organic carbon content of soil. Identification of critical soil pH and EC in maintenance of soil structure, TOC and hydraulic properties is very much essential. Comparative study can be made in future to find out the prediction efficiency of different geostatistical techniques and machine learning approaches. As plant growth is a direct indicator of soil health, plant parameters can be included in input dataset to check the model efficiency.

Agricultural Statistics

Manoj Varma

Name of the Student : **Manoj Varma**
Roll No. : **21238**
Chairperson : **Dr. K. N. Singh**

Dr. K. N. Singh

Title of the Thesis

Forecasting Crop Yield Using Feature Selection And Machine Learning Algorithms

Crop yield forecast is valuable to many players in the agri-food chain, including farmers, agronomists, commodities merchants, and policymakers. As the crop yield is determined by numerous input parameters, it is important to identify the most important variables and eliminate the ones that may reduce the prediction model's accuracy. The feature selection algorithms assist in selecting only those features that are relevant in the predictive algorithms. Instead of a complete set of features, feature subsets give better results for the same algorithm with less computational time. Feature selection has the potential to play an important role in the agriculture domain, with the crop yield depending on multiple factors such as land use, water management, fertilizer application, other management practices and weather parameters. As crop yield prediction is a complex phenomenon and has many underlining nonlinear patterns. Such, datasets are difficult to deal with stringent assumptions of the statistical models. Hence, machine learning (ML) techniques which has very few prior assumptions and are data driven provides great deal of flexibility for modelling and forecasting the crop yield. In the present study, feature selection algorithms such as Forward Selection, Backward Selection, Random Forest feature selection, LASSO and Correlation Based Feature Selection (CBFS) have been applied to three different datasets. Regression forecasting models have been developed with selected features for all the algorithms. Machine learning techniques such as Random Forest Regression and Support Vector Regression are also applied. Also, RF regression and SVR have been compared with the stepwise regression method. The Forecasting performance of the proposed modelswere compared using statistical measures such as Root Mean Square Error (RMSE), Mean Absolute Prediction Error (MAPE) and Mean Absolute Deviation (MAD). A comparison has been made between all the feature selection algorithms and between the machine learning algorithms. Finally, the machine learning technique has been compared with the regression model coupled with feature selection with the help of random forest. The CBFS, LASSO and RF has been found to be the best feature selection algorithm for prediction with a regression model for different datasets. Support Vector regression was observed as the best machine learning technique except for Medak district rice yield. The feature selection with the regression frameworkwas found to be more efficient as compared to machine learning technique.

Agronomy


Anamika Barman

Name of the Student : Anamika Barman
Roll No. : 50048
Chairperson : Dr. V.K. Singh


Dr. V.K. Singh

Title of the Thesis

Deficit Irrigation Management in Mustard Using Drip Under Agri-Horti System

---

The field experiment on "Deficit irrigation management in mustard using drip under Agri-Horti system" was conducted during *Rabi season* 2020-2021 at ICAR-IARI, New Delhi. The experimental site was sandy loam in texture with neutral to alkaline in reaction. The experiment was carried out in split plot design, with five main plots having different Agri-Horti system (AHS) viz. Moringa-based AHS (M_1), Phalsa-based AHS (M_2), Karonda-based AHS (M_3), Aonla-based AHS (M_4) and Guava-based AHS (M_5). The sub-plot consisted three deficit irrigation scheduling treatments (DIS) viz. S_1 (rainfed), S_2 (IS at 0.4 IW/CPE ratio), S_3 (IS at 0.6 IW/CPE ratio). The yield attributes and yield of Indian mustard were significantly influenced by AHS under various irrigation scheduling. The Moringa based system had 7.7%, 15.9% and 36.9% higher numbers of siliqua/plant over Phalsa, Karonda and Aonla based AHS. The highest numbers of siliqua were in a 0.6 IW/CPE ratio (396) that are statistically superior to those with a 0.4 IW/CPE ratio (354). The significantly higher seed yield (1939 kg ha^{-1}), stover yield (6067 kg ha^{-1}), and biological yield (8143 kg ha^{-1}) were recorded under Moringa-based AHS. In case of DIS, 0.6 IW/CPE had maximum yield followed by 0.4 IW/CPE and rainfed. There was 10.9 % and 36.1 % higher seed yield and 7.6% and 16.1% rose in stover yield recorded with 0.6 IW/CPE treatments over 0.4 IW/CPE and rainfed treatment. The interaction effect between DIS and different AHS had turned out non-significant. Under the 0.6 IW/CPE treatment, the maximum total N uptake by seed and stover (91 kg ha^{-1}), total P uptake (17 kg ha^{-1}), and total K uptake (106 kg ha^{-1}) were recorded. Under Moringa based AHS increased in WUE of Indian mustard was recorded by 13.8%, 16.7% 19.7% and 30% higher over Phalsa, Karonda, Aonla and Guava based AHS, respectively. In terms of WUE of Indian mustard 0.6 IW/CPE treatments remained superior over 0.4 IW/CPE treatments. In the deficit irrigation schedule treatment, the lowest penetration resistance (1548 k Pa) was found in the 0.6 IW/CPE group, the highest in the rainfed group (1768 k Pa), and medium in the 0.4 IW/CPE group (1666 k Pa). Maximum net returns (52516 Rs ha^{-1}) in 0.6 IW/CPE. The treatment with 0.4 IW/CPE had the highest net B:C ratio (1.86), followed by rainfed (1.83). Moringa-based AHS had the highest net B:C ratio (2.22), followed by Phalsa-based AHS (1.85) and Guava-based AHS (1.44), with the lowest B:C ratio (1.44). The best monetary efficiency was achieved with the 0.6 IW/CPE treatment (438 Rs ha^{-1} day^{-1}), followed by the 0.4 IW/CPE treatment (410 Rs ha^{-1} day^{-1}) and rainfed (333 Rs ha^{-1} day^{-1}).

Biochemistry


Debarati Mondal

Name of the Student : **Debarati Mondal**
Roll No. : **21251**
Chairperson : **Dr. Veda Krishnan**


Dr. Veda Krishnan

Title of the Thesis

Starch-Lipid Interactions and its Influence on Inherent Glycaemic Potential

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The Inherent glycemic potential (IGP) is an index of starch bioavailability in terms of eliciting postprandial glycemic response of staple cereals which leads to chronic hyperglycemia such as type 2 diabetes mellitus (T2DM), cardiovascular diseases (CVD) and their sequelae. Directed investigation in this direction is thus required to understand the role of explanatory variables governing IGP as well as to develop a model system for limiting high blood glucose of staple cereals. Therefore, in the present study, we have addressed few basic questions to share a comprehensive understanding on various illustrative variables possessing roles like: does inherent indices like microstructure, matrix compositions/ interactions and molecular configurations affect starch digestibility and ultimate IGP? This study inscribes these questions by considering two starch sources of varying inherent matrix composition as pearl-millet (PM) and rice with five cooking fats (*ghee, coconut oil, sunflower oil, mustard oil, til oil*) as well as on the basis of the observations from microstructure, fatty acid profiles through gas chromatography (GC-MS), starch-lipid (S-L) complexation (CI and iodine spectra), food matrix interactions via CLSM, *in-vitro* starch dynamics (SHK), molecular mechanism like short range and long range molecular organization through FTIR and XRD, *in-vitro* glucose diffusion assay (GDRI) to predict *in-vivo* starch bioavailability into the system. Based on results, *in-vitro* oral-gastro intestinal simulation revealed PM to have low IGP (63.71%) compared to rice (65.89 %) and it was well correlated with microstructural parameters [pericarp thickness (22.71 ± 0.20 μm), granule size (2.16 ± 0.12 μm), endodermal surface area (1199.64 ± 2.86 μm^2)]. It was also found that dense food matrix components and higher S-L interaction visualized by CLSM contributes to the resistance towards digestive enzymes. The molecular structures were explored using FTIR, XRD to understand the synergistic effects of short range and longer-range molecular patterns ($R_{1047/1022}$: 0.80& CD %: 21.73%) of PM starch, which revealed the superior crystalline compactness as vital towards low IGP. Further, exogenous addition of cooking fats revealed that PM-mustard oil (PM-MO) and rice-mustard oil (R-MO) complexes were found most promising with least IGP of 57.17 % and 59.65 % respectively. Molecular structural differences (short range and long range) of these two complexes were also found in line with previous results ($R_{1047/1022:}$ 0.85 & 0.80, CD %: 50.13 %, 31.09 %). Therefore, our research for the first time unraveled a perspective relation of IGP with various intrinsic characters and also deciphered the mechanism of modulating IGP of archaeological nutri-cereal *i.e.,* PM as compared with staple cereal-rice through formation of a *lipid induced digestive model*, acting as one of significant approaches of lowering IGP against current situation of diabetic and pre-diabetic scenario.

Bioinformatics

Asif Ali V.K.

Name of the Student : **Asif Ali V.K.**
Roll No. : **21259**
Chairperson : **Dr. Anu Sharma**

Dr. Anu Sharma

Title of the Thesis

Phylogenetic Marker Genes Based Approach for Binning of Metagenomics Data

The study of microbes was traditionally focused on single species in pure culture, which made the interpretation of these complex communities very difficult. The science of 'Metagenomics' enables us to investigate microbes in their natural environments, the complex communities in which they normally live. Metagenomic sequence binning is one of the important steps of metagenomic data analysis so as to produce meaningful 'bins' or groups. There are several techniques for grouping, among which binning is most widely used. Binning indicates to the process of classification of DNA sequences into clusters that might be the true representative of an individual genome or genomes from taxonomically related microorganisms. Binning uses any of the several clustering techniques available such as K-Means, DBSCAN, spectral clustering, hierarchical clustering *etc*. But each of these clustering techniques has its own drawbacks. In the past, only few efforts have been seen on the use of single-copy phylogenetic marker genes for the clustering of metagenomic data. The phylogenetic marker genes are protein encoding genes that are universal, single-copy marker genes and are rarely subjected to horizontal gene transfer (HGT). They had been used to accurately and consistently delineate prokaryotic species.Here in this research a semi-supervised clustering approach is adopted to cluster the metagenomic data using marker genes. Initially, contigs harbouring marker genes are identified by running the Prodigal, FetchMG and USEARCH applications sequentially. Then the K-Means clustering technique is applied on the metagenomic data which has been already reduced to two dimensions using BH-TSNE algorithm. In the end, correction of the generated clusters was carried out based on the sequences harbouring marker genes with the help of spectral clustering. K-Means clustering itself generated 8 clusters with a rand index of 0.973, a F1 score of 0.71 and an overall accuracy of 0.9 for a 10s genome dataset using tetranucleotide frequency as initial input feature matrix. While cluster correction resulted in the generation of 10 clusters with a rand index of 0.981, a F1 score of 0.91 and an overall accuracy of 0.95 for the same dataset. In a nutshell,the cluster correction using sequences harbouring marker genes produced better clustering results.

Computer Application

Pratiksha Subba

Name of the Student : **Pratiksha Subba**
Roll No. : **21265**
Chairperson : **Md. S.N. Islam**

Md. S.N. Islam

Title of the Thesis

Development of Mobile Application on Integrated Farming System

---

Agriculture is one of the indispensable segments to Indian economy. Our farmers have contributed a lot to growth prosperity of agriculture. However, the marginal and small farmers do not get the desired output due to the lack of knowledge and information about the cropping systems. Most of them follow mono-cropping system and traditional way of farming that lacks diversification.Integration of multiple enterprises such as livestock, poultry, fisheries, mushroom production, and bee keeping along with traditional crops is needed for a better income for farmers. However, farmers are not aware about the cropping system to be followed with the available land and resources that can fetch him a better return. Multiple efforts have been taken to develop models of integrated farming system by the scientists of agriculture research network. Models have been developed based on agro climatic condition, area, resources available and factors that effects production, productivity and returns.These models need to be reached out to the farmers in a scientific way so that they may adopt it for a better return. A decision support system is needed that can guide them in this connection. There are numerous mobile applications that are used all over the world for various purposes, including agricultural activities. Smartphones and mobile apps have become an essential part of everyday life. Even though there are numerous mobile application developed for agricultural issues, still there is a need for the development of mobile application to guide the farmers to choose different enterprise and follow different cropping sequence that will help them obtain maximum output with sustainable lifestyle. The developed mobile application is a decision support system for the farmers to select the right IFS model according to their need. It guides him about the different enterprise to be followed up and also about the cropping sequence that may be adopted for a better return. The decision support system has been developed by using Android Studio 2.3, Java and XML has been used to programming. Tools used to develop this decision support system are SQLite, Android Studio IDE and Android Device Monitor. This app provides user friendly interface that helps the user to select the suitable IFS model. This Mobile Application is an effort to bring a better possible return for farmers.

Entomology

Komal J.

Name of the Student : **Komal J.**
Roll No. : **21269**
Chairperson : **Dr. P.R. Shashank**

Dr. P.R. Shashank

Title of the Thesis

Taxonomic Studies on Microlepidoptera of Pusa Campus, New Delhi

Lepidoptera is one of the largest insect orders and artificially divided into macrolepidoptera and microlepidoptera. Microlepidoptera includes smaller moths which have wingspan ranging from 5-20 mm. They play major roles as pests on a variety of food and cash crops, as pollinators, as ecological indicators implying profound economic and ecological significance. There are limited studies that have examined the regional moth diversity with upto date taxonomic treatment, especially in major metropolitan cities such as Delhi, the National capital territory of India and one of the fastest growing cities in the world. Here, we present an updated checklist of the moths of Delhi and biosystematics study of micromoths of Pusa campus, New Delhi. The checklist comprises of 331 species of moths belonging to 32 families in 14 superfamilies from Delhi along with their synonyms, updated taxonomic treatment and occurrence and also provided with illustrations of 195 species. Noctuioidea was observed as the most numerous superfamilies comprising 164 species accounting for about 49.5% of all the moths followed by the superfamily Pyraloidea which constitutes about 18.4% of the moths and includes 62 species. Erebidae is the dominant family with 95 species. Further, we recorded 37 species of microlepidoptera belonging to 8 families under 7 diverse superfamilies from the Pusa campus of which larval biology (4 species), redescriptions (15 species) and diagnostic report (22 species) were provided with photographic illustrations of larvae, pupae, adult moths and genitalia.

Environmental Science

Pooja L.R.

Name of the Student : **Pooja L. R.**
Roll No. : **21277**
Chairperson : **Dr. Renu Singh**

Dr. Renu Singh

Title of the Thesis

Reducing Ammonia Volatilization using Organic And Inorganic Amendments in Wheat (*Triticum aestivum L.*)

In agricultural systems, applied N fertilizer to the crop is mainly prone to losses through ammonia (NH3) volatilization, nitrate (NO3-) leaching, and denitrification. These reactive nitrogen species cause negative effects on biodiversity, eutrophication, and nitrate accumulation in waters, acidification of soil and water bodies. Therefore the need of the hour is using organic and inorganic amendments to reduce these losses. A study was conducted with an objective to unveil the effect of organic and inorganic amendments on NH3 volatilization on the nitrogen use efficiency and productivity of wheat. Under this study, 10 treatments were applied in experimental RBD design, and they are T1 (Control with no recommended dose of nitrogen), T2 (RDN), T3 (RDN+ N-(n-butyl) thiophosphoric triamide (NBPT)), T4 (RDN + Hydroquinone (HQ)), T5 (RDN+ Calcium carbide (CaC_2)) T6 (RDN+ Vesicular Arbuscular Mycorrhiza (VAM)), T7 (RDN +Azotobacter), T8 (RDN +Garlic powder), T9 (RDN +Linseed oil), T10 (RDN + Pongamia oil). The highest volatilization losses were observed in T2 (RDN) of about 20.4 kg ha-1 season-1. Significant reduction in NH3 volatilization losses were observed in T3 (RDN+NBPT) by 40%, T4 (RDN + HQ) by 27%, and T8 (RDN +Garlic powder) by 17%. In all amendment added plots, it was observed that there was an increase in nutrient availability (N, P, K) and soil organic carbon. An upsurge in soil microbial activity was found in T7 (RDN +Azotobacter) and T6 (RDN+VAM). Soil urease activity was found decreased in plot receiving amendments i.e. NBPT (T3), HQ (T4), and CaC_2 (T5). The available N forms, majorly ammonical N (NH_4^+-N) and nitrate N (NO_3^-N), decreased from the plant tillering stage to the plant physiological maturity stage due to uptake and losses. The highest grain yield was observed in the T7 (RDN +Azotobacter) treated plot with 5.09 t ha-1, and straw yield was increased in T4 (RDN + HQ). So it is important to develop more inorganic and organic amendments which are economically affordable to reduce N losses and save our environment from these harmful reactive nitrogen species.

Floriculture & Landscape Architecture

Ediga Amala

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Roll No. : **21284**
Chairperson : **Dr. Kanwar Pal Singh**

Dr. Kanwar Pal Singh

Title of the Thesis

Cold Tolerance Studies in Marigold (*Tagetes species*)

Marigold (*Tagetes* spp.) is one of the popular ornamental crop belonging to family Asteraceae. It is extensively grown for production of loose flowers for making garlands, religious offerings, social functions and pigment extraction in addition to its use for garden display as bedding, pot plant etc. Cold tolerance is an important genotypic traitto be considered when selecting marigold cultivars for growing under low temperature stress conditions as its growth and flowering are drastically reduced at low temperature. In the present study, twenty marigold genotypes i.e. ten genotypes from African marigold (*Tagetes erecta* L.) and ten genotypes from French marigold (*Tagetes patula* L.) were taken to observe their responses to morphological, physiological, biochemical and image based (high through-put phenotyping) parameters in relation to lowtemperature stress. The plants of these genotypes were grown in pots during winter season, in two environments i.e. outside polyhouse and inside polyhouse under two sets of experiment (first set of experiment from mid-November to mid-February and second set of experiment from December end to April end) to study the effect of lowtemperature prevailing during December and January in Delhi conditions on variousmorphological, physiological, biochemical and image based (High through-put phenotyping) parameters of young plants (in second set of experiment) and well grown plants (in first set of experiment) of these genotypes grown outside polyhouse and inside polyhouse. In African marigold genotypes, the morphological parameters likeplant height, number of primary branches, stem diameter, leaf length, leaf area, flowerdiameter, length of the petal and flower longevity on the plant were outperformed ingenotype Af./W-4 followed by the genotypes Pusa Bahar, Pusa Basanti Gainda, Af/W- 1 and Af./W-7. Among the physiological and biochemical parameters, maximum Relative Water Content, photosynthetic and transpiration rate, chlorophyll a, b & total chlorophyll content, total carotenoids, Super Oxide Dismutase, Catalase, Guaiacol Peroxidase antioxidant enzymes, Total Phenolic Content, proline content, protein content and minimum Electrolyte Leakage Rate and Malondialdehyde content werealso found in genotype Af./W-4. Under non-destructive image analysis studies through high through-put phenotyping, genotype Af./W-4 was found to have higher plant area, convex hull, greenness, water content, compactness and caliper length compared to the other genotypes. In French marigold genotypes, Pusa Arpita genotype outperformed the others in terms of morphological parameters such as plant height, plant spread, number of secondary branches/plant, flowering duration, weight of the single flower,flower yield/plant, number of petals per flower and flower longevity on the plant followed by the genotypes Hisar Beauty and Hisar Jafri. Among the physiological andbiochemical parameters, Hisar Beauty genotype had the highest Relative Water Content, Super Oxide Dismutase, Catalase, Guaiacol Peroxidase antioxidant enzymes, Total Phenolic Content, proline content and the lowest Electrolyte Leakage Rate andMalondialdehyde content followed the genotypes Hisar Jafri and, Pusa Arpita. In image-based traits, the genotype Hisar Jafri had higher plant area and greenness while genotype Hisar Beauty had higher water content and compactness and the genotype Pusa Arpita had higher caliper length. When comparing the two sets of experiments,the first set of experiment showed a higher level of cold tolerance based on the assay of various morphological, physiological, biochemical and image based (high through-put phenotyping) traits compared to the second set of experiment in both African and French genotypes.

Fruit Science


Rutuparna Senapati

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Chairperson : **Dr. Madhubala Thakre**


Dr. Madhubala Thakre

Title of the Thesis

Understanding the Basis of Pulp Colour in Black Guava (*Psidium guajava* L.)

The present study was carried out during 2020-21 with the objectives to estimate metabolites responsible for pulp colour in Black guava, and to characterize gene(s) involved in metabolite synthesis in Black guava. Black guava along with seven other guava genotypes, namely, Hisar Surkha, Punjab Pink, Lalit, Pant Prabhat, Shweta, Trichy-1, Allahabad Safeda have been used in the present study. Peel and pulp colour of Black guava belonged to greyed orange group 174A and 186B, respectively, which was completely unique as compared to other seven guava genotypes. Black guava had maximum total anthocyanin content (9.663 mg/100 g). HPLC and LCMS analysis indicates that three anthocyanins, *viz*., delphinidin-3-glucoside, petunidin-3-glucoside and cyanidin-3-glucoside were present in Black guava, and responsible for purplish peel and pulp colour. Hisar Surkha having pink pulp colour had maximum lycopene (8.798 mg/100 g) and second highest anthocyanins (7.863 mg/100 g) contents. It was also applicable for Lalit which contained lycopene and anthocyanins both. This indicated that lycopene and anthocyanins are responsible for pink pulp colour in Hisar Surkha and Lalit. It was also postulated that in pink pulped guava genotypes, lycopene pathway and anthocyanin pathway both were working and contributing to pulp colour. In Punjab Pink, lycopene (3.334 mg/100 g) was present and it had minimum anthocyanin content (0.108 mg/100 g). Irrespective of pulp colour of guava genotypes, carotenoids were also present in all guava genotypes (0.203 mg/100 g - 0.730 mg/100 g). It indicated that the complete lycopene pathway was working in all guava genotypes including white pulp also without accumulating the intermediates like lycopene responsible for pink colour. This may be the possible reason for different colour shades in white pulped guava genotypes, *i.e.*, white, cream and intermediates of both are available. In nut shell, the pulp colour in guava was governed by presence of more than one pigment and the final colour depends on the relative proportion of these pigments. In case of Black guava, more anthocyanins and less lycopene was present resulted in purplish pulp colour. In Hisar Surkha, both lycopene and anthocyanins were contributing for pink to red pulp colour. However, in Punjab Pink, lycopene is playing major role, and in white pulped guava, total carotenoid was responsible for pulp colour from white to cream. At this stage, in guava for pulp colour the statement “pigments in proportions” is correct. The primers for *DFR* and *CHS* gene of anthocyanin pathway amplified in Punjab Pink and not in case of Black guava. This may be due the fact that both genes belong to multigene family and gene responsible for anthocyanins in Black guava may be structurally different than the other guava genotypes.

Genetics and Plant Breeding


Uttarayan Dasgupta

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Roll No. : **21295**
Chairperson : **Dr. Gyan P. Mishra**


Dr. Gyan P. Mishra

Title of the Thesis

Comparative RNA-seq Analysis and Antioxidant Studies to Understand the Complex Regulatory Network of MYMIV Resistance in Mungbean (*Vigna radiata* (L.) R. Wilczek)

Yellow Mosaic Disease (YMD) in mungbean [*Vigna radiata* (L.) R. Wilczek] is one of the most damaging diseases in Asia. In the northern part of India, the YMD is caused by mungbean yellow mosaic India virus (MYMIV), while in southern India this is caused by mungbean yellow mosaic virus (MYMV). The molecular mechanism of YMD resistance in mungbean remains largely unknown. RNA-seq was conducted between a resistant (PMR-1) and a susceptible (Pusa Vishal) mungbean genotype, under both MYMIV infected and control conditions to understand the regulatory network operating for the YMD resistance imposition. Overall, 76.8 million raw reads could be generated and mapped to the reference genome. The resistance showed a complicated gene network, which begins with the production of general PAMPs (pathogen-associated molecular patterns), then activation of various signaling cascades like kinases, jasmonic acid (JA) and brassinosteroid (BR), and finally the expression of specific genes (like PR-proteins, virus resistance and R-gene proteins) leading to resistance response. The function of WRKY, NAC and MYB transcription factors in imparting the resistance against MYMIV could be established. The PPI analysis also revealed the role of proteins involved in kinase, viral movement and phytoene synthase activity in imparting YMD resistance. Additionally, a set of 513 novel stress-related EST-SSRs were identified and 76 primers were used on 32 genotypes, of which 12 were found polymorphic, but none could clearly differentiate between resistant and susceptible genotypes. Secondary metabolites such as phenolics and flavonoids were also estimated on the selected mungbean genotypes in four stages viz., 03-day sprouts, 07-day seedlings, 30-days old plant leaves and 60-days old plant leaves. At the initial stage (i.e. sprouts and seedling), no correlation between any of the studied secondary metabolites and resistance could be recorded. However, in the MYMIV infected samples (at 30-DAS), the TPC was recorded in the range of 5.86±0.577 (Pusa 9531) to 10.54±0.471 (MH421) mg GAE/g DW; whereas at 60-DAS this was recorded in the range of 4.58±0.336 (Sona Moong) to 10.56±0.097 (PDM 139) mg GAE/g DW. Interestingly, TPC was found positively correlated with YMD resistance. In addition, the resistant genotypes under infection (both 30- and 60-DAS), expressed higher TPC than the susceptible genotypes. Unlike for TPC, no correlation was recorded between TFC with YMD resistance in mungbean. Thus, this study is a step ahead in understanding the complex regulatory network of genes which results in the YMD resistance in mungbean.

Microbiology


Sonam Priyadarshani

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Ms. Anju Arora

Title of the Thesis

Demonstrating Lignocellulolytic Potential of Actinobacteria for Application in Biomass Processing

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Deficiency of non-renewable energy sources and environmental issues such as air pollution and global warming has in recent years, raised the demand of identifying an alternate carbon neutral renewable energy resource. Lignocellulosic (LC) biomass is a great solution, due to its low cost and natural abundance. However, its conversion and processing is challenging. Several methods including chemical, physical, physico-chemical and biological are used to deconstruct LC biomass and increase enzyme accessibility for cellulose and hemicellulose degradation. Biological processing is preferred due to its less energy requirement, cost effectiveness and environment friendly nature. Several microbes like white rot fungi, bacteria and actinomycetes possess the ability to degrade lignocellulosic biomass in natural niches and these microbial consortia actively participate in the global C cycle. One such habitat, compost, supports huge microbial diversity, and actinobacteria form a dominant proportion of community. The presence of different pH and temperature regimes in these habitats, make these actinobacteria potential sources of enzymes with desirable properties in biomass processing and biorefineries. The current study was thus aimed at isolation and characterization of actinobacterial strains for lignocellulolytic enzyme production and delignification of rice straw for enhanced saccharification. Of the thirteen actinobacterial strains isolated from compost samples after enrichment on rice straw at 40 ºC and pH 8, two strains were selected and found to be potentially significant lignocellulose degraders through qualitative and quantitative enzymes assays of lignocelluloytic enzymes. Both were identified to be *Streptomyces thermoviolaceous* S1 and *Streptomyces thermophilus* by PCR based molecular characterization. Under submerged fermentation, production of lignocellulolytic enzymes (CMCase, FPase, β-glucosidase, Xylanase, Laccase, Lignin peroxidase) was favoured in the presence of rice straw as a carbon substrate, than cellulose. Except β-glucosidase, all enzyme activities were found to be higher on the 21st day, compared to 10th day of incubation. Under solid state fermentation, higher lignin degradation by *S. thermophilus* S2 was observed, as evident from the higher absorbance values in alkali extracts of fermented rice straw at 205 nm. Higher enzymatic activities were obtained in buffer extracts of *S. thermophilus* S2 inoculated rice straw during solid state fermentation compared to *S. thermoviolaceus* S1. Removal of lignin resulted in enrichment of 53.03% and 49.01% holocellulose with *S. thermophilus* S2 and *S. thermoviolaceus* S1 respectively correlating with the levels of degraded lignin in its alkali extracts. Structural and compositional analysis using electron microscope, XRD and FTIR also substantiated the evidence for cellulose disintegration and lignin removal in pretreated rice straw compared to uninoculated rice straw. Buffer extracts of solid-state fermented rice straw were found to be a good source of lignocellulolytic enzymes for biomass hydrolysis. These findings highlight *S. thermophilus* S2 and *S. thermoviolaceus* S1 as promising source of enzymes and biocatalysts for biomass processing

Nematology

Gagandeep Singh

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Dr. Vishal Singh Somvanshi

Title of the Thesis

Detection of Entomopathogenic Nematodes by Loop-Mediated Isothermal Amplification

Entomopathogenic nematodes (EPNs) are well known for their biocontrol potential against a broad range of insect pests. They can actively search for their host in soil, and are safe to the environment. Due to their eco-friendly nature, EPNs are emerging as an alternate to the harmful insecticides. Soil baiting with the insect *Galleria* is used to isolate the EPNs from field soils. However, insect baiting turns out to be expensive for large area surveys because it is time consuming, requires high labour cost and large number of insect larvae. In addition, an expert taxonomist is required for proper identification of isolated EPNs. Here, we designed two loop-mediated isothermal amplification (LAMP) assays for rapid detection of *Heterorhabditis* and *Steinernema* genera from the total soil DNA. The designed assays are named Ste-LAMP for *Steinernema* spp. and Het-LAMP for *Heterorhabditis* spp. A set of 5 oligonucleotide primes were designed for each assay using ITS and 18S regions of the ribosomal DNA, respectively, for *Heterorhabditis* and *Steinernema*. The reaction of the Het-LAMP worked best at 66 ^{o}C for 60 minutes, and Ste-LAMP optimized at 68 ^{o}C for 60 minutes followed by termination of reaction at 85 ^{o}C for 5 minutes. The designed assays successfully detected DNA of a single EPN infective juvenile from the total DNA of 250 mg soil sample. The Het-LAMP and Ste-LAMP assays were very specific to their target, amplifying only *Heterorhabditis* spp. and *Steinernema* spp. respectively. Furthermore, the assays are very sensitive and can detect 0.02 to 96 picograms of DNA in a 25 µl reaction volume. These assays can be used in large scale surveys of EPNs and can speed up the EPN isolation and save a large number of insect larvae. The soil samples may be tested first by LAMP assays followed by insect-baiting only the samples testing positive for presence of EPNs. These assays can give results within 2 to 3 hours from sampling to detection as compared to insect-baiting methods. In the future, lateral-flow kits for point of care or field labs can be developed based on these assays.

Plant Genetic Resources


Sandip Kumar Panigrahi

Name of the Student	:	**Sandip Kumar Panigrahi**
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Dr. Kavita Gupta

Title of the Thesis

Assessment of Genetic Diversity and Differential Reaction of Black Gram (*Vigna mungo*) Germplasm to Pulse Beetle *Callosobruchus maculatus*

Black gram is a potential grain legume constituting a major part in the primarily vegetarian Indian diet. However, its production and storage is greatly affected by bruchid infestation. Natural and reliable resistance or tolerance sources have not been reported in cultivated black gram mainly owing to limited screening attempts and low seed yield due to narrow genetic base. Therefore, a diverse set of 69 germplasm accessions, representing landraces of *Vigna mungo* and its CWR, were evaluated for resistance against *Callosobruchus maculatus* (Fab**.**) followed by SSR-based genetic diversity analysis employing 50 microsatellite markers. Considerable variation was observed in terms of physical seed parameters viz., width, length, shape, texture, coat color, hilum concavity and hardness. The accessions also exhibited significant differences in terms of growth parameters viz., total oviposition, emergence holes, adult emergence (AE), percent seed weight loss (PSWL) and growth index (GI). Based on three key traits viz., AE, PSWL and GI the accessions were categorized into six classes viz., immune (I), resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS). After validation screening, IC259504 (*V. vexillata*) and IC424616 (landrace, *V. mungo*) were observed to be immune and resistant against bruchid infestation respectively, which was authenticated through X- ray radiography. Correlation heat matrix indicated GI had significant positive correlation with AE (r= 0.780) and PSWL (r= 0.574). Seed hardness showed significant negative correlation with AE (r= -0.379). The genetic diversity parameters viz., allele number, PIC values, observed heterozygosity indicated considerable diversity among the accessions at the DNA level. The immune and resistant accessions reported in the above study could be utilized in breeding programs for generation of bruchid resistant/tolerant cultivars in black gram and its other related *Vigna* species.

Plant Pathology


Shaivya Singh

Name of the Student : **Shaivya Singh**
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Chairperson : **Dr. K. K. Biswas**


Dr. K. K. Biswas

Title of the Thesis

Identification of Putative Mild Cross Protecting Strains of Citrus Tristeza Virus (CTV) for Management of Severe Decline Disease in Citrus

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Citrus tristeza virus (CTV), a *Toxoptera citricidus* transmitted closterovirus, destroys millions of citrus trees worldwide including India. The virus contains flexuous filamentous particles (2000 x 11 nm), +ve sense ssRNA (~19.3kb with 12 ORFs encoding 19 proteins) genome. CTV infects most of the cultivated citrus causing symptoms like decline, yellowing, growth stunting and stem pitting with poor fruit yield and quality. CTV is a century old problem and killed more than one million trees in India. CTV occurs in all the citrus growing geographical zones of India and infects all the commercial citrus and its relatives. Several citrus samples were collected from seven citrus cultivars belonging to four citrus species viz., *Citrus reticulata* cvs Khasi, Kinnow and Nagpur mandarin; *C. sinensis* cvs Sweet and Valencia orange; *C. limon* cv. Assam lemon; *C. jambhiri* cv. Rough lemon, of three citrus farms of Assam, HRS farm, AAU farm, Guwahati; CEC farm , Kamrup Rural, and URF, AAU, Jorhat. Based on DAC-ELISA and PCR the overall incidence of CTV was estimated upto 65.7% ranging from 40.9- 85.54% in different farms. Twenty one CTV isolates randomly, designated as CTV-Asm 1 to CTV-Asm 21 were characterized based on cloning and sequencing 404 nt fragment of 5'ORF1a gene of CTV genome. In the phylogenetic analysis, the present CTV isolates segregated into two genogroups; of them 16 isolates fell into one genogroup along with VT/Kpg3/K5 and other five isolates, fell into another genogroup along with Indian CTV isolate AR-1. Intra-farm genetic diversity among CTV isolates were observed from HRS farm and in URF farm, AAU, Jorhat. The present study revealed that occurrence of decline CTV genptypes VT/Kpg3 are prevalent in citrus growing areas of Assam causing citrus decline. In the present study, effort has been made to identify mild cross protecting strain (MCPS) of CTV with the help of *in silico* molecular-based techniques based on codon usage bias (CUB) analysis. The CP gene of 12 CTV isolates from Northeast India and some globally recognized CTV genotypes were taken for the study. The N_C vs GC3 plot analysis indicated that codon choice of CTV is influenced by translational selection, gene length, and gene function along with mutational bias. GC1/GC2 vs GC3 plot analysis showed unique pattern of higher GC1 and lower GC2 value similar to *Citrus* sp. which indicate that codon biasness of CTV is more dependent on host tRNA pool. Most of the Indian CTV isolates tested has higher Nc value, indicating that they might be severe and atypical type. Based on CUB analysis, thus, three isolates Mnp1, MB3 and K10 were considered to be mild isolates as they fell into same category with Florida mild CTV strain, T30. Based on nucleotide sequences of CP gene, these three isolates showed 93% nt identity with T30, whereas based on amino acid sequence, Mnp1 and K10 had 96-97% aa identity but MB3 had 94% aa identity with T30. Therefore, MB3 would be a strong putative mild strain.. These findings will be effective for designing a proof concept experiment to identify MCPS after biological evaluation challenging with severe strain.

Plant Physiology


Sinto Antoo

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Dr. Lekshmy Sathee

Title of the Thesis

Interactive Effects of Elevated [CO_2] and Nitrogen Fertilization on Yield and Nitrogen Response of Bread Wheat

The nitrogen (N) and protein concentration of wheat crop and grain declines in response to growth under elevated CO_2 (EC) conditions. The present study was conducted to determine the effect of reproductive stage N application on grain yield and NUE of wheat genotypes under EC. Another aim was to understand the interactive effects of EC and N dosage on the expression of genes involved in N metabolism (source and sink), ROS metabolism (source and sink), and grain size (sink). The changes in growth, yield parameters, grain ionome, and grain protein content, were examined in response to three N levels (LN: 30 kg/ha^{-1} (0:30:0), ON:120 kg/ha^{-1} (60:30:30), HN: 150 kg/ha^{-1} (60:45:45) and atmospheric CO_2 enrichment in six wheat varieties in season 1 and two varieties in season 2. There was a conspicuous decline in leaf nitrogen metabolism by EC; depicted as a reduction in the activity of GS and GOGAT and grain protein content. The altered transcript abundance of key genes like *TaYSL*/*TaNAMB1 etc.* supports the decline in grain ionome and suggests a transcriptional reprogramming by EC. The enhancement in RNS and ROS in the HN application re-confirmed the futility of applying excess N to alleviate the grain protein decline in EC. Grains collected from AC and EC conditions had variations in germination rates, suggesting that the multigenerational exposure to EC will have major implications in crop establishment and performance, as evinced by the rate of germination and altered crop phenology in the season 2 experiment. Plant responses to N availability under EC are genotype dependent, hence the fertilizer regimes need to be revised based on the N use efficiency of cultivars. The reproductive stage N application could alleviate the decline in grain protein content at EC conditions. The HN application was less beneficial than HRN in wheat plants grown under EC. Attention also needs to be given to the altered crop phenology observed under EC, which again can contribute to variation in N consumption.

Seed Science & Technology


Sushma M.K.

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Chairperson : **Dr. S.K. Yadav**


Dr. S.K. Yadav

Title of the Thesis

Effect of Nanoparticles on Seed Quality, Yield Attributes and Storability in Chickpea (*Cicer arietinum* L.)

The studies were carried out on chickpea variety Pusa 547 during 2020-21 with the objectives to study the effect of nanoparticles on seed quality parameters, yield attributes and storage potential. The seeds were dry dressed and infused with each of nano and bulk forms of Zinc oxide, Titanium oxide, Silicon dioxide @ 50, 100, 250, 500 and 750ppm along with the two controls i.e., untreated and treated with recommended PoP (Thiram treated @ 2g/Kg of seeds). Treated seeds along with controls were also stored in different packaging material i.e., Polythene and cloth bags under ambient conditions upto six months to study the storage efficacy. Significantly highest radicle emergence percentage (80%), germination percentage (92%), average shoot length (14.31cm), average root length (21.19cm), average normal seedling length (35.5cm), seedling dry weight (0.513g), seedling vigour index I (3265), seedling vigour index II (47.16), dehydrogenase enzyme activity (OD value 1.126) and lowest dead seeds percentage (4%), electrical conductivity (0.0557 µS/cm/g) were recorded for the seeds treated with dry nano ZnO @ 250ppm compared to both the controls. Significantly lowest pathogen infection percentage (13.33%) was recorded in seeds treated with dry nano ZnO @ 250ppm, dry nano ZnO @ 500pm and dry nanoTiO2 @ 100ppm compared to both the controls. Lowest insect infestation percentage was observed in seeds treated with dry nano ZnO @ 250ppm and dry nano ZnO @ 500ppm compared to both the controls. Seed treated with dry nano ZnO @ 250ppm also recorded highest field emergence percentage, days to 50% flowering, plant height, number of branches per plant, number of pods per plant, seed yield per plant, harvest index and test weight. Highest germination percentage (80.67%), seedling vigour index I (2781), seedling vigour index II (38.16), field emergence percentage (76.67%) and lowest values of dead seeds percentage (8.67%), moisture content (11.97%) were recorded in dry nano ZnO @ 250ppm after six months of storage when stored in polythene bags. Dry nano ZnO @ 250ppm was found to be most effective treatment for seed quality, yield attributes and storage potential in chickpea.

Soil Science & Agricultural Chemistry


Sharat Kothari

Name of the Student	:	**Sharat Kothari**
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Chairperson	:	**Mr. Kapil A. Chobhe**


Mr. Kapil A. Chobhe

Title of the Thesis

Synthesis and Evaluation of Novel Nitrogenous Fertilizer Products for Enhancing Nitrogen Use Efficiency

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As the production sector of N fertilizer challenged by energy crisis of the world and consumption sector is challenged by the environmental impacts, there is an urgent need to improve the nitrogen use efficiency for the sustainable growth of agriculture sector. Controlled release N fertilizers products are the promising tools in this regard which helps to balance between the economy and ecology as they improve the agricultural productivity, reduce pollution hazard and benefit the fertilizer industry. So the present investigation aims to synthesise and characterize novel controlled N fertilizer products i.e. N loaded nano clay biopolymer composites and coated urea fertilizer formulations and estimate the extent of N release from them. Efforts were also carried out to assess the effect of applied nitrogen on yield and nitrogen use efficiency of maize. The novel controlled release N products were characterized using XRD, FTIR and SEM which revealed the participation of bentonite and starch in the polymerization reaction at the nano level in case of the polymer composites. The incubation study in soil and water disclosed the slow release N property of these materials comparing to normal urea. The column study emphasized the significantly lower nitrate leaching potential of these material comparing to normal urea. In the field study, even when the N dose was reduced by 25% and applied through these novel products, the resulting yield was similar with that of 100% N application through urea indicating the scope to reduce 25% N dosage through these products. The improvement in the NUE was in the range of 0-17% without any compromise in the yield of maize. So these materials can be successfully used as controlled release N fertilizers products permitting more sustainable and high efficient use of fertilizers.

Vegetable Science


Geeta P. Karigar

Name of the Student : **Geeta P. Karigar**
Roll No. : **50056**
Chairperson : **Dr. Shrawan Singh**


Dr. Shrawan Singh

Title of the Thesis

Studies on Heterosis for Quality Traits in Cauliflower

Heterosis breeding has been instrumental in improving the productivity and profitability of vegetable sector. Introgression of cytoplasmic male sterility (CMS) system in cauliflower ensured affordable hybrid seed production since, the self-incompatibility (SI) mechanism has stability and maintenance issues. Therefore, the present study was conducted to study heterosis for quality traits in cauliflower with emphasis on heterosis and combining ability analysis for yield and quality traits. For this, 12 important agro-morphological traits were observed in 24 parental lines (10 CMS and 5 testers in Early group; 5 CMS and 4 testers in Mid group) and 70 F1 crosses (50 in Early and 20 in Mid group) and observed significant level of heterosis. Wide range of heterosis was revealed by the study of curd yield attributes i.e. curd length, curd width, marketable curd yield and net curd weight. CMS N-2-121, CMS 999-23, DC 67 and DC 71 of Early group and CMS 8401 and DC 401 of Mid group were best combiners for curd yield traits. Further, analysis of nine dietary minerals namely iron (Fe), zinc (Zn), copper (Cu), manganese (Mn), magnesium (Mg), sodium (Na), potassium (K), calcium (Ca) and sulfur (S) content in curd portion at harvest stage indicated wide range of mineral content as well as both mid parent and better parent heterosis. Combining ability analysis indicates for available strong combiners for different dietary minerals in both Early and Mid groups of Indian cauliflower. Promising combiners for multiple minerals were identified as CMS 999-41-5 (Fe, Mn, Mg, Na, Ca, S), CMS 4348-41-5 (Fe, Zn, Na, Ca, S, K), DC 98-2 (Fe, Cu, Na, Ca, S) and DC 67 (Zn, Mn, Na and S) in Early group. In Mid group, CMS 8401 (Fe, Na, Ca, K), CMS 1944-309 (Zn, Ca, S), DC 401 (Fe, S, K) and DC 476 (Cu, Mn, Na) were most promising combinations. Further, the total glucosinolates, sinigrin, glucoerucin and progoitrin content were detected in significant levels in cauliflower parental lines and F1 hybrid of Indian cauliflower. These compounds showed wide range of heterosis. It also revealed potential combiners on the basis of GCA effect and promising F1 combination on the basis of SCA effect. Expression analysis of eight key genes from different branch points from glucosinolates biosynthesis process and amplification of 16 gene specific markers also indicated variable expression pattern in Indian cauliflower. It was first systematic attempt to study the heterosis for dietary minerals and glucosinolates and also for understanding the glucosinolates pathway genes in Indian genotypes of cauliflower. The study will be useful for breeding cauliflower hybrids rich in dietary minerals, antioxidants and beneficial glucosinolates.

Ph.D.
Thesis Abstracts

Agricultural Chemicals


Ashish Khandelwal

Name of the Student : **Ashish Khandelwal**
Roll No. : **10223**
Chairperson : **Dr. Neera Singh**


Dr. Neera Singh

Title of the Thesis

Bioremediation of Aliphatic and Polyaromatic Hydrocarbons (PAHs) from Oil Contaminated Soil using Microbial Consortia

Exposure to crude oil, naturally or accidentally, deteriorates the productivity and biodiversity of agricultural lands. Adaptability of native microbes to sustain in contaminated environment, opens the avenue for treating contaminated soils in an effective way. Therefore, 17 bacteria (genus *Bacillus, Pseudomonas, Arthrobacter, Kocuria, Lysinibacillus, Nocardioides, Sporosarcina* and *Staphylococcus*) and 3 fungi (genus *Aspergillus* and *Trichoderma)* were isolated from the crude oil contaminated soil. Isolated microbes were evaluated to degrade aliphatic hydrocarbon in crude oil (1%) and PAHs mixture (naphthalene, fluorene, phenanthrene, anthracene and pyrene, 10 $\mu g\ g^{-1}$ each) in medium, without and with Tween-80 (0.1%). Bacteria, *Pseudomonas* sp. A3, and *Bacillus amyloliquefaciens* A9 and fungus *Aspergillus sydowii* AK20 were identified as the best aliphatic hydrocarbon degrader, whereas, *Kocuria rosea* AK4 and *Aspergillus sydowii* AK20 were the best PAH degrader. Tween-80, in general, affected degradation of aliphatic hydrocarbons/PAHs by bacteria. Based on degradation results and mutual compatibility studies, consortium of *Pseudomonas* sp.+*Bacillus amyloliquefaciens* and *Aspergillus sydowii* were identified as best microbial agents for crude oil degradation. They were evaluated for degradation of total petroleum hydrocarbon (TPH) in crude oil in naturally contaminated (25% oil) loamy soil (Assam) and found that bacterial consortium ($t_{1/2}$ 47.5 d) and fungus ($t_{1/2}$ 58.2 d) showed fast degradation as compared to uninoculated control soil ($t_{1/2}$ 135.9 d). Microbial population and N-assimilating genes increased after bacterial and fungus inoculation in the contaminated soil. Microbes exhibiting best crude oil/PAHs degrading ability were formulated in three types of bio-formulations, viz. bentonite-alginate beads, WDG of guar gumnanobentonite and composite of carboxymethyl cellulose-bentonite. Identified microbes (without and with nutrients) and bio-formulations were evaluated for TPH (Gujarat crude oil, 1%) degradation in a sandy loam soil. Compared to the uninoculated control ($t_{1/2}$ 69.7d), free cultures of bacterial consortium ($t_{1/2}$ 10.8d) and fungus ($t_{1/2}$ 21.4d) were highly effective in degrading TPH in crude oil and the $t_{1/2}$ decreased by 350-600%. Addition of ammonium sulfate (1%) slightly enhanced degradation by bacterial consortium ($t_{1/2}$ 10d) and fungus ($t_{1/2}$ 12.7d), while no effect of compost was observed. Bio-formulations were at par with the free cultures in degrading TPH. Degradation of TPH decreased with increase in the crude oil content from 1 to 5% and compared to bacterial consortium, fungus was more resilient to crude oil content. Microbial consortia was effective in degrading PAHs mixture in the sandy loam soil, but, efficiency varied. Compared to control, consortium decreased the

$t_{1/2}$ by 521-807% (naphthalene), 337-883% (fluorene), 387-533% (phenanthrene), 315% (anthracene) and 220-312% (pyrene). No significant effect of nutrients was observed on PAHs degradation. Bioformulations were as effective as free cultures of microbes. Inoculation of soil with crude oil/PAHs degrading microbes increased microbial diversity and nitrogen activity in soil and negated the effect of contaminants. Present study suggested that microbes identified in the present study were highly effective in degrading crude oil's TPH and PAH in medium and soils. Bioformulations of identified microbes, which are easy to handle and store, can be successfully used to remediate these contaminants in environment.

Agricultural Economics


Nithyashree M. L.

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Chairperson : **Dr. Suresh Pal**


Dr. Suresh Pal

Title of the Thesis

Investment and Development of Food Processing Industry: Firm-Level Evidence from India

During the developmental transition, the country needs to create more value addition to the commodities produced from the primary sector. In this context, the food processing industry has a significant role to play. Realizing the potential, the food processing sector is recognized as the sunrise sector in India, and during the last two decades, concerted efforts have been made to attract investment to expand industry growth. Despite this, the level of processing and India's global share in the processed food commodities are often reported as sluggish and it lacks competitiveness as compared with the global pioneers. Past studies suggest that the processing sector in the country is mainly constrained by limited resource utilization and stagnant technological change, but there is a scarcity in understanding the diverse factors associated with these. To fill this research gap the present study has undertaken the analysis of the structure, productivity and efficiency pattern of the food processing industry. The efforts have also been made to capture the role of foreign investment in the development of the food industry in India. The results of the study indicated that expansion of the industry output has largely been driven by the combined input growth followed by technical change. The resource use efficiency is although rising, slowly and the potential benefit of the capital investment was found to be very low. Raising the working capital turnover and timely availability of quality raw materials to the firms, macro environmental variables in terms of regional policy, openness to access the modern inputs and encouraging the innovations at the industry level will have a significant role in raising the efficiency of resource use. Rising consumer demand for high-value commodities and consciousness for nutritional content and safety necessitates sophistication of the food industry, thus technology upgradation. The foreign direct investment in this context has a significant role to play. The study has assessed the spillover effect of foreign investment in the food industry. The results indicated that the presence of foreign affiliates largely benefited in rising the domestic firms' productivity and they are mainly channelized through backward vertical linkages. Further analysis of these effects by the country source of origin and mode of investment suggested that the firms in the food industry were able to reap the benefit mainly from the developing countries via automatic route. To conclude, the study found evidence that the strategy for the development of the food processing industry lies in investment growth by attracting foreign capital and rising domestic ventures. Incentivizing the R&D activity, expansion of the scale of operation, efficiency gain and stabilization of the market prices of agricultural produce are likely to be equally important for the benefits of the food processing sector.

Agricultural Extension


Sangeeta Bhattacharyya

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Dr. R.R. Burman

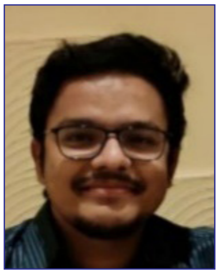
Title of the Thesis

Socio-economic Impact of Sansad Adarsh Gram Yojana in Maharashtra and Telangana

Villages have been the fundamental units of human civilization since time immemorial. Certain villages have reached the epitome of development and have been declared as Model Villages. The Central Government had launched an ambitious rural development program named *Sansad Adarsh Gram Yojana* (SAGY) in 2014 where each Member of Parliament adopts a village for transforming it as a Model Village. It was a matter of interest to probe whether the villages adopted under SAGY had reached/exceeded the level of development of already declared Model Villages of their respective states. Hence, a research investigation was planned to study the structural and functional mechanism of SAGY, identifying and standardizing indicators of Model Village, assessing the performance of SAGY villages, analyzing the perceived facilitating and inhibiting factors and studying the socio economic impact of these model villages and designing suitable strategies for convergence of agencies involved in developmental intervention in the adopted villages. The study was conducted in 10 villages located in 4 districts of purposively selected states of Maharashtra and Telangana because these states have highest concentration of Model Villages, which could serve as a comparison for evaluating SAGY villages appropriately. The total sample size for the study was 390 comprising of all categories of stakeholders. For comparative assessment of Model and SAGY villages on various developmental parameters, 7 rural development indices were developed through the NUEPA Method. In Maharashtra, SAGY villages scored more index values in terms of health and farming as compared to already declared Model Villages of the state. In Telangana, SAGY villages scored more index values in terms of education, farming, livestock, ecological status as compared to already declared Model Villages of the state. A multidimensional perception scale constructed for the study revealed that government-public liaison (671.86) was perceived to be the most dominant factor in facilitating the effective implementation of SAGY followed by factors like infrastructure and education (383.14), local political environment (267.42), collective power of villagers and youth (255.98), equality (236.71) and cultural and inherent values (143.03) existing among villagers. Amongst inhibiting factors, the lack of separate funding (-12.88), presence of factions within village (25.05), lack of coordination amongst Govt. departments (59.65) and faulty policy of village adoption (130.85) were prominent. SAGY had significant impact ($p<0.05$) in terms of increase in monthly family income, number of earning members in family, material possession status, social connectedness, family educational status and satisfaction level of villagers. By using Alfares method the strategy of convergence in funding (W=85.25) was ranked of top priority. Ensuring

convergence of schemes and its proper implementation on priority basis, leveraging on facilitating factors like community participation and social mobilization of the village community, instilling a spirit of brotherhood and cultural bonding to speed up different developmental activities of the program and involvement of NGOs, community bodies, line dept officials were suggested for promoting effective implementation of SAGY.

Agricultural Physics



Koushik Banerjee

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Dr. P. Krishnan

Title of the Thesis

Thermal Imaging for Characterization of Abiotic Stresses in Wheat Under Field Condition

Wheat crop growth and yield are closely related to the existence of favourable conditions. However, the presence of abiotic stresses restricts the crop growth and development which ultimately affect crop yield and biomass. Thus abiotic stress characterization and screening of wheat genotypes into tolerant/ moderate/ sensitive is necessary for gaining optimum crop yield under different abiotic stress conditions. Thus, field experiments (two study years), one at IARI (2016-17 and 2017-18) and another at CSSRI Karnal (2017-18 and 2018-19), were conducted for characterizing and screening wheat genotypes under water, temperature, nitrogen, double, triple and salinity stress conditions. From the observed biophysical parameters, PCA-based screening indices (NWSTI for water stress, NTSTI for temperature stress, NNSTI for nitrogen stress, NDSTI for double stress, NTSTI for triple stress and NSSTI for salinity stress) were developed, which best showed their potential to distinguish different wheat genotypes into tolerant (screening value >0.66), moderate (screening value 0.33-0.66) and sensitive (screening value <0.33) categories under different abiotic stress conditions. Heat mapping additionally showed association (strong or weak) among wheat genotypes cluster and biophysical parameters. Thus, the indexing approach developed in this study may play a potential role in the screening and selection of drought tolerant wheat genotypes in semi-arid condition. Latter, a set of fourteen thermal and RGB image-based indices were used for discriminating wheat genotypes grown under different abiotic stresses based on discriminant analysis (DA). At first sensitive image-based indices were identified using correlation analysis with PCA based indices under each abiotic stress conditions which were further used in DA analysis. DA also picked out the important thermal and RGB based indices that could play a potential role in the discrimination of wheat genotypes under different abiotic stress conditions. In addition to these, based on the thermal and RGB images of wheat canopy grown under different levels of water stress conditions, a new index called Normalized sunlit shaded index –NSSI was developed to characterise the sunlit and shaded areas of the crop canopy. The NSSI index showed significant relation with radiation use efficiency and thermal image-based stress indices i.e., CWSI and IG. Further, in this study, upscaling of sensitive RGB based indices (which were found important at ground level, in characterizing and discriminating wheat genotypes under water stress condition) was done using remote sensing data. Time series (2000 to 2019) MODIS imagery (in R, G, B and NIR bands) were collected over three wheat growing regions of Rajasthan. Drought years were identified by calculating standardized precipi-

tation index (SPI) for February and March over three districts i.e, Alwar, Ganganagar and Hanumangarh. Latter regression analysis was done using trend adjusted indices and SPI4 over three districts to understand their relationship under drought conditions. The study additionally predicted the wheat yield using ten different multivariate models for the three districts with the, image-based indices as input and found support vector machine to be the best model to predict the wheat yield.

Agronomy

Sonaka Ghosh

Name of the Student : **Sonaka Ghosh**
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Chairperson : **Dr. T. K. Das**

Dr. T. K. Das

Title of the Thesis

Nitrogen Management and Weed Dynamics in A Conservation Agriculture-Based Maize-Wheat-Mungbean System

A field experiment, involving maize-wheat-mungbean cropping system was undertaken during rainy (*kharif*), winter (*rabi*) and summer (*zaid*) seasons of 2018-19 and 2019-20 at ICAR-Indian Agricultural Research Institute, New Delhi. The objectives were: to appraise the conservation agriculture (CA) effects on weed seed bank on crop productivity and profitability; to work out the use efficiencies of water, nutrient and energy; and to assess its effects on selected soil physical, chemical and biological parameters and for mitigation of greenhouse gases (GHGs). The experiment was conducted in the 9th and 10th year of a long-term CA experiment. Ten treatments with three replications were laid out in a randomized complete block design. In this system, different CA-based practices were compared with conventional tillage (CT) practice. Different methods of crop establishment [permanent narrow bed (PNB), broad bed (PBB) and flat bed (FB) with and without residue retention (R) of maize, wheat and mungbean)], along with 75% and 100% recommended doses of nitrogen (75N and 100N) were integrated with CA practices. Results showed that, compared to CT practice, the CA-based practices resulted in reduction in weed seed density in soil by 2.5-45.1%, 5.0-53.1%, and 3.4-47.6% at 0-7.5 cm, 7.5-15 cm and 0-15 cm soil layers, respectively. The PBB+R+100N treatment resulted in 22.1%, 27.1%, 56.8% and 31.3% increase in maize, wheat, mungbean yields and system productivity, respectively compared to CT practice. The PBB+R+75N treatment was comparable with it in this regard. In both years, the PBB+R+100N gave significantly higher gross returns, net returns and net benefit: cost ratio and also resulted in 36.9%, 56.5% and 99.7% higher total water productivity, respectively in maize, wheat and mungbean crops compared to CT practice. The PNB+R+75N was the next best treatment in this regard. The 75% N application had higher partial factor productivity of N in maize and wheat than 100% N. Application of 75% N and 100% N were at par on energy productivity and energy ratio. The treatment PBB+R+100N significantly improved water stable aggregates across the soil depths. The soil organic carbon stocks were comparable between the PBB+R+100N and PBB+R+75N at 5-15 cm and 15-30 cm soil depths. Also reduction in GHGs (CO_2, N_2O) emission was observed in this study under PBB+R and PNB+R. The treatments PBB+R+100N and PBB+R+75N were comparable on above parameters in maize-wheat-mungbean system. The PBB+R+75N system, however, led to a saving of 75 kg N/ha. Hence, the CA-based PBB+R system with 100% N in the initial years of adoption and 75% N over a long period may be recommended for sustainable intensification of maize-wheat-mungbean system in the Indian Indo-Gangetic Plains and similar agro-ecologies of the tropics and sub-tropics.

Bioinformatics

Bulbul Ahmed

Name of the Student : **Bulbul Ahmed**
Roll No. : **10780**
Chairperson : **Dr. Anil Rai**

Dr. Anil Rai

Title of the Thesis

Development of A Deep Learning Based Methodology for Functional Protein Classification

Cereals are staple crops widely cultivated across the world. These are highly nutritious, rich in vitamins, minerals, carbohydrates, fats, oils, proteins and fibers but are low in essential amino acids such as lysine. Cereal crops belong to *poaceae* family, having wider applications in production of flour, bread, rice, cakes, corn etc. The other by-products of these crops are beverages and wine. Moreover, consumption of these crops reduces the coronary heart disease, diabetes, colon cancer, diverticular disease etc. India is the third largest cereal producer after China and USA but it has been producing to a great extent which could be achieved to 4.9% increase in production from base year 2020 to 2027. The production of these crops is highly affected by biotic and abiotic stresses which adversely affected crop growth and development, further resulting in crop loss that leads to economic loss. Hence, it is required to understand and study the genes involved in order to minimize the biotic and abiotic stresses. The genes start adapting under stress factors and produce proteins that can tolerate such changes by changing signalling pathways in protein-protein interaction. Finding these proteins are highly expensive, time consuming and required a highly experienced person. In order to reduce cost and time, rapid classification and prediction of such proteins using computation approaches is required. Further, these proteins are complex in nature with high dimensions which are very difficult to study using conventional approaches. This study was oriented towards the application of different machine learning techniques (namely, support vector machine and random forest) and deep learning (long short-term memory) for development of classification models for abiotic stresses (heat, cold, salinity and drought) protein sequences from *poaceae* family. Also, an activation function, Gaussian Error Linear Unit with Sigmoid function (*SiELU*) has been developed for deploying in a deep learning model which shows an increased efficiency of the model. Lastly, a web-based tool for prediction of stress associated proteins from *poaceae* family has been developed implementing the proposed long short-term memory deep learning methodology with developed activation function *i.e.*, *SiELU* and tuning of other hyper-parameters.

Entomology

Sunitha P.

Name of the Student : **Sunitha P.**
Roll No. : **11021**
Chairperson : **Dr. Vinay K. Kalia**

Dr. Vinay K. Kalia

Title of the Thesis

Colonization of Entomopathogenic Bacteria in Brinjal Plant and Interaction with Brinjal Shoot and Fruit Borer, *Leucinodes orbonalis* (Lepidoptera: Crambidae)

Brinjal shoot and fruit borer (BSFB), *Leucinodes orbonalis* Guenee is the key pest of brinjal that causes a significant yield loss. Farmers spray wide range of insecticides right from vegetative stage till last harvesting stage to protect the crop from the notorious BSFB, which leads to pesticide residue and insecticide resistance problems. To overcome this, now focus has shifted to biopesticides but their commercial application is limited due to their susceptibility to abiotic factors. To overcome these bottlenecks, a hidden ecological role played by entomopathogenic bacteria as endophytes was sought. Here in the present investigation bioefficacy of the twenty six *Bacillus* strains comprising of *Bacillus thuringiensis, Bacillus subtilis*, *Bacillus pumilus*, *Bacillus atrophaeus* and *Bacillus amyloliquifaciens* along with reference strain *i.e. B. thuringiensis* sub species *kurstaki* HD1were screened against neonates of BSFB using diet incorporation method under controlled conditions in laboratory using acetone precipitated spore crystal complex. On 7th day after treatment the highest mortality was observed in *Btk* HD1 (100%) followed by 96% (VKK-13 and VKK-BB2) and 80% (VKK-BB1) mortality with native *Bt* strains. Further, endophytic bacteria *Bacillus atrophaeus*, VKK-6OL and *B. subtilis* strain attained 68% and 52% mortality respectively. Median lethal concentration (LC_{50}) of the potential *Bt* strains revealed that *Btk* HD1 (LC_{50}=0.49µg/g of diet) and *Bt*VKK-BB2 (LC_{50}=0.59µg/g of diet) were found to be at par as their fiducial limits are overlapping. Moreover, these *Bacillus* spp. were screened for the insecticidal activity in CFU form at 1x 10^8 CFU/ml against neonates of *L.orbonalis*. Two native *Bt* strains (VKK-BB2 and VKK-13) and two brinjal seed endophytic *Bacillus safensis* strains (BSEB-6 and BSEB-9) along with reference *Bt* (*Btk* strain HD-1) could record above 50% mortality. Three potential *Bt* strains (*Bt* VKK-BB2, *Bt* VKK-13 and reference *Bt*, Btk-HD1) were inoculated to brinjal plants via seed treatment, soil application and foliar spray @ 1x 10^8 CFU/ml in pot culture experiments. Besides, GFP tagging of *Bt* strain VKK-BB2 was carried out to study the translocation of Bt in the plant and confirmed by Confocal Laser Scanning Microscope (CLSM). Inoculation of GFP tagged *Bt* VKK-BB2 to brinjal by three inoculation methods as mentioned above. Presence of bacteria within the leaves was confirmed by amplification of *gfp* and *cry* gene in the re-isolated *Bt* colonies from brinjal leaves and shoot. In case of seed treatment, *Bt* colonies could survive up to 30th days after inoculation. The native

Bt strain VKK-BB2 was found to be potential colonizer with the highest recovery in all three inoculation methods. Leaves taken from the colonized brinjal plants were able to cause up to 44% mortality when fed to neonates of *Leucinodes orbonalis*. To our knowledge, this is the first report on endophytic ability of native *Bt* strains in brinjal and its effect on larval herbivory. Establishment of native *Bt* strain as endophytes in plants opens new horizons for the development of a novel pest-resistant crops which could be an alternative to Bt transgenic crops.

Floriculture and Landscape Architecture


Rihne T.

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Chairperson : **Dr. Namita**


Dr. Namita

Title of the Thesis

Characterization and Management of Phytoplasmas in Rose (*Rosa* × *hybrida* L.) Genotypes

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Disease incidence of 12.5 to 87.5 per cent of phytoplasma suspected symptoms of phyllody, flower malformation, little leaf and flat stem were recorded in sixteen rose genotypes from four states (Delhi, Manipur, Uttar Pradesh and Maharashtra) of India during 2018-2020. Phytoplasmas association was confirmed in all the sixteen symptomatic *Rosa* × *hybrida* and *Rosa damascena* genotypes using primer pairs of *16S rRNA*, *secA* and *rp* genes in nested PCR assays. Sequence comparison, phylogenetic and *in silico* RFLP analysis of 16S rRNA gene sequences allowed the identification of the rose infecting phytoplasma strains into 16SrI-B and 16SrII-D subgroups. Utilization of the *rp* gene specific primers for 16Sr I (rpF1/rpR1 and rp(I)F1A/rp(I)R1A) and 16SrII groups (rp(II)F1/rp(I)R1A and rp(II)F2/rp(I)R1A) could confirm the mixed infection of 16SrI-B and 16SrII-D subgroups of phytoplasma in five rose genotypes: Pusa Muskan, Pusa Manhar, Haseena, Deepak and MS Randhawa from New Delhi. Leafhoppers collected from rose fields at New Delhi (*Empoasca motii* and *Hishimonus phycitis*) and Uttar Pradesh (*H. phycitis*) were tested positive with 16SrII-D subgroup of phytoplasma and suggested as putative vectors. Besides, five species of weeds from New Delhi were identified as hosts of 16SrI (*Coccinea sp, Galinsoga sp* and *Poa annua*) and 16SrII (*Catharanthus roseus* and *Parthenium hysterophorus*) group and four species from Uttar Pradesh as hosts of 16SrII (*P. hysterophorus, Cannabis sativa, Datura stramonium* and *Phyllanthus niruri*) group growing in and around the rose fields using 16S rRNA gene sequence comparison analysis. The report of association of 16SrI-B phytoplasma subgroup related strain in *Coccinea sp* and *Galinsoga sp* are the first records in the world and *Poa annua* is the first record of phytoplasma's host in India. A multiplex PCR assay was also developed and optimized for detection of *Ca*. P. asteris strain associated with rose samples by employing primer pairs of 16S rRNA (P1/P7, R16mF2/R16mR2, R16F2n/R16R2) and *sec*A genes (secAfor2/secArev3) in a single PCR reaction by increasing the PCR mastermix, reducing the primer quantity and optimizing annealing temperature at 55°C. Management of phytoplasma was attempted using three antibiotics (oxytetracycline, streptomycin and erythromycin A) at different concentrations (60mg/L, 80mg/L, 100mg/L) in the infected rose genotype MS Randhawa under *in vitro* and *in vivo* conditions. All the concentration of oxytetracycline was found effective in elimination of phytoplasma both under *in vitro* and *in vivo* condition. However, 60mg/L concentration was observed to be better in terms of normal growth and development of treated rose plants in comparison to other tested concentration under *in vitro* condition. Hence, 60mg/L concentration of oxytetracycline can be recommended for management of rose associated phytoplasma disease infections. Streptomycin and erythromycin A treatments failed to show elimination of phytoplasma in rose genotype MS Randhawa both under *in vitro* and *in vivo* conditions as manifested by positive PCR results for phytoplasma presence in treated rose genotype.

Genetics and Plant Breeding

Neeraj Kumar

Name of the Student : **Neeraj Kumar**
Roll No. : **10613**
Chairperson : **Dr. C. Bharadwaj**

Dr. C. Bharadwaj

Title of the Thesis

Mapping Genomic Regions (QTLs) Imparting Salt Stress Tolerance in Chickpea (*Cicer arietinum* L.)

Salinity is a major abiotic stress that hampers crop production and productivity, it reduces chickpea annual yields by 8–10% worldwide. Understanding the genetic basis governing this complex trait is utmost important to breed salt tolerant chickpea. In our study recombinant inbred line (RILs) population derived from ICCV 10 (salt tolerant) x DCP 92-3 (salt sensitive) was evaluated. Higher salinity induced reduction in yield and physiological traits like, relative water, chlorophyll and proline contents and increased electrolyte leakage and shoot Na^+/K^+ concentrations. Axiom®CicerSNP array was used to construct a high-density linkage map comprising 1856 SNP markers spanning a distance of 1106.3 cM across eight chromosomes. Leading to identification of 28 major and minor effect QTLs explaining up to 28.40% of the phenotypic variance. Comparative RNA- seq data between tolerant (ICCV 10, JG 11) and sensitive (DCP 92-3, Pusa 256) were also used to understand the complex molecular mechanisms underlying salinity tolerance. A total of 530 million reads were generated from stressed and non-stressed root tissues using Illumina HiSeq-2500. A total of 21,698 differentially expressed genes (DEGs) were identified, of which 11,456 and 10,242 were up- and down-regulated, respectively. These DEGs were associated with crucial metabolic pathways, including hormone signaling, photosynthesis, lipid and carbohydrate metabolism, and cell wall biogenesis. Gene ontology (GO) examination revealed an enrichment of transcripts involved in salinity response. A total of 4257 differentially expressed GO terms were categorized into 64 functional groups of which, GO terms like, integral component of membrane, organelle, and cellular anatomical entity were highly represented in tolerant genotypes under salt stress. Major QTL regions were enriched with key genes, such as calcium-dependent protein kinases, histidine kinases, cation proton antiporter, WRKY and MYB transcription factors, which are reportedly involved in salinity stress tolerance. Results also depicted that both tolerant genotypes deployed more sophisticated and efficient mechanisms of stress tolerance via actively upregulating candidate genes under stress. This study provides useful information to discern the genetics of salinity tolerance, which could ultimately pave the way to harness molecular breeding tactics to elevate salinity tolerance in chickpea breeding programs.

Molecular Biology and Biotechnology

Kishor Uttamrao Tribhuvan

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Roll No. : **10841**
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Dr. Kishor Gaikwad

Title of the Thesis

Understanding the Molecular Mechanism of Flowering in Response to Photoperiod in Pigeon Pea (*Cajanus cajan* (L) Millsp)

Pigeonpea (C. *cajan* (L) Millsp), a staple pulse crop of SE Asia is a short-day plant that shows a strong photoperiod response for induction of flowering under sub tropic conditions. Understanding the molecular mechanism behind photoperiod sensitivity in *C. cajan* is a prime requirement for the development of photoperiod insensitive varieties that can withstand a wider range of agroecological environments as well as suited for growing in multiple seasons. For expanding the scope of investigations, in the present study, three photoperiod-insensitive genotypes viz ICP20338, ICP14952, and ICP 14923 of *C. cajan* were identified by screening under short day and long day photoperiod. Variant analysis between photoperiod-sensitive (MAL3) and photoperiod-insensitive (ICP20338) genotypes identified 1.31- and 0.24 million SNPs and InDels, respectively. An annotation and pathway analysis revealed that SNPs and/or InDel containing genes associated with 391 metabolic pathways. A total of 21 genes of plant circadian rhythm pathway, a key regular of photoperiod dependent flowering harbors SNPs and InDels either in their regulatory, coding, or intronic region. qRT-PCR based expression analysis showed that *GI*, *CRY1*, *CRY2*, *LHY*, *CHS,* and *PRR5* showed a differential expression pattern between RL tissues of ICP20338 and MAL3. The altered expression pattern of these genes due to the presence of SNPs and InDels makes them the probable candidate genes for photoperiod sensitivity. A genome-wide survey for photoperiod response genes revealed the presence of 13 PEBP (FT) and 33 CCT genes in *C. cajan*. Expression analysis across gene atlas data and qRT-PCR identified two FT genes viz *CcFT6* and *CcFT8* and two CONSTANS viz *CcCCT4* and *CcCCT23* up-regulated in reproductive leaf. Expression analysis in photoperiod sensitive, MAL3 genotype revealed that *CcFT6* and *CcCCT23* are upregulated under SD. However, in photoperiod insensitive genotype (ICP20338) both *CcFT6* and *CcFT8*; and *CcCCT4* and *CcCCT23* were upregulated in SD, while *CcFT8* and *CcCCT4* were upregulated only under LD. Further characterization revealed that MAL3 utilized photoperiod dependent induction of flowering with the involvement of *CcFT6*, *CcCCT23*, whereas ICP20338 seems to utilize an additional photoperiod independent pathway comprising of *CcFT8* and *CcCCT4* proteins. Interestingly, in ICP20338, photoperiod dependent pathway appears to be shut down or least effective under LD. This study will pave the way for the detailed characterization of the genes involved in the photoperiodic regulation of flowering in *C. cajan.*

Nematology

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Chairperson : **Dr. Uma Rao**

Dash Manoranjan Pitabas

Dr. Uma Rao

Title of the Thesis

Molecular Dissection of Rice-*Meloidogyne graminicola* Interactions: Effectors And Their Targets

Meloidogyne graminicola has emerged as the most destructive plant-parasitic nematode disease of rice (*Oryza sativa* L.). The compatibility of plant-nematode interactions is dependent on host defence responses that are modulated by nematode secreted effectors. In a previous study, activation tagged mutants were developed in an indica rice landrace (acc. JBT 36/14). Four mutant lines, viz. line-8, 9, 11 and 15, showed resistance to *M. graminicola*. Here, we sequenced the genome of JBT 36/14 along with line-8, 9, 11 and 15 to identify the structural genomic variations putatively involved in incompatible interaction with *M. graminicola*. Sequencing identified 293,238 to 553,648 unique SNPs and 32,395 to 65,572 unique InDels in the mutant lines, of which 93,224 SNPs and 8,170 InDels were common between all the mutant lines. Functional annotation of genes containing these variants showed their involvement in metabolism and growth pathways, rice traits and families of transcription factors (e.g., FAR1, NAC, bHLH), and putative susceptibility (S) genes (e.g., PME3, FAD8). Our results indicate that subject to further genetic validations; these structural genetic variations may be involved in conferring nematode resistance to the rice mutant lines. Further, RNA-sequencing was used to investigate the molecular mechanisms conferring nematode resistance to mutant line-9. At 24 h post-infection, 674 differentially expressed genes were found in line-9 compared to JBT 36/14. Early regulation of genes putatively related to nematode damage associated molecular pattern recognition (e.g. Wall associated receptor kinases), signalling (NLRs), pathogenesis-related genes (PR1, PR10a), defense-related genes (NB-ARC domain-containing genes) as well as a large number of genes involved in secondary metabolites including diterpenoid biosynthesis (CPS2, OsKSL4, OsKSL10, Oscyp71Z2, oryzalexin synthase, and momilactone A synthase) was observed in *M. graminicola* resistant mutant line-9. We identified 561 secretory proteins and 52 orthologs of putative nematode parasitism genes from *M. graminicola* genome. Thirteen of these were functionally evaluated for their importance in parasitism and reproductive fitness using RNAi. Perturbations in rice root tissue penetration and nematode multiplication factor were observed post gene silencing on Pluronic gel. Silencing of *Mg-msp-3*, *Mg-flp-18*, *galectin* and *Mg-msp-27* showed the highest attenuation in nematode multiplication (63 to 43 %) and root penetration (68 to 37%). Lastly, four cognate rice proteins interacting with *M. graminicola* CLE proteins were identified through a yeast two-hybrid screen. These proteins were involved in apoptosis, transcription, translation and modulation of brassinosteroid hormone biosynthesis genes in rice, suggesting the role of CLE gene in modulation of basic cellular mechanisms and rice defence responses.

Plant Pathology


Kuleshwar Prasad Sahu

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Dr. Aundy Kumar

Title of the Thesis

Structural and Functional Analysis of Rice Phyllospheric Bacteria for Their Antimicrobial Properties and Defense Elicitation Against Blast Disease

Rice is among the most consumed grain crop in the world. Rice blast disease caused by the fungus *Magnaporthe oryzae* is one of the threats in rice production globally. Present blast management strategies including host resistance and fungicide spray are either non-durable or not compatible with environment and trade. Therefore, new management options are needed for sustainable rice production. With its adapted microbiota, the phyllosphere brings a unique microbiome to the plant-holobiont-pool with a potential for modulating plant traits. However, the ecological forces driving the phyllomicrobiome assemblage and functions are among the underestimated aspects of plant biology. In the present study, we combined the mNGS with microbiological methods to decipher the core-phyllomicrobiome of rice-genotypes differing for their reaction to blast disease grown in contrasting agroclimatic zones. Principal coordinate analysis indicated an influence of environmental factors rather than the genotype *per se* on phyllomicrobiome assembly. The predominance of phyla such as **Proteobacteria, Actinobacteria,** and **Firmicutes** encompassing the core-microbiome consisting of *Acidovorax, Arthrobacter, Bacillus, Clavibacter, Clostridium, Cronobacter, Curtobacterium, Deinococcus, Erwinia, Exiguobacterium, Hymenobacter, Kineococcus, Klebsiella, Methylobacterium, Methylocella, Microbacterium, Nocardioides, Pantoea, Pedobacter, Pseudomonas, Salmonella, Serratia, Sphingomonas* and *Streptomyces* was observed on the phyllosphere. SparCC network analysis showed a complex intra-microbial interactions on the phyllomicrobiome. The microbiological validation of mNGS data confirmed *Acinetobacter, Aureimonas, Curtobacterium, Enterobacter, Exiguobacterium, Microbacterium, Pantoea, Pseudomonas,* and *Sphingomonas* on the phyllosphere. Images captured by scanning electron microscope revealed the physical presence of bacterial aggregates. All the cultured isolates were functionally characterized for antagonism against blast fungus *M. oryzae*. Most of the isolates displayed secretory compounds, as well as a volatile compound, mediated antagonism against the blast fungus. Upon seed bacterization, these isolates showed induction of MAMP triggered immunity on rice seedlings. Further, blast disease suppression assay under artificial epiphytotic conditions culminated in the identification of 17 bacterial isolates which gave more than 50 % disease suppression on blast susceptible variety Pusa Basmati 1. Transcriptional profiles of innate immunity marker genes such as *OsCEBiP, OsCERK1, OsPAD4, OsNPR1, OsEDS1, OsPDF2.2, OsFMO1, and OsPR1.1* in rice were found altered or up-regulated in bacterized rice seedlings. GC-MS analysis of the bacterial volatiles indicated the presence of antifungal volatile compounds. GC-MS analysis of rice leaves leads to the identification of rice-associated volatile compounds. Multi-pronged activities of phyllomicrobiome on *Magnaporthe oryzae* (antifungal activity), rice (defense elicitation), and blast disease (blast suppression) have been elaborated for management of blast by phyllomicrobiome reengineering.

Post Harvest Technology

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Title of the Thesis

Studies on the Influence of UV-C and Chemical Elicitors on Quality and Shelf Life of Bitter gourd Fruit

Bitter gourd is a cucurbitaceous crop rich in several bioactive compounds and also possesses antidiabetic potential used for treating diabetes and other human ailments. It is highly perishable due to short shelf-life (4-5 days) under ambient condition and spoils rapidly due to excessive moisture loss, tissue softening, yellowing, and quality loss. To address these problems, three objectives were formulated. In the first objective, UV-C radiation (20,30 and 40 min) were used as an elicitor for reducing the microbial load and retaining the biochemical attributes of bitter gourd fruit during cold storage [10 ^{0}C, 85-95% RH (relative humidity)]. Results showed that UV-C treatment for 40 min has retained 57% higher antioxidant activity, 61% higher total phenols, 51% higher antidiabetic potential and 5% higher saponin content compared to control on 16th day of storage at 10 °C and 85-95% RH. It also induced the abiotic stress hence accelerated the synthesis of MDA and proline. UV-C also reduced the microbial load in stored bitter gourd for 16 days. This suggests that the application of UV-C for 40 min can be gainfully utilized for microbial load reduction, shelf-life enhancement and secondary metabolites retention during storage. In the second objective, bitter gourd fruits were dipped in different concentrations of salicylic acid (SA 3, 5, 10 mM), putrescine (PUT 1, 2, 3 mM), and calcium lactate (50, 75 and 100 mM) and stored at 10 ºC 85–95% RH for 20 days. Among the treatments, SA 7.5 mM retained 16% higher total carotenoid, and 80% higher ascorbic acid while SA 10 mM retained 85% higher total phenol, two-times higher anti-oxidant capacity and 19% higher antidiabetic potential compared to control on 20th day of cold storage. Higher fruit firmness, lower PLW and PME activity were also recorded in SA 10 mM treated fruits. PUT 3 mM was best in retaining two times higher fruit firmness, 45% higher ascorbic acid, 36% higher antioxidant, 35% higher antidiabetic potential and 4% higher saponin compared to control on 20th day of storage. CL has also shown positive effect in shelf-life extension of bitter gourd up to 20 days under cold storage. CL 100 mM dose was more effective in reducing the PLW to 6.46% and decay rate to 33.33% on 20th day of storage. CL 100 mM was found to maintain the firmness by three times, ascorbic acid by 1.5 times, antidiabetic potential by two times and increased saponin by one-fold compared to control on 20th day of storage. Hence, SA, PUT and CL could be considered as an eco-friendly approach for shelflife extension of bitter gourd with higher retention of nutraceutical attributes. Third objective was aimed to quantify charantin content in bitter gourd treated with physical and chemical elicitors. Results showed that PUT 3mM retained higher charantin content (723.03µg g^{-1}DW) compared to control and other treatments, hence this was subjected to gene expression study of *McCAS1* and *McSE* gene responsible for charantin biosynthesis which showed some other gene could also be responsible for its biosynthesis due to their spatial, temporal and tissue specific expression during storage.

Vegetable Science


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Title of the Thesis

Joint Multiple Family Linkage Analysis for Resistance to Watermelon Bud Necrosis Virus and Fruit Quality Traits in Watermelon

Since past three decades, tospoviruses have been impacting severe economic losses causing heavy yield reduction in many crops. Watermelon bud necrosis disease caused by watermelon bud necrosis orthotospovirus (WBNV) is one such tospovirus that has emerged as a devastating disease of watermelon in India. Citron (*Citrullus amarus*) a wild relative of watermelon is reported to possess resistance to this disease. However, being white fleshed with coarse texture and bland/bitter taste; citron may cause undesirable effect on quality in watermelon. Hence, it is important to understand the genetics and genomic regions/ genes governing fruit quality, while using this species in WBNV resistance breeding. Genetic analysis in two prebred lines *viz.,* BIL-53 and BIL-99 derived from citron suggested that the genetics of most of fruit quality traits are governed by one or two genes suggesting simple inheritance. QTL mapping for fruit shape identifies eleven major QTLs on chromosome 3, 4 and 11. Candidate gene analysis in chromosome (Chr) 3 revealed a novel allele of *Cla011257* gene with two SNPs resulting in oblong fruit shape and predicted *Cla016683* gene as a putative candidate for fruit shape in a novel QTL region on Chr. 11. Similarly, for rind color and pattern consistent QTLs were detected across two populations (F2 and BC1F2) on chromosome 9. Comparative genomics analysis of this region revealed two genes namely *Cla016148* and *Cla016150* as probable potential candidate genes for stripe and interstripe color. QTL analysis for seed traits revealed two QTLs viz., *q_100SW_2.1* and *q_100SW_6.1* for 100seed weight; three QTLs viz., *q_SCC_3.1*, *q_SCC_5*.1 and *q_SCC_5.2* for seed coat color. Results validated the previously reported QTLs viz., *ss2.1* and *qSS6* for seed weight/size and *qsc-c3-1* for seed coat color of watermelon. Similarly, one novel QTL was identified for total soluble solids on Chr. 11; candidate gene analysis in it predicted *Cla016890* and *Cla016891* genes as putative candidates. For flesh color, we made first attempt to map the genes/QTLs governing flesh color at the different regions of fruit through visual and colorimetric analysis. Results revealed fifteen major QTLs on Chr. 2, 4, 5, 6, 7 and 10 for flesh color at different regions. Candidate gene analysis predicted *Cla020214* and *Cla020121* on Chr.2; *Cla005011* on Chr. 4; *Cla018767, Cla018768, Cla018769, Cla018770, Cla018771* on Chr. 6; *Cla017416* and *Cla017593* on Chr. 10 as a probable candidates genes governing flesh color at different regions. For WBNV resistance, efforts have been made to integrate WBNV resistance QTLs from wide range of populations and screening experiments for a comprehensive analysis through QTL-meta-analysis and joint inclusive composite interval mapping (JICIM). Comprehensive analyses for

QTLs suggested *MQTL_WBNV_2.1* on Chr. 2, *MQTL_WBNV_3.2* on Chr. 3 and *MQTL_WBNV_7.2* on Chr. 7 as potential candidate QTL regions for WBNV resistance. The genes identified in these QTLs *viz*., *Cla020173* encoding PR-1, *Cla001733* encoding pathogenesis-related transcriptional factor and ethylene-responsive transcription (ERF), *Cla001590* and *Cla001591* genes encoding acid phosphatase, *Cla019476* encoding TIR-NBS and *Cla011771* belonging to TIR-NBS-LRR gene family may be investigated as putative candidates for WBNV resistance in watermelon. Overall results suggest that the breeders can use citron species as a source of resistance in breeding programs without apprehension of linkage drag on fruit quality traits. The results obtained in the present study may provide way for functional validation of putative candidates and development of suitable markers for marker assisted selection (MAS) to WBNV resistance with improved fruit quality traits in watermelon.


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