



# Fifty Ninth Convocation

## Significant Post Graduate Students' Research

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### Abstracts

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**M.Sc.**  
**Thesis Abstracts**





## Agricultural Chemicals



Partha Chandra Mondal

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Dr. V. S. Rana

### *Title of the Thesis*

### **Extract from *Eucalyptus globules* and *Cymbopogon flexuosus* against *Bemisia tabaci***

Due to hazards of synthetic pesticides to environment and living being, search for green pesticides of biological origin are preferred. Thus, *Eucalyptus globules* and *Cymbopogon flexuosus*, not yet evaluated against *B. tabaci*, were explored. *E. globules* leaves were found to contain 0.86% oil and 10.22% acetone extract, while, *C. flexuosus* contained 0.81% oil. 1,8-Cineole (60%), limonene and p-cymene were identified as main compounds in *Eucalyptus* oil while *C. flexuosus* oil contained citral (82%). 1,8-cineole and citral from oils, ursolic acid lactone and ursolic acid from extract were also isolated by column chromatography. These oils, 1,8-cineole, citral and extract were evaluated for their pest control activity against *B. tabaci* and results showed concentration dependant activity. Tested samples at 0.3% concentrations, possessed 50% or more than 50% mortality of whiteflies after 48 hours under lab conditions. The acetone extract of *E. globules* and lemongrass oil were found most effective followed by *Eucalyptus* oil, citral and 1,8-cineole. Similarly, results of ovipositional deterrent activity showed that essential oils from *Eucalyptus* and lemongrass possessed highest deterrent activity followed by 1,8-cineole, citral and acetone extract against *B. tabaci*. The contact toxicity and ovipositional deterrent activity of tested samples have been found for first time against *B. tabaci*.



## Agricultural Economics



Shenaz Rasheed

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Dr. P. Venkatesh

### *Title of the Thesis*

### **Valuation of ecosystem services of paddy landraces and assessment of eco-compensation in Wayanad district of Kerala**

Landraces of paddy are highly adaptive, tolerant to local stresses and integral part of local food culture, nutrition and agrobiodiversity. However, growing preferences for high-yielding varieties and more remunerative crops led to several landraces going extinct and paddy being replaced. The dual issues of conversion of paddy ecosystems and declining landraces poses threat to food security, agrobiodiversity and environmental health. Thus, a study was conducted to understand and evaluate paddy ecosystem services and disservices, and assess if incentivizing farmers through eco-compensation or payments for ecosystem services could help in conserving fragile and important agroecosystems. Etymologically ‘the land of paddy fields’, Wayanad district in Kerala state, has been witnessing massive losses of its paddy fields and diversity of landraces over the past decades. Hence, Wayanad was selected for the study and 225 paddy farmers were surveyed using a pretested schedule in February, 2020. In the study, Markov chain analysis indicated greater stability in area under banana and plantain in Wayanad and Kerala reflecting a shift in cropping pattern towards these crops. As observed from structural break analysis in the study, the ‘Kerala Conservation of Paddy Land and Wetland Act, 2008’ prohibiting the conversion of paddy fields in the state, could significantly arrest annual reductions in area under paddy to an extent of 11,253 ha in Kerala and 129.4 ha in Wayanad. Farmers of Wayanad grow paddy landraces mainly for self-consumption. Farmers also grow landraces as part of their tradition and for conservation, and are highly aware of paddy ecosystem services and probable ecological effects of paddy land conversions. Using market price, replacement cost and benefit transfer methods, it was estimated that the paddy ecosystem of Wayanad generates Rs.6,26,919 per ha worth of ecosystem services annually, of which 77 percent is non-marketed. ‘Wayanad Package Scheme, 2018’ was aimed at financial assistance for farmers growing indigenous paddy in Wayanad but only around 10 percent farmers were aware of the scheme. However, around 95 percent of farmers showed willingness to enroll in eco-compensation programmes as payments for preserving ecosystems would augment farm income and also incentivize conservation. Single bound contingent valuation analysis found a mean compensation of Rs.7,933 per ha required for cultivating paddy landraces which was lower than that proposed by the Government. But these amounts are extremely low in comparison to the annual value of services generated by the ecosystem. Thus, the value of ecosystem services needs to be accounted for in eco-compensation framework and farmers should be duly recognized and paid for the invisible fruits of their toil.



## Agricultural Engineering



Manabraj Manna

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Dr. D. K. Singh

### *Title of the Thesis*

### **Study on impact of backwater flow and rainfall on soil and groundwater quality in deltaic region**

A study was conducted in Kaikhali and Bonegheri villages of South 24 Parganas district of West Bengal which is a part of Sundarbans delta. These villages are located between two tidal streams namely Matla and Nimaniam within the elevation of 1.0 m from mean sea level. Salinity of water in Matla varies from 22.0 dS/m to 41.0 dS/m whereas in Nimaniam, it varies from 17.0 dS/m to 35.0 dS/m. Scarcity of irrigation water and soil salinity during summer, ponding of water in cultivable land during monsoon months and lack of location specific technologies are major reasons for low agricultural productivity. Land shaping technologies such as ponds in 20% of the area, ridges at the side of pond locally known as *Ail* and embankments and ditches in 5% of the area are enabling farmers to grow vegetables and pulses crops during winter. However, hydrological impacts of these structures on water resource availability and irrigation need to be analyzed. The major objectives of the study were to evaluate the recharge characteristics of the study area, to determine spatio-temporal variations in soil and groundwater salinity and to compute water balance for developing water utilization plan for enhancing irrigation intensity. Groundwater levels and salinity were monitored through the observation wells installed at various locations and depths in the study area. Soil samples from different locations at different times were collected to determine the soil salinity (EC), soil pH and soil texture. The infiltration rate at different locations was measured. Water level in the ponds was measured at regular interval to determine the volume of water stored in ponds in different months. Interactions with the farmers were done to collect data and information for estimation of the water requirement and performance evaluation of the structures. Estimation of the reference crop evapotranspiration (ET<sub>o</sub>) and crop water requirement were done using the CROPWAT. The HYDRUS-1D model was calibrated and validated for estimation of the recharge flux from paddy field and the evaluation of recharge characteristics. Water balance method was used to determine recharge from the pond. The maps showing the spatio-temporal variations in soil and groundwater salinity in the study area were generated using the ARCGIS 10.2.2. Statistical analysis was performed to determine the difference in the performance of land shaping interventions with respect to yield of paddy. Irrigation water demand and water availability in the pond were estimated to suggest water utilization plan for enhancing irrigation intensity in the study area. Very low infiltration rate (1.94 cm/day) and higher silt and clay content in the soil suggest that study area is not favourable to



groundwater recharge. The cumulative bottom flux from the paddy field was 13.61 cm. Cumulative surface runoff, cumulative evaporation, and cumulative actual root water uptake were 2.77 cm, 13.19 cm and 11.57 cm, respectively. Percolation from pond in 135 days was 25.1 cm but it did not contribute to groundwater recharge in adjacent areas. Hence, pond in the area can be used for rainwater harvesting and storage not for groundwater recharge. Soil salinity in the area varies with the season and location. Salinity in pre-monsoon period was higher than the post-monsoon period due to leaching of salt during monsoon. Soil salinity was more in the areas which were near to Nimanika creek than the areas which were away from the creek. This suggests that lateral migration of the salt is not much due to low hydraulic conductivity and hydraulic gradient. Soil salinity in the April- 2019 varied from 0.23-0.80, 0.80-0.96, 0.96-1.17, 1.17-1.55, 1.55-2.60 dS/m whereas in September it varied from 0.02-0.28, 0.28-0.36, 0.36-0.44, 0.44-0.61, 0.61-0.96 dS/m only. Groundwater salinity was more in the pre-monsoon period and reduced subsequently during the post-monsoon period. Groundwater salinity was more in the areas close to Nimanika creek and Matlariver which carry a very high saline water. Groundwater salinity in April- 2019, varied from 1.14-3.64, 3.64-4.16, 4.16-4.71, 4.71-5.37, 5.37-6.85 dS/m whereas in September- 2019, it varied from 0.75-1.32, 1.32-1.53, 1.53-1.78, 1.78-2.08, 2.08-3.21 dS/m. There was significant difference between the treatments (Land shaping interventions and farmers practices) and locations, however there was no significant difference among the replications. The treatment 1 (20 % area under pond) was found to be best. Irrigation intensity in the field of 0.2 ha could be increased by 53% if farmers cultivate tomato on entire *Ail* area (64.48 m<sup>2</sup>) Rabi paddy in half of the area of main land (570 m<sup>2</sup>).



## Agricultural Physics



Tridiv Ghosh

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Dr. Pragati Pramanik Maity

### *Title of the Thesis*

### **Effect of porosity and pore size distribution on soil carbon mineralization under conservation agricultural practices**

To study the changes in porosity and pore size distribution of soils and their effects on carbon mineralization under different tillage practices an investigation was carried out in a long term experiment which is in progress since 2010 at the Agricultural Research Farm of ICAR- Indian Agricultural Research Institute. Porosity and pore size distribution were studied using X-ray computed tomography with a system resolution of 60  $\mu\text{m}$ . To evaluate the effect of porosity and pore size distribution on soil carbon mineralization, incubation study was done for 28 days, keeping the moisture content fixed at 60% of water filled pore space (WFPS). Based on the resolution of the instrument, pores were classified into four classes i.e. Class 1: 60-100  $\mu\text{m}$ ; Class 2: 110-500  $\mu\text{m}$ , Class 3: 510-1500  $\mu\text{m}$  and Class 4: >1500  $\mu\text{m}$ . Results showed that total numbers of detected pores in 0-5 cm of soil were the highest in ZT+R, followed by PBB+R and the lowest number of pores was observed in PBB followed by ZT. In CT plots, the number of detected pores was higher by 12.38% than ZT whereas, number of detected pores was higher by 88, 18.28 and 92.74% in PBB+R, PNB+R and ZT+R, respectively. In class 2, residue applied plots had 60.40% more pores than non-residue applied plots. Under CT, 197.12% more pores were found in class 3 than all CA based plots. Sphericity increased, irrespective of treatments as the soil depth increased from 0-5 cm to 5-15 cm. Compactness also increased in all the treatments as the soil depth increased. In 5-15 cm of soil layer, average numbers of pores in all CA based treatments were 153095 which was 3.67% more as compared to CT. In 0-5 cm soil depth, the average TOC content of all the plots was 9.3 g/kg soil. CT had the lowest TOC value of 7.50 g/kg at sowing and it was significantly lower than all other CA treatments. PBB+R had significantly higher TOC than all other treatments. As compared to CT, all the CA plots had on an average 56.6% more mineralization except PNB which had lower cumulative mineralization than all other plots. In 5-15 cm of soil depth, lowest  $C_m$  value was obtained for CT and the trend followed was: PBB+R>PBB>PNB+R>ZT+R>PNB>ZT>CT. As the depth increased from 0-5 to 15-30 cm, the TOC % mineralized decreased by 5.48% in CT whereas, in CA plots average decrease was 5.7%. Mineralization rate was positively and strongly correlated with porosity, MWD, macroporosity and TOC. Porosity was positively correlated with different classes of pores but the correlation was significant with class 2 pores. As the present study was a first attempt to characterize porosity and pore size distribution using X-ray computed tomography, more research emphasis should be given to determine the different categories of pores and their influence on water, air and nutrient movement in soil profile because enhancing the input use efficiency is our prime goal.



## Agricultural Statistics



Bijoy Chanda

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Dr. Arpan Bhowmik

### *Title of the Thesis*

### **Trends efficient minimally changed run sequence in factorial experiments**

Randomization of run sequences in multi factor experiments may result in large number of factor wise level changes which will make the experimentation costly, time-consuming and difficult. Experiments in which it is hard to change the levels of factor(s), use of minimally changed run orders may often be favoured to a random run orders as minimally changed run order will minimize the cost of the experiments as cost is directly proportional to number of factor level changes. Minimally changed run orders are also not unique. Further, due to limited randomization; they are expected to witness the influence of systematic trend. In the present investigation, exhaustive search algorithm has been developed to obtain comprehensive list of minimally changed run order for 22, 23 factorial and half replicate of 23 fractional factorial. It has been observed that except for half replicate of 23 factorials in all cases, there do exist minimally changed run orders which are moderate to highly trend resistant. For 24 factorial, comparisons in terms of trend resistance have been made based on four different minimally changed run order and it has been observed that there do exist moderate trend resistant to nearly trend free run orders. Since, exhaustive search algorithm is very time consuming and is difficult to implement when there exists many minimally changed run orders, therefore, the restricted exhaustive search algorithm was developed and implemented for half replicate of 24 factorial where there exists many minimally changed run orders. It has been observed that, for half replicate of 24 minimally changed run order, out of 13, 824 minimally changed run orders, 768 run orders are nearly trend free. Present investigation also deal with comparisons of minimally changed run orders w.r.t. trend effect with other run orders having higher number of changes for a specific factorial combinations and it have been observed that minimally changed run orders also outperforms many run orders with higher number of factor level changes in terms of trend effects. Thus, minimally changed run orders which are moderate to high trend resistant should be preferable to the experimenters as their adaption leads to cost minimization from experimenter's point of view and also they are moderate to high trend resistant as compared to those run orders which are costly due to large factor wise level changes. The algorithms for the present investigation have been implemented using SAS 9.3.



## Agronomy



Sasmita Tripathy

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Dr. S. L. Meena

### *Title of the Thesis*

## **Integrated phosphorus management for upland direct-seeded rice in North-Eastern Hill region**

A field experiment was conducted at the experimental farm of ICAR Research Complex for NEH Region, Umiam, Meghalaya, India (Latitude 25°41' N; longitude 91°55' E; 950 m ASL; humid-sub tropical climate) during *Kharif* season of 2019 to study the effect of nutrient management practices on productivity and quality of rice along with evaluation of those practices on nutrient uptake of rice along with its economic calculations. The experiment consisted of 8 treatments *viz.* control, 100% of recommended dose of P (RDP), 50% RDP+ 50% through farmyard manure (FYM), 50% RDP + 50% through vermicompost (VC), 50% RDP + 50% through poultry manure (PM), 50% RDP + Phosphorus solubilizing bacteria (PSB) + Arbuscular mycorrhiza fungi (AMF), 75% RDP + PSB + AMF and the last 25% FYM + 25% VC + 25% PM + PSB. The experiment was set up in randomized block design being replicated three times. The soil of the experimental site was red lateritic type and owing to high rainfall and leaching of bases, it showed acidic reaction (pH 4.2) with oxidizable-soil organic carbon (SOC) 1.62%, available-N 256 kg ha<sup>-1</sup>, available-P 6.3 kg ha<sup>-1</sup>, and available-K 354 kg ha<sup>-1</sup>.

The results revealed that all the growth parameters like plant height, dry matter accumulation along with growth indices like leaf area index, crop growth rate, relative growth rate were found to be significantly higher in the 100% organically managed plot comprising of diverse organic nutrient sources 25% FYM + 25% VC + 25% PM + PSB. This was followed by 100% RDP and 75% RDP + PSB + AMF. In a similar way, yield attributes like higher numbers of panicles m<sup>-2</sup>, higher filled grains panicle<sup>-1</sup>, higher spikelet fertility (%) and higher grain (4.97 t ha<sup>-1</sup>) and straw yield (8.85 t ha<sup>-1</sup>) were achieved in organically treated plots. Treatments subjected to organic nutrient sources gave higher grain quality with bold, plump grains having a higher percentage of head rice recovery. Protein content along with protein yields were significantly higher in plots fully supplied with organic manures. Calculation of net returns were the highest for 25% FYM + 25% VC + 25% PM + PSB (Rs.1,01,186 ha<sup>-1</sup>) followed by 100% RDP (Rs. 96,640 ha<sup>-1</sup>) and 75% RDP + PSB + AMF (Rs.93,950 ha<sup>-1</sup>). Available NPK nutrient status in soil was found to be the highest under 25% FYM + 25% VC + 25% PM + PSB closely followed by 100% RDP and 75% RDP+ PSB+ AMF. Microbiological parameters like soil microbial biomass carbon, dehydrogenase activity, acid phosphatase activity and urease activity showed a higher increment under organic treatment. To conclude,



an integrated combination of organic nutrient sources like FYM, VC, PM along with microbial consortia of PSB proved to be the best treatment in terms of growth, yield, soil health and available nutrient status. However, the benefit-cost ratio from chemically treated plot supplied with recommended fertilizer doses was comparatively higher than organically treated plot. But continued use of organic nutrient sources may surpass inorganic treatment in terms of economics and become more profitable with time along with sustenance of soil health and preservation of biological diversity in North-Eastern Hill region.



## Biochemistry



Deepanyeta Goswami

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Dr. Vinutha T.

### *Title of the Thesis*

### **Profiling of nutritional composition and bioactive compounds in chickpea and pigeon pea**

Legumes are known as ‘Poor man’s meat’ because of their high protein content and are considered as staple food for those who cannot afford animal proteins or are vegetarian by choice and thus have the potential for improving nutritional status of the people and combating the Protein Energy Malnutrition (PEM). Chickpea (*Cicer arietinum* L.) and pigeonpea (*Cajanus cajan* L.) are the two most important food legumes in India both in terms of production & consumption. Considering these points, a study to determine the protein digestibility-corrected amino acid score, essential amino acid score (EAAS), quality protein and antioxidant potential of chickpea and pigeonpea genotypes was conducted. Twelve each of *Desi* and *Kabuli* genotypes of chickpea and ten genotypes of pigeonpea were investigated. Crude protein content along with the amino acid composition for each of the chickpea and pigeonpea varieties were studied. The results showed the highest and the lowest protein content of 27.49 g/100g in Pusa 362 and 16.75 g/100g in Pusa 547 belonging to *Desi* chickpea genotypes. Similarly, Pusa 1003 (24.11 g/100g) and Pusa 5023 (14.19 g/100g) of *Kabuli* genotypes of chickpea showed the highest and the lowest protein content, respectively. Among pigeonpea genotypes, TJT 501 (24.46g/100g) and Bahar (14.48 g/100g) were found to have the highest and the lowest protein content, respectively. The results of amino acid composition showed balanced amino acid score and % daily value (DV) for all the essential amino acids with respect to FAO pattern (1991) except for methionine and cysteine in chickpea and pigeonpea genotypes. The amino acid profile of pigeonpea and chickpea showed that they can contribute 45%–100% DV for a 60 kg adult (based on per capita consumption of pulses) of various essential amino acids except methionine. Thus, our results clearly showed that, the amount of essential amino acid content can be met with 100% DV with the daily intake of 100 g dhal/whole seeds of chickpea and pigeonpea except for methionine. The PDCAAS (Protein Digestibility Corrected Amino Acid Score) reflects an attempt to measure the overall quality of a protein as the product of the digestibility of the protein and its amino acid score. Among chickpea genotypes, *Desi* types showed the highest protein digestibility of 86% (Pusa 256) with PDCAAS values of > 0.5 as compared to *Kabuli* types. The pigeonpea genotypes were found to have a PDCAAS (%) in the range of 39.00% (BSMR 736) to 82.84 % (ICP 87). Since the protein content of all the varieties of chickpea and pigeonpea analyzed in the present study showed higher protein content between 14 % to 23 %, which is higher than that in



egg (13 %), and milk (3.4%), suggesting that, high protein chickpea and pigeonpea can be of alternative to egg and milk to meet 100% DV of all the essential amino acids except methionine. Pulses are useful source of bioactive polyphenols, carotenoids and tocopherols which may provide additional health benefits through their antioxidant activity. In this regard, the chickpea and pigeonpea genotypes were analyzed for antioxidant activity through DPPH and FRAP assays. We found significantly higher antioxidant activity in pigeonpea (58.70% to 92.41%) genotypes as compared to chickpea genotypes (13.56% to 29.95%). Effect of cooking (boiling) and canning on protein digestibility and antioxidant potential was carried out on two contrasting genotypes of chickpea and pigeonpea for total protein content. PDCAAS (%) was found to be higher in 'high' protein containing lines than 'low' protein containing lines in case of chickpea. However, no significant variation in PDCAAS (%) was found between 'low' and 'high' protein pigeonpea genotypes. Both PDCAAS and antioxidant activity was found to increase in chickpea and pigeonpea genotypes after cooking and canning. The generated information will thus help in identifying promising chickpea and pigeonpea genotypes with high nutritional quality and aid in future breeding programmes.



## Bioinformatics



Pranita Das

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Dr. Monender Grover

### *Title of the Thesis*

### **Study on differential expression of coding and non-coding RNAs and post-translational modifications in wheat rust resistance**

Bread wheat ( $2n=42$ ), belonging to the family Poaceae, is one of the most important food crops on the global scenario and known as “the King of Cereals”. It is extensively cultivated for its seeds as a staple food for human as well as for livestock feed across the world. Due to global warming and climate change, the most emerging problems are biotic and abiotic stresses. Stripe rust of wheat, caused by *Puccinia striiformis f. sp. tritici* (*Pst*) is one of the largest biotic stress factor among them, limiting wheat production worldwide. Despite the efficiency of fungicide treatments, genetic resistance is considered to be the most economical and environmentally friendly way to control the disease. The present study is based on the paired-end reads of control and *Pst* treated leaf samples of two near isogenic lines of wheat generated using HiSEQ 4000. The study aims at identification of differentially genes in response to wheat stripe rust between the susceptible line PBW343 and resistant line FLW29 and their transcriptional profiling, identification and characterizations of lncRNAs in stress conditions, transcription factors, pathways etc and lastly the prediction of PTM sites in the translated DEGs. A total of 164095 transcripts, 409 differential expressed genes, 1503 transcriptional factors, and several protein domains and families were identified from reference based assembly. Myeloblastosis related proteins (MYB), WRKY domain, Basic helix-loop-helix (bHLHs) found in this study are reported to be associated with plant tolerance against biotic stress. A total of 6807 putative lncRNAs have been identified under three different time points i.e. 12 hpi, 48 hpi and 72 hpi out of which only 13 are differentially expressed. These are related to the pathogenesis-related protein 1 and disease resistance protein RGA2. These findings should facilitate the development of effective strategies for the breeding of resistant wheat varieties to obtain a better control of stripe rust. Lastly, the study on PTM has been carried out on the protein coded DEGs in sequence level and palmitoylation sites has been found more in case of down-regulated genes compared to the up-regulated ones indicating palmitoylation may play some important role in disease resistance mechanism.



## Computer Application



Tamal Kundu

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Dr. Mukesh Kumar

### *Title of the Thesis*

### **Decision support system for biomechanical evaluation of agricultural activities with Human Physical Drudgery Index (HPDI)**

As we know that the use of mobile phones or we can say the smart phones is increasing at a greater pace. This is because the smart phones are getting cheaper day by day and the cost of using internet is also getting cheaper. Standing in such a favorable situation the use of smart phones in developing the agriculture is no doubt be a great decision. Following this pathway, different mobile applications are being developed by various research institutes for helping the farmers in their cultivation practices. These mobile applications are used by farmers belongs to any age groups. In my research work, a mobile application named “HPDI Ergon” has been developed with the aim to make the farmers comfortable in their working environment. It is a fact that the farmers and the agricultural workers always face difficulty and stress in their working environment. It is because that there is no improved tools or farming equipments available to them. As a result, they have to totally depend on their muscular force and cardiac capability. These causes the farmers and the agricultural workers to undergo physical and mental stress. This type of muscular force intensive work needs huge energy which affects their cardiac health and as a result, they suffer from cardio logical stress. Besides these the drudgery experienced by them in their daily work life causes to lowering their working efficiency. In this respect, the app named HPDI Ergon is developed to remove the drudgery involved in the work. In this app, farmers are assessed based on different physical parameters and conclusion is drawn regarding their efficiency and constraints. The app is developed using Android Studio and Java programming language. In the app, there will be registration for both the users and the farmers under the users. Individual registered farmers are selected to undergo different ergonomic analysis and drudgery analysis. The data generated by different analysis is stored in the database which is implemented using SQLite database. After the complete analysis of a farmer, all the results of all the parameters is shown on the screen for drawing better conclusion by the user or researchers. Based on the results of all the ergonomic analysis and drudgery analysis using HPDI conclusion is drawn regarding whether there is any need of changing or improving the working condition or not. Accordingly, different suggestions and various improved tools are provided to the farmers for reducing their both physiological stress and drudgery in their working environment and consequently making them more efficient in their working environment.



## Entomology



Adrish Dey

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Dr. Pathour R. Shashank

### *Title of the Thesis*

### **Systematic studies on Lepidopteran stem borers of Gramineous crops with emphasis on molecular diversity of *Sesamia inferens* (Walker)**

The larvae of certain species of Crambidae, Pyralidae, Noctuidae and also Tortricidae feed by boring into the grasses of family Poaceae and produce a characteristic damage symptom called 'dead heart'. This polyphyletic group of insects are commonly known as 'stem borers'. The stem borers are economically important because they affect members of the family Poaceae which includes economically important crops like major cereals and sugarcane. In the present study, 13 species of stem borers have been re-described with current valid names, synonyms, authors, type information, distribution, and host plants. The specimens were identified from characters of the genitalia such as shape of uncus, gnathos, valva, projections of the costa or tegumen, and shape of aedeagus. High quality photographs are provided for each species which included the male and female habitus, and the genitalia of both sexes. The molecular diversity of *Sesamia inferens* studied from four different Agro-ecological zones of India. The mitochondrial cytochrome oxidase subunit I gene region were sequenced for twenty-nine specimens. The analysis showed that among the Indian populations, a low level of genetic variability and so no clustering was observed with regards to geographic position. It can be inferred from the low genetic variability within the populations. The neutrality tests conducted for the sequences of *S. inferens* showed no evidence of population expansion. The  $F_{ST}$  values obtained suggested that the populations are not completely isolated and there is absence of significant variations among populations analysed.



## Fruit Science



Vishal Balasaheb Mhetre

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### *Title of the Thesis*

### **Evaluation of new growth regulators for quality grape production**

The present study was conducted on five-years-old grapevines of 'Flame Seedless' and 'Beauty Seedless' at the experimental field of the Division of Fruits and Horticultural Technology, ICAR-Indian Agricultural Research Institute, New Delhi. Nine treatments of plant bioregulators, viz. abscisic acid (ABA 200 ppm & 400 ppm), benzothiadiazole (BTH) (0.3 mM & 0.6 mM), ethephon (200 ppm & 400 ppm), prohexadione-calcium (Pro-Ca) (200 ppm & 400 ppm), including a control were investigated using standard methodologies for their effect on grapevine growth, physiological and biochemical parameters of vines of grape cv. Beauty Seedless and cv. Flame Seedless. The study was conducted in a randomized block design and the data obtained were analysed using SAS software. The RNA-Seq analysis was carried-out for three samples of berries of grapevine cv. Flame Seedless treated with ABA 400 ppm, ethephon 400 ppm along with control. The highest leaf net photosynthesis rate ('PN') and stomatal conductance ('gs') were recorded with Pro-Ca 400 ppm treatment while the least 'PN' was recorded with ABA 400 ppm and 'gs' with ethephon 400 ppm in Beauty Seedless and Flame Seedless cultivars, respectively. Treatment of ethephon 400 ppm resulted in the maximum berry TSS in cv. Flame Seedless (20.77° Brix) and Beauty Seedless (20.03° Brix). The highest ascorbic acid content (22.89 mg 100 g<sup>-1</sup>, 26.24 mg 100 ml<sup>-1</sup>) was obtained from berries treated with ethephon 400 ppm in Beauty Seedless and 200 ppm in Flame Seedless, respectively. Uniformly coloured berries due to higher accumulation of monomeric anthocyanins were observed with application of ethephon 400 ppm in Beauty Seedless (579.62 C<sub>3</sub>GE mg l<sup>-1</sup>) and Flame Seedless (570.56 C<sub>3</sub>GE mg l<sup>-1</sup>) followed by ABA 400 ppm (562.10 and 549.40 C<sub>3</sub>GE mg l<sup>-1</sup>, respectively). Also, both ethephon 400 ppm and ABA 400 ppm treatments produced maximum total phenolics content (153.60 and 150.99 GAE mg 100 ml<sup>-1</sup>), respectively and total flavonoids content (62.73 and 61.77 QE mg 100 g<sup>-1</sup>, respectively) in Beauty Seedless cultivar as well as total phenolics (157.19 and 155.13 GAE mg 100 ml<sup>-1</sup>, respectively) and total flavonoids (65.67 and 64.23 QE mg 100 g<sup>-1</sup>, respectively) in Flame Seedless cultivar. Ethephon 400 ppm and ABA 400 ppm treatments resulted in the maximum antioxidant activity in cv. Flame Seedless (8.63 and 8.35 TE μmol g<sup>-1</sup>, respectively) and Beauty Seedless (8.30 and 7.98 TE μmol g<sup>-1</sup>, respectively). RNA-seq analysis revealed several DEGs associated with anthocyanin biosynthesis pathway controlling berry colour were found to be highly expressed, such as UFGT (VIT\_16s0039g02230) and GST (VIT\_04s0079g00690). These results indicated that exogenous application of plant bio-regulators significantly influenced the



several physio-biochemical parameters. Both ethephon (400 ppm) and ABA (400 ppm) treatments were found to be promising for improving the quality of Beauty Seedless and Flame Seedless cultivars under Delhi conditions. It was also revealed that the other new plant bio-regulators (BTH and Pro-Ca) did not prove better over ethephon and ABA, although both were found little superior over control for most of the berry quality parameters.



## Genetics and Plant Breeding



Nunavath Aswini

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Dr. V. S. Hegde

### *Title of the Thesis*

### **Characterization of a recombinant inbred line population for pod and seed traits and validation of markers linked to flowering time genes in chickpea (*Cicer arietinum* L.)**

Breeding for early flowering is an important strategy to increase productivity of chickpea and stability of its production in environments characterized by terminal drought and heat stresses. The present investigation was aimed at: characterization of a recombinant inbred lines (RIL) population of chickpea for flowering time, pod & seed traits; identification of early flowering and high yielding RIL(s); and validation of molecular markers linked to time of flowering genes. A set of 250 RILs derived from Pusa 362 (Late) x BGD 132 (Early) were studied for various genetic parameters in rabi 2018-19 and 2019-20. Analysis of variance showed that there was significant difference among parents and RILs included in the study for all the agronomic characters and seed yield in both the seasons. Large genetic variation was observed for flowering time, pod and seed traits during the two seasons and therefore there is a scope for maximizing genetic gain from selection in the population. A significant amount of transgressive segregation was present both for high and low parents for plant height, all the pod and seed traits and seed yield per plant in both the seasons. However, time flowering was the only trait that did not show any transgressive segregation for low or early flowering parent in the two seasons. The heritability estimates were high, and it ranged from 0.96 to 0.99 for different traits studied in both the seasons. High significant positive correlations observed among pods/plant, seeds/plant seed yield/plant in both the seasons. Based on the phenotyping data of 2018-19, ten each of early and late flowering high yielding RILs were selected and evaluated them in a randomized block design with 3 replications along with 2 parents and 2 controls to identify a RIL(s) having the best combination of earliness and high seed yield. A ToFRIL 214 that matured in 125 days produced seed yield of 2992.4 kg/ha with per day productivity of 23.3 kg/ha which is comparable to the high yielding late parent Pusa 362 (3253.4 kg/ha; 23.8 kg/ha/day) and earliness of early parent. Seed yield showed strong positive association with per day productivity. Selection for medium duration chickpea with moderate height and seed size is expected to result in high yielding variety having higher per day productivity. Bulked segregant analysis was carried out to validate the markers reported to be linked to flowering time in chickpea. Markers selected from both chickpea and *Arabidopsis* were used for validation. One SSR marker, TA64, found to be linked with early flowering trait that can be used for marker assisted selection (MAS). Graphical genotyping technique suggested a similar pattern of amplification in chickpea and *Arabidopsis*.



## Microbiology



Aditi

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Dr. K. Annapurna

### *Title of the Thesis*

### **Symbiotic effectiveness of inoculation with *Bradyrhizobium* sp. on soybean genotypes under different N levels**

Understanding how plants respond to nitrogen in their environment is crucial for determining how they use it and how it affects other processes related to plant growth and development. Under N limitation, the activity and affinity of uptake systems is increased in roots, and lateral root formation is regulated to adapt to low N levels and scavenge from soil. Legumes associate with rhizobia and develop nitrogen fixing nodules and this association is tightly regulated by external N levels. Nodulation relies on two closely coordinated processes: the infection process, including the colonization of the bacteria inside the host plant, and the organogenic process, in which the nodule tissue is formed to accommodate the bacteria. The present investigation is focused towards gaining in-depth understanding of the role of nitrate application and its impact on the symbiotic nitrogen fixation (SNF) process in soybean-*Bradyrhizobial* interaction. Six soybean genotypes viz: PUSA-12, SL-958, PUSA-9814, SL-688, PUSA- 9712 and PS- 1347 were initially screened hydroponically for a comparative analysis of their responses to different N-levels ranging from low (0.1 mM) to medium (4 mM) and high (9.5 mM). This was followed by their evaluation in terms of their symbiotic potential with four slow (KAS-1, IND II, PV 3.4, PV 3.24) and two fast growing root nodulating bacteria (DS-1, LSR-8). Genotype PUSA- 9712 showed highest overall positive response under hydroponic conditions at different nitrogen levels. Among the strains, the slow growing *Bradyrhizobium yuanmingense* strain KAS-1 showed an overall positive effect across the genotypes. The study of symbiotic effectiveness of strain KAS-1 and genotype PUSA- 9712 was undertaken at the molecular level, in terms of gene expression in the presence of 4 mM nitrate. Nitrate was added at two-time intervals; one as basal dose along with the *B. yuanmingense* (KAS-1) inoculation and the other 15 days after inoculation. Reduction in nodule number at the basal N treatment indicates that nodule infection might have been severely affected. N application after 15 days of plant growth and inoculation did not impact negatively, as infection and pre-initiation may have occurred during the first 15 days. This finding was found to be correlated with *Enod-40A* gene expression which is known to be involved in nodule initiation and its development is significantly affected by N treatment. *Enod-40A* expression at 18<sup>th</sup> DAI (days after inoculation) showed a reduction of 49.4% (in samples receiving basal N) and 78.3% (in samples receiving N on 15<sup>th</sup> DAI), as compared to the values recorded at 7<sup>th</sup> DAI with basal N application, suggesting the short-term inhibitory effect of



N application on the SNF physiology. A similar trend with nodule dry weight (NDW) was also recorded with reduction of 92.8% and 17.5% in recorded in N as basal and N (18 DAI) application. However, ARA decreased by 47.9% and 43.7, respectively in plants harvested at 35 DAI after basal or 15 days application (at 18 DAI). This suggests that the soybean variety 9712 and *B. yuanmingense* KAS-1 partnership is extremely sensitive as regards rhizobial infection but resistant in terms of nodule development and nitrogen fixation, in response to time of external N application.



## Molecular Biology and Biotechnology



Priyanka Kumari

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### *Title of the Thesis*

### **Understanding self and non-self root-root interaction on root system architecture and expression of putative nitrate transceptor gene in bread wheat under nitrogen limited condition**

One of the major reasons of roots to modulate their architecture is due to the recognition of kin (self) and non-kin (non-self) root growing together in one soil volume. Weed appears as non-kin plants to crop plants in agricultural field. The wheat varieties bred during green revolution are less competitive, and demands high inputs (irrigation and fertilizers). The high application of nitrogenous fertilizers led to the increased weed infestation, and consequently *Phalaris minor* evolved as one of the major weeds in rice-wheat growing tracts. *P. minor* causes yield reduction by 20-30% by depleting as much as 28 kg N/ha from soil. Ironically, the nitrogen use efficiency (NUE) of wheat is abysmally low, i.e., 30-35% which means rest of the 65-70% N applied is lost to environment in various forms. Therefore, enhancing nitrogen use efficiency (NUE) traits of wheat has become a major goal of wheat improvement programme. In Arabidopsis, *AtNRT1.1* has been reported as nitrate transceptor, i.e., functions as both receptor and transporter. Therefore, considering its transceptor activity, it is hypothesized that its ortholog may play some role in lateral root elongation/differentiation in wheat in the presence of one of its major weeds, i.e., *P. minor*. Here in this study, self and non-self root-root interaction on root system architecture and expression of putative nitrate transceptor gene in bread wheat (*Triticum aestivum* L.) under nitrogen limited condition are reported.

*P. minor* has profound effect on root system architecture, biomass and nitrogen uptake ability of wheat in nitrogen limited condition. Root biomass (length, fresh and dry weight) of wheat invariably increased under N-starvation condition which further increased when *P. minor* is present in the same condition. To compensate the increased growth of root system, the corresponding parameters of shoot have been found to be reduced. The growth of root was further corroborated by changes in its architecture under these conditions. Both length-based root traits, e.g., TRS, MRP and LRS, as well as numbers-based traits, e.g., first and second order lateral root numbers have been found to be increased by the presence of *P. minor*, specially under N-starved condition. *AtNRT1.1* (*Atlg12110*) sequence is first used as seed sequence to identify the orthologs in wheat. Thirteen orthologs have been identified in wheat reference genomes that are located on 1<sup>st</sup>, 2<sup>nd</sup>, 4<sup>th</sup>, 5<sup>th</sup> and 7<sup>th</sup> chromosomes of all three sub-genomes. Rice nitrate transceptor (NRT1.1B) was used to identify the closest sequence (s) among 13 identified from Arabidopsis that resulted into 4 putative nitrate transceptor of wheat (*TaNPF6.4*), located on 4<sup>th</sup>, 5<sup>th</sup> and 7<sup>th</sup> chromosome. These sequences



were also reported to be closest orthologs of *AtNRT1.1*. The homeolog specific expression of *TaNRT1.1* (*TaNPF6.4*) in wheat genotype K9107 reveals that sub-genome A is highest expressing homeolog in both seminal and lateral roots. In order to understand the mechanism of different expression pattern of these four homeologs under different conditions in the present study, 2Kb upstream sequences of all three homeologs were cloned and analysed bioinformatically. The upstream sequences of homeologs revealed variation in number of CREs.



## Plant Pathology



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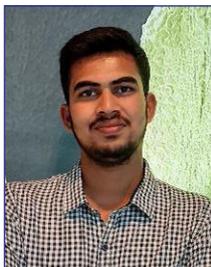
### *Title of the Thesis*

### **Pathogenic and genetic variation among *Fusarium* spp./isolates causing head scab of wheat and identification of resistant sources**

*Fusarium* head blight (FHB) or head scab of wheat caused by *Fusarium* spp., is a global concern as recent outbreaks reported in Canada, Europe, Asia, Australia and South America. Presently, FHB is a minor disease in India but can cause significant yield loss if rain occurs during mid anthesis in the foot hills of Punjab, Himachal Pradesh, Uttarakhand and hilly areas in Tamil Nadu. Among 110 head scab infected wheat ear heads collected from Dalang Maidan, Lahaul valley of Himachal Pradesh and Wellington, Nilgiris hills, Tamil Nadu, dominance of *F. graminearum* was observed. Twenty nine *Fusarium* isolates were identified as *F. graminearum* based on morphological, cultural and ITS based approaches. Pathogenic variation among 29 *F. graminearum* isolates was observed on wheat varieties (UP 2338, PBW 343, Sonalika, HD 2967, HD 3086, HD 29, MACS 5049, HS 645, VL 1013). After 7 and 14 days of inoculation, isolates Fg-W10 and Fg-W24 were found highly pathogenic while Fg-W7 and Fg-W26 were found least pathogenic. Out of 23 SSR markers designed using whole genome sequence of *F. graminearum* PH-1 strain, 21 SSRs amplified *F. graminearum* isolates. Cluster analysis separated the isolates into two main groups. Group A consisting two isolates one from Wellington (Fg-W27) and another from Lahual Spiti (Fg-L2). Group B contained all other 27 isolates. This study has shown that there is considerable pathogenic and genetic variability among *F. graminearum* isolates obtained from infected wheat earheads from different geographic regions of India. One hundred sixty four wheat genotypes were screened for FHB resistance under artificially inoculated conditions. On the basis of categorization of varieties based on AUDPC values, only three wheat genotypes were grouped between 101-200 group (HD3377, NIDW1149 (durum) and HI 1612). In rest of genotypes, AUDPC values were more than 200 while maximum AUDPC value of 900 was obtained in highly susceptible variety, Sonalika. Only four genotypes viz., HI 1612, MACS 6747, UP 3016 and MACS 4059 (durum) were having rAUDPC values less than 25 % of susceptible variety, Sonalika. Since most of popular cultivars grown in India are susceptible to head scab, so there is a need to screen more indigenous and exotic wheat lines for incorporating head scab resistance in popular wheat cultivars.



## Plant Physiology



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### *Title of the Thesis*

### **Investigating the role of DUF1645 proteins in abiotic stress tolerance and grain yield in rice**

Rice is the world's most important staple food and will continue to be so in the coming decades. Climate change is adversely affecting rice production and developing climate-smart rice is the need of hour. Identification of stress-responsive genes is the first step towards developing climate-smart crops. However, a significant number of proteins in the Pfam database lack annotation. Our study attempts to characterize the Domain of Unknown Function (DUF) 1645 and suggests the great need for annotation of hypothetical proteins to utilize in crop improvement. We identified fifteen novel DUF1645 protein-coding genes in the rice genome. Interestingly, the DUF1645 family of proteins is endemic to plants and highly conserved motifs in these proteins suggest their crucial role in plants. It has been noticed that DUF1645 gene promoters are enriched with binding sites for stress responsive transcription factors and also cis elements related to hormonal regulation. Expression analysis suggested the role of these proteins in multiple stress tolerance, genes were significantly up-regulated in plants subjected to cold, salinity and osmotic stress. These proteins have a highly disordered structure, suggesting their enhanced propensity to interact with multitude of protein or DNA. We noted a significant number of highly conserved MAP kinase binding sites across the family, their co-expression with transcription factors and their localization in the nucleus. Our results suggested that DUF1645 may be a novel DNA binding domain of transcription factors. Further, we used remote homology search tools to find distant relatives of DUF1645 in protein databases. We found that DUF1645 is distantly similar to various DNA binding folds. However, to prove this hypothesis we need to further look on the mechanistic insights about DUF1645 proteins and their interaction partners. Our study along with previous studies indicate strongly the importance of phosphorylation and interaction of DUF1645 proteins with MAP kinase for their functioning, leaving us to speculate their involvement in MAP kinase cascade regulating stress response and grain length in rice.



## Post Harvest Technology



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Dr. R. R. Sharma

### *Title of the Thesis*

### **Postharvest disease management and shelf life extension of nectarine**

Nectarine is an important emerging stone fruit due to its attractive appearance, pleasing flavor and presence of secondary metabolites that increase the nutritional value of the fruit (e.g., vitamins and various phenolics). However, due to its typical climacteric ripening pattern, nectarine fruit exhibits a sharp senescence in postharvest period followed by quality deterioration and its post harvest life is limited to 3-4 days at ambient storage. Apart from quality deterioration, nectarines are highly prone to postharvest diseases during storage due to succulent nature and high juice content. The major postharvest diseases of nectarines are brown rot caused by *Monilinia fructicola*, Rhizopus rot caused by *Rhizopus stolonifer*, Pencillium rot caused by *Pencillium expansum* and gray mold caused by *Botrytis cinerea*. To address this problem, we carried out eco-friendly approach of edible coatings and plant extracts to enhance the life and reducing the spoilage from postharvest pathogens. Three objectives were proposed under this study, in the first objective *in vitro* efficacy of aqueous and methanolic plant extracts (neem, ocimum, marigold, eucalyptus, moringa and mixture of all the plant extracts -MPE) were tested against *Rhizopus stolonifer* and *Pencillium expansum* at different concentrations (50,100,200 and 400 $\mu$ l). *In vivo* studies on 'Snow Queen' nectarines were carried out under 2<sup>nd</sup> objective by using best concentration (200  $\mu$ l) of plant extract obtained under *in vitro* condition by two methods , method I (Plant extracts followed by pathogen), and method II (Pathogen followed by plant extracts were applied in the hole).In the 3<sup>rd</sup> objective, shelf life and quality attributes of nectarines treated with plant extracts and edible coatings such as mixed plant extracts (MPE), chitosan (CH), carboxy methyl cellulose (CMC), CH+CMC, CH+MPE, CMC+MPE, CH+CMC+MPE were evaluated under supermarket condition and low temperature condition over control fruits (water dip fruits as control). Our results reported that at 200  $\mu$ l concentration methanolic extract of mixed plant extracts followed by moringa leaf extract exhibited higher inhibition (76% ,73%) of *R. stolonifer* and *P. expansum* compared to other plant leaf extracts and concentrations. Under *in vivo* studies, Method I showed good results with respect to decay area (21.3 % , 14.92%), decay (21.31% , 14.94%) and lesion diameter (12.5%, 7.5%) better over method II in *R. stolonifer* and *P. expansum*, respectively. Nectarines stored at  $1\pm 1^{\circ}\text{C}$  retained their edible quality (8.10 ) upto 25 days in layer-by-layer coating CH+CMC+MPE fruits, whereas nectarines stored under  $18\pm 2^{\circ}\text{C}$  had their shelf life upto 16 days and layer-by-layer coated fruits exhibited highest edible quality (7.72) as compared to other treatments and control (6.45).



## Seed Science & Technology



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Dr. S. K. Chakrabarty

### *Title of the Thesis*

### **An assay on phenol colour reaction in seed of rice (*Oryza sativa* L.)**

In order to address the problem of non-uniformity of phenol colour reaction to seeds of paddy varieties, to help variety identification and to understand biochemical basis of this character an investigation was made. An experiment was conducted to evaluate sixty rice varieties for phenol color reaction (rapid chemical test) during 2019-20. A standardization of phenol colour test was done to classify paddy varieties in five distinct colour groups. Difference in phenol colour in seeds within a plant *i.e.* inter-panicle and intra-panicle in a variety was studied revealing some intra-panicle variation than inter-panicle. The phenol content in different panicles in a plant and seeds at different portions of a panicle in a variety indicated non-significant differences. Further, polyphenol oxidase activity in the seed coat governed by tyrosinase enzyme and other substrates like pyro-catechol and L-DOPA were studied. These substrate's activity and phenol content along with phenol color *per cent* have shown higher values in old seed lots of varieties (except a few varieties) than that in fresh seed lots. A distinct difference in phenol content, L-DOPA, tyrosinase and pyrocatechol activity was found among the varieties belonging to different phenol colour groups. The results of the study indicated that rice varieties showed a very high level of phenol colour reaction to its seeds corresponding to the phenol content and poly phenol oxidase activity. This information would be useful in clearly characterizing a rice variety for phenol colour reaction and determine its varietal admixture.



## Soil Science & Agricultural Chemistry



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Dr. Sarvendra Kumar

### *Title of the Thesis*

### **Soil nitrogen transformation in pigeon pea and cotton under conservation agriculture**

In the present investigation, microbial functions, soil nitrogen release and distribution of nitrogen fractions in pigeon pea (*Cajanus cajan L.*) and cotton (*Gossypium hirsutum L.*) crops under conservation agriculture (CA) was studied. To achieve these objectives, soil samples were collected from three depths (0-5, 5-15 and 15-30 cm) in pigeon pea and cotton crops under pigeon pea-wheat and cotton-wheat systems from existing long-term CA (since 2010) experiments at ICAR-Indian Agricultural Research Institute, New Delhi. The samples were collected from seven treatments *viz.* conventional tillage (CT), permanent narrow bed (PNB), PNB with residues of previous crop (PNB+R), permanent broad bed (PBB), PBB with residues of previous crop (PBB+R), flat bed (FB) and FB with residues of previous crop (FB+R) at four physiological crop growth stage of pigeon pea and cotton. The soil samples were collected at pre-flowering, flowering, pod filling and harvesting stages of pigeon pea. Whereas, at pre-flowering, flowering, boll formation and harvesting stages in cotton during *kharif* season of 2019-20. The samples were analysed for dehydrogenase activity (DHA), arginine deaminase activity (ADA), nitrogen mineralization potential (PMN), ammonium (NH<sub>4</sub>-N) and nitrate nitrogen (NO<sub>3</sub>-N). The sample collected at harvesting stage (0-15 cm soil depth) had been also analysed for different fraction of nitrogen. The result indicated that crop residue retention increased DHA, ADA and PMN over without residue retention and CT treatments irrespective of crop growth stages and depth of soil. Among treatments, PBB+R recorded highest values of studied parameters in both the crops at different crop growth stage and soil depth. In 0-5 cm of soil depth of pigeon pea, highest DHA was noticed in PBB+R plots (14.1 µg TPF g<sup>-1</sup> soil h<sup>-1</sup>) followed by FB+R > PNB+R > FB > PBB > PNB > CT plots at pod filling stage. The ADA in pigeon pea soil increased with the advancement of crop growth stages, quantitatively it increased by 20, 60 and 39% from pre-flowering to pod filling stage in 0-5, 5-15 and 15-30 cm soil depth respectively. Most importantly, ADA responded N application and decreased after N fertilizer application *i.e.* from pre-flowering to flowering stage in cotton. In both the crops maximum NH<sub>4</sub>-N was observed in flowering stage followed by pod filling/ boll formation > pre-flowering > harvest stage up to 15 cm soil depth. In pigeon pea, mean NO<sub>3</sub>-N concentration decreased from pre-flowering (18.1 mg g<sup>-1</sup>) to flowering stage (15.7 mg g<sup>-1</sup>), and increased at the pod filling stage (21.2 mg g<sup>-1</sup>) and substantially decreased at harvesting stage (7.95 mg g<sup>-1</sup>) in 0-5 cm soil depth. Adoption of CA practices significantly increased hydrolyzable amino-N, hydrolyzable amino acid-N and total-N fractions in both the



crops. In nutshell, zero tillage with crop residues retention especially PBB+R plots increased DHA, ADA, PMN and total-N of soil. The increased activity of N cycling enzymes reflected increased  $\text{NH}_4\text{-N}$  &  $\text{NO}_3\text{-N}$  concentration and decreased unidentified organic fraction of N in soil. Thus, PBB+R practice may be a viable option for enhancing N content and soil health status especially in semi-arid and arid conditions.



## Vegetable Science



Rakshitha K. N.

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Dr. Shrawan Singh

### *Title of the Thesis*

### **Association mapping of heat stress related curding traits in Indian cauliflower**

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is a thermo-sensitive crop for the development of its economic part 'the curd'. Based on temperature requirement for curd induction and development, there are four prevalent groups in cauliflower in India. The genetic investigation so far showed its quantitative inheritance but the present investigation was aimed to assess the association of curding traits with temperature stress factor and assess genetic diversity and association using SSR markers and genotyping by sequencing (GBS). To investigate this, the present study was undertaken at two locations IARI, New Delhi and ICAR RC for NEH Region, Barapani using 91 genotypes as common for both locations during 2019- 20. The trial was done in complete randomized block design with three replications at each location, however, the sowing time was delayed by two months at Barapani location to escape heavy rainfall. Standard crop management practices were followed at both locations and eight curd related traits were recorded from each genotype and analysed using statistical software. For molecular diversity and GBS analysis, the genomic DNA was extracted from 96 genotypes (including orange cauliflower, two of each broccoli and tropical cabbage) and analysed using 90 SSR markers. Of them, clear 59 were polymorphic. The observation on agro-morphological traits revealed high phenotypic coefficient of variation and genotypic coefficient of variation (20%) for net curd weight (g), marketable curd weight, and gross plant weight in both the location. High heritability is observed for days to 50% curd initiation and days to 50% curd harvest, marketable curd weight and net curd weight. Genotypic correlation coefficients indicate that most of the traits showed positive and highly significant correlation. Under both environment conditions it was found that Kt-25, Kt-22, BR- 2 and Pusa Meghna for Delhi condition, CC-14, DC-310-22, DC-135-199, Kt-20 and Kt-16 are the best suitable for Barapani condition. Agro-morphological traits based clusters showed clear groups and matching with traditional groups of maturity except few interchanges in early and mid-early groups. Molecular diversity analysis revealed significant diversity among the cauliflower genotypes and the polymorphic information content (PIC) values was highest for BoGMS0742 (0.68) followed by OI10D03 and BoGMS0162(0.51) while its mean value was 0.18. The STRUCTURE analysis could show four sub-populations with low to high admixture. The GBS analysis using the Illumina sequencing platform for 96 genotypes for assessing diversity and association mapping showed average of 3.146 million reads per plant sample. Total 35831 SNPs were detected from all the nine chromosomes and the highest from chromosome



3. Three QTLs were detected for marketable curd weight (MCW-1) on chromosome 4, curd width (CW\_1) on chromosome 5 and number of leaves per plant (NL\_P\_1) on chromosome 9 located within detected QTL regions. The genomic information on curding traits in cauliflower particularly Indian type will facilitate designing robust molecular for use in breeding varieties with adaptive plasticity for temperature related curding traits to meet the long-time demand of growers.



## Water Science and Technology



Ankit

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Dr. D. S. Gurjar

### *Title of the Thesis*

### **Standardization of sensor-based wastewater irrigation scheduling for chrysanthemum (*Chrysanthemum morifolium* Ramat.)**

A study was conducted to standardize the FDR sensor based wastewater irrigation scheduling for chrysanthemum (*Chrysanthemum morifolium* Ramat.) at Water Technology Centre, ICAR-Indian Agricultural Research Institute, New Delhi during the year 2019-2020. Standardization of irrigation scheduling was done by assessing the impact of wastewater irrigations, scheduled at different MAD, on soil health, flower export grading/quality standards and productivity of chrysanthemum using an approach of maximum allowable depletion (MAD) of available soil moisture. Hence, an experiment was laid-out in a randomized block design with four replication and six treatments namely, T1: Groundwater irrigation scheduled at 25% MAD, T2: Groundwater irrigation scheduled at 50% MAD, T3: Groundwater irrigation scheduled at 75% MAD, T4: Wastewater irrigation scheduled at 25% MAD, T5: Wastewater irrigation scheduled at 50% MAD, T6: Wastewater irrigation scheduled at 75% MAD, in a open field condition. Results of the study revealed that wastewater irrigations scheduled at 50% MAD has significantly improve the soil health parameters (EC, pH, OC, NPK and micronutrients) as compared to groundwater irrigation. Flower quality and yield in terms of flower turgidity, flower size, vase life (20.50 days), flowers yield (6.12 t/ha) and water use efficiency (10.41 kg/ha-mm) were found enhanced under wastewater irrigations scheduled at 50% MAD. The highest economics in-terms of benefit cost ratio (3.35) were also occurred under wastewater irrigations scheduled at 50% MAD. Hence, a standard value for wastewater irrigation scheduling for chrysanthemum was considered as 50% MAD. Therefore, the present study concluded that irrigation scheduling at 50% MAD may enhance the quality and productivity of chrysanthemum without an adverse impacts on soil health for short-term application of wastewater. However, a long-term application of wastewater irrigation at 50% MAD needs to be monitored.



**Ph.D.**  
**Thesis Abstracts**





## Agricultural Chemicals



Dinesh Kumar

Name of the Student : Dinesh Kumar  
Roll No. : 10727  
Chairperson : Dr. Shakil N. A.



Dr. Shakil N. A.

### Title of the Thesis

## Synthesis of ferrocenylchalcones and their evaluation against plant pathogenic fungi and root knot nematode

Chalcones and their derivatives are conventionally known to possess biological activity due to their highly reactive unsaturated carbonyl group and have been a subject of interest for the scientists all over the world. However, poor solubility is a major concern and prevents their use in crop protection. In order to overcome this, thirty four substituted ferrocenylchalcones have been synthesized by microwave method and compared the reaction time and yield of products with that of conventional method (CM). The use of microwave has several advantages such as shorter reaction times, higher yields, ease of manipulation and lower costs. Environmentally benign character of the microwave method is desirable for large scale industrial applications. A series of ferrocenylchalcones was synthesized by base-catalyzed condensation of acetylferrocene with different benzaldehydes and ferrocenecarboxyaldehyde with different acetophenones, characterized by various spectroscopic techniques viz. IR, <sup>1</sup>H-NMR, <sup>13</sup>C-NMR and LC-HRMS and tested against *Meloidogyne incognita*, *Sclerotium rolfsii* and *Alternaria solani*. Although all the compounds possessed activity against *M. incognita*, but, compounds 3b, 3f, 3h, 3m, 3o, 6g, 6h, 6j, 6k and 6p were found to be more potent. However, all the synthesized compounds were found to be less active than commercially available carbofuran and velum prime. Pot study revealed that, all plant growth parameters (shoot length, shoot weight, root length, root weight, average no. of galls/plant and yield) were positively influenced by these compounds. The activity was highest in compounds 3f, 3h, 6g and 6h @ 80 ppm at 30 days after inoculation (DAI) and 60 DAI. The activity was higher in soil drenching method compared to root dipping method.

As regards fungicidal activity, among (3a-3p) series compounds, 3o [(2E)-1-ferrocenyl-3-(2,6-dichlorophenyl)-prop-2-en-1-one] showed highest fungicidal activity against *S.rolfsii* with ED<sub>50</sub> of 23.24 ppm. But, in case of *A. solani*, among (3a-3p) series compounds, 3c [(2E)-1-ferrocenyl-3-(4-fluorophenyl)-prop-2-en-1-one] (ED<sub>50</sub> = 29.9 ppm) showed highest activity. Among (6a-6r) series compounds, 6o [(2E)-1-(5-chloro-2-hydroxyphenyl)-3-ferrocenyl-prop-2-en-1-one] showed the highest fungicidal activity against *S. rolfsii* with ED<sub>50</sub> of 21.50 ppm. In case of *A. solani*, among (6a-6r) series compounds, 6b [(2E)-1-(4-bromophenyl)-3-ferrocenyl-prop-2-en-1-one] showed the highest fungicidal activity with ED<sub>50</sub> of 31.14 ppm. Based on *in vitro* results, three most effective compounds 3b, 3o and 6o were chosen for pot



experiment against *S. rolfsii*. The percent disease incidence was significantly decreased as compared to control. The percent disease incidence was found to be minimum in plants treated with 3b @ 1000 ppm. The disease incidence was minimum in soil drenching method compared to root dipping method. This is the first attempt to synthesise a series of ferrocenylchalcones by Microwave Synthesis Reactor. Study revealed that microwave method was quick and green method as compared to conventional method. All the synthesized compounds were found to have good to moderate nematocidal and fungicidal activity.



## Agricultural Economics



Suresh Kumar

**Name of the Student** : Suresh Kumar  
**Roll No.** : 10937  
**Chairperson** : Dr. D. R. Singh



Dr. D. R. Singh

### *Title of the Thesis*

### **Economics of soil and water conservation: a case study of drought prone areas of Karnataka**

In India, around 30 per cent of the total geographic area is witnessing problem of land degradation, posing a threat to agricultural sustainability and thereby livelihood of millions of poor farmers. Karnataka is the second highest drought prone state in India after Rajasthan. Therefore, the study was undertaken in drought prone areas of Karnataka to examine the adoption behaviour of farmers relating to soil and water conservation (SWC) measures and their investment, the impact of *in-situ* SWC measures on equity, efficiency, profitability and production risk in major crops and identify the constraints to adoption of SWC measures. This study is based on primary data collected from 593 selected farmers cultivating 1239 number of plots. Multivariate and Ordered Probit models were fitted to identify the factors affecting the adoption SWC technologies and their intensity of adoption, respectively. For assessing impact of adoption of soil bunds on productivity and technical inefficiency, endogenous switching regression model was used. DEA-double bootstrapped approach and meta technology ratio were also used to assess the bias-corrected technical efficiencies and impact of soil bunds on improvement in the efficiencies. Further, stochastic dominance analysis and moment-based approach were employed for estimating the effect of soil bunds on downside risk exposure, i.e., crop failure. The results show the farm level investment in SWC technologies was found poor in study area. The physical features of land, perception of farmers and institutional factors rather than the household characteristics are key determinants of adoption of soil bunds. The soil bund adopter farmers realized higher and more inclusive profitability in crop production than that of non-adopter farmers. The average treatment effect on treated (ATT) indicates that the adoption of soil bunds leads to significant increase of 26 and 36 per cent in the yield and reduction of 28 and 13 per cent in technical inefficiency in maize and sorghum production in comparison to their counterfactuals, respectively. The average treatment effect on untreated (ATU) also showed similar impacts on non-adopter farms. Meta-technology ratio also indicates a potential of increasing the output when switching from the non-adoption to adoption. The adoption of soil bunds not only improve the crop revenue but also reduce its variability and reduces the chances of downside risk, i.e., crop failure. The adoption of soil bunds was found economically feasible even under increasing (even up to two-thirds) probability of consecutive droughts. Lack of technical support, lack of interest of land owners, secondary occupation status of farming and non-assurance of next year leasing-in of plot were identified as major constraints in the adoption of



SWC technologies. The adoption of soil bunds was found to be very effective for enhancing productivity and profitability, improving inclusiveness and efficiencies, and reducing production risk and crop failure in crop production in the drought prone study area. Therefore, concerted efforts should be made to enhance the level of adoption in treated areas and need to scale-up in the untreated areas. Furthermore, the adoption of soil bunds should be prioritized as an important risk mitigation strategy and climate resilient technology in the view of increasing climate variability. Finally, the study support investment in SWC technologies for sustaining livelihood of resource-poor farmers of ecologically fragile regions such as the semiarid tropics.



## Agricultural Engineering



Nickhil C.

**Name of the Student** : Nickhil C.  
**Roll No.** : 10742  
**Chairperson** : Dr. Debandya Mohapatra



Dr. Debandya Mohapatra

### *Title of the Thesis*

### **Ozone treatment for disinfestation of chickpea (*Cicer arietinum*) in bulk storage**

In many developing countries, chickpea is consumed by a sizable vegetarian population as a major and cheap source of proteins in the form of dhal, flour, sprouted, and dry seeds. Chickpea grains are mostly attacked by insects during storage, thus reducing their nutritive as well as market value. To avoid the incidence of the insects, the approach of gaseous ozone treatment is a suitable disinfestation technique for grains stored in bins, for its potential oxidizing and residue-free nature. The present study attempts to disinfest the stored chickpea grain infested with *C.maculatus* and analyse the quality profile of various nutritional aspects of chickpea grains. The simulation of gaseous ozone in the bulk storage was also attempted at various fill of chickpea grains and for different inlet position of the storage bin. The disinfestation studies were evaluated at different ozone gas concentrations (500-1000 ppm) varying moisture content (10-14%wb), storage temperature (18-31°C), and grain bed thickness (5-10 cm) as major factors. At a higher ozone concentration approach, the results revealed 100 % and 0 % of adult and egg mortality, reduction of the microbial load to 4.25log CFU/ g, and having 79% germination percentage. The surface morphological studies spotted the collapse of the eggshell of the insect to the tune of 5-38µm in dimension. Besides, minor skin cracks on the chickpea pericarp ranging 317 to 711 nm and irregular changes in the inner globules of the cell wall were also revealed. A reduction in the minor protein content (17.62 to 17.17%), the amino acid (869.25 to 600.7 mg/g) without a change in the protein profile having 8 bands in 16-250 KDa molecular weight range and increase of biological value from 36.93 to 38.95% were also indicated. The increase in S-S content (9.64 to 9.71µ mol/g), oleic (0.84 to 0.91 %), linoleic (54.72 to 56.16) at higher ozone concentration signifies increased stability of protein and gaining of beneficial omega fatty acids. The increase in dehulling efficiency (93- 96.1%) and reduction in cooking time (39-23 min) were also achieved.

The numerical simulation of ozone flow in the grain storage bin revealed that the mass fraction at different inlet conditions at the bottom, middle and top was 1 at the lower, center and top region of the storage bin in the 100 % grain fill condition having diffusion coefficient between  $1 \times 10^{-10}$  to  $1.725 \times 10^{-5}$  ( $m^2/s$ ) after 15 min. Top inlet full-grain fill percentage has better distribution and density of ozone that helped uniform diffusion of ozone inside the bin. The half fill grain condition has the poor distribution of ozone at all the inlet conditions. The oxygen diffusion coefficient increased from  $2.99 \times 10^{-8}$  to  $3.65 \times 10^{-7}$



after the ozone flow for 12 minutes. In pilot scale for 6-month storage, ozone-treated samples achieved 100 % adult mortality, 0% egg hatching, 13 % amino acid reduction, 89 % dehulling efficiency, and 29 min cooking time, whereas the untreated sample has 12.7 % adult mortality, 81 % egg hatching, 26 % amino acid reduction, 42.1 % dehulling efficiency and 32 min cooking time.



## Agricultural Extension



Priti Priyadarshni

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Dr. R. N. Padaria

### *Title of the Thesis*

### **Theory Building and Impact Analysis of Social Learning in Agricultural System**

Social learning has been cited in several researches as potential approach for achieving sustainability through collective action as well as interaction. Researches have also presented the challenge of ambiguity in the concept of social learning. Considering the potential and gap in research on social learning this study was framed to build theory on social learning for different social contexts and analyze its impact at different levels of crop management. The study was conducted in state of Kerala, Bihar and Nagaland. Experimental study on social learning for organic farming was conducted in Thiruvananthapuram, Kerala and Gaya district of Bihar. Two case studies on social learning based marketing of organic produce and six case studies on value addition were conducted in Thiruvananthapuram and Vellanad in Kerala, respectively. The total sample size of the study was 365 framers. For social learning based ecosystem management, two case studies viz., collective management of integrated land and water through indigenously developed Zabo system in Phek district and collective management of indigenous Alder based Jhum cultivation in Kohima district of Nagaland were undertaken. The farmers' belief (behavior) model for communities of practice for ecosystem management showed path of causal relationship of normed shared belief, shared values and trust with community orientation whereas social relationship was antecedent for social cohesiveness and social cohesiveness led to community orientation which was found to be immediate precursor for the collective active for resource management. This model was absolutely fit with value of RMSEA=00.09, GFI=0.96, non-significant chi-square (which is required for model fit), CFI=0.92, IFI=0.93 and NFI=0.86. The resultant validated factors for farmers' belief (behavior) model in case of social learning through interaction were awareness, motivation, participation, trust social relationship, attitude and behavioral intention. Awareness and motivation were antecedent factor for participation in learning process which was found as precursor for trust and social relationship development. These social capitals formed path to attitude which was found to be the immediate precursor for behavioral intention. This model was also absolute fit with values of model fit as; RMSEA=0.07, GFI=0.97, RMR=0.029 and non-significant chi-square. The obtained stages for social learning in the case of communities of practice were reflection, scoping, integration, negotiation, reproduction, action and development. Self-reflective capability was found to be the significant influencing factor ( $p < 0.01$ ) at reflective stage. Cooperativeness significantly influenced scoping ( $p < 0.05$ ), integration ( $p < 0.01$ ), negotiation ( $p < 0.05$ ) and reproduction ( $p < 0.05$ ) stages.



Trust was found to be significant influencer at negotiation ( $<0.01$ ) and reproduction ( $<0.05$ ) stages, while self-efficacy was significantly influencing reflection ( $<0.01$ ) and reproduction. Self-esteem was significant factor at action ( $p<0.05$ ) and development ( $p<0.01$ ) stages. Stages for social learning through interaction were Stimulation, attention, retention, reproduction, motivation, action and feedback. Awareness was found as a significant factor ( $p<0.01$ ) influencing the stimulation stage. Stage attention was significantly influenced by factor value orientation ( $p<0.01$ ) while interaction ( $p<0.01$ ) was significantly influencing retention ( $p<0.01$ ) and reproduction ( $p<0.01$ ) stages. Consequence was found as significant factor for the stages reproduction ( $p<0.01$ ), action( $p<0.05$ ) and motivation( $p<0.01$ ). Self- efficacy was influencing factor for stages motivation ( $p<0.01$ ) and action ( $p<0.01$ ), while welfare orientation was influencing factor for honest feedback ( $p<0.05$ ). The independent t-test in Gaya and Kerala showed significant difference ( $p<0.01$ ) between control and treatment group except for civic culture in the case of Kerala ( $>0.05$ ). Significant value of dependent t-test for human and social capital ( $p<0.01$ ) for both Kerala and Gaya showed social learning had made enhancement in these capitals. Again, for civic culture in Kerala, dependent t-test was insignificant ( $>0.05$ ). Social learning based marketing of organic farming enabled marginal farmers to earn Rs. 700-3100 per week as net profit. Perceived enhancement in human capital and social capital was high to very high for the most of the farmers. Collective action for integrated land and water management through Zabo system enabled farmers to get 133% more yield than the state average under Jhum, while in case of collective management for Alder based Jhum cultivation it was 110%. Social learning has huge potential which can be harnessed for markets and market information brokerage, farmer organization development, facilitation of joint farmer-researcher learning & promoting innovations, and development of entrepreneurial skills and attitude.



## Agricultural Physics



Rajkumar Dhakar

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Dr. V. K. Sehgal

### *Title of the Thesis*

### **Regional wheat yield prediction using remote sensing inputs with dynamic crop-weather models**

A reliable crop yield forecast system is an imperative for stabilized food security. The study attempted to develop a novel regional wheat yield forecasting system by assimilating remote sensing derived LAI and weather forecast into crop simulation model i.e. InfoCrop-wheat, using minimum observations as model inputs. The CSM model was calibrated and validated using experiments at research farm of IARI, as well as the model was validated for 42 farmers' fields selected in Pataudi block of Haryana during *rabi* season 2015-16 and 2016-17 and showed good performance of the model at both the scales. Field experiments showed a complex interaction of water and terminal heat stress on water productivity and conclude that maintaining balance between radiation and water productivity may result into higher yield under multiple stresses. The developed forecasting framework consisted of four components, viz., (1) retrieve LAI from multi-spectral remote sensing images, (2) assimilate LAI into modified InfoCrop model, (3) Incorporate bias corrected WRF modeled weather forecast and (4) computer coded prototype system for spatial implementation. The LAI was retrieved through inversion of PROSAIL RTM from Sentinel 2A MSI and Landsat-8 OLI imageries and validated using in-situ LAI measurements of farmers' fields and also assessed the effect of atmospheric correction algorithms, inversion approaches and image resolutions on LAI retrieval. Among the two atmospheric correction algorithms, MODTRAN outperformed libRadtran, while among the inversion approaches, Look-Up-Table outperformed ANN. The inclusion of additional two red-edge bands as available in MSI significantly reduced the uncertainty in LAI retrievals over that obtained by using six bands, while inclusion of only additional VNIR band did not show any significant effect on LAI retrievals. MODTRAN and LUT based inversion reduces average error in LAI retrieval to 0.44 from 1.19  $m^2/m^2$ . Then, we developed the novel modified InfoCrop-LAI assimilation framework through successful implementation of Ensemble Kalman filter and Forcing algorithm of multiple LAI assimilations with crop phenology adjustment. Our study demonstrated that assimilation of LAI through EnKF improved not only crop yield prediction performance but also phenology and growth of wheat with our novel approach using standard management inputs and minimum actual observations. Finally, we demonstrated the novel wheat growth and yield forecasting system assimilating LAI through ensemble kalman filter and bias corrected weather forecast from dynamical WRF model into InfoCrop-wheat model for a region. The workable system has shown the acceptable accuracy in forecasting phenology, total dry matter and yield of spring wheat at fine scale and minimized the large management input data requirements. It has potential to be adopted for actual applications in many national projects like FASAL and PMFBY of Govt. of India.



## Agricultural Statistics



Mohd. Harun

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Dr. Cini Varghese

### *Title of the Thesis*

### **Statistical techniques for triallel and tetra-allele cross experiments**

The major objective of a breeding programme is to release new hybrids with enhanced genetic potential which is based on information on general and specific combining abilities, information related to variance components and predictor of yielding capacities of crosses. Further, designs used for attaining these goals should be robust against disturbances like missing observation. Higher order crosses like triallel and tetra-allele crosses are considered as they being genetically more viable and consistent performers, can provide more information on combining abilities. Under a fixed effects model including specific combining abilities, the estimates of combining abilities have been obtained for both triallel and tetra-allele crosses. A method of construction of partial triallel crosses arranged in blocks has been obtained based on two-associate triangular association scheme along with the information matrices, eigen values, variance factors, efficiency factor and degree of fractionation. Another two methods of constructing partial triallel cross designs have also been obtained using various types of Lattice designs and Kronecker product of incidence matrices respectively. All these methods are efficient along with lower degree of fractionation. A class of orthogonal tetra-allele cross designs for estimating contrasts pertaining to general combining ability effects has been obtained under a reduced model including lower order specific combining ability effects using mutually orthogonal Latin squares. The obtained class satisfies the condition of optimality for equi-replicated designs for tetra-allele crosses and has low degree of fractionation. Also, under a random effect model excluding specific combining ability effects for tetra-allele crosses, the Best Linear Unbiased Predictor (BLUP) for yielding capacity of cross has been obtained. A lower bound to mean square prediction error for characterizing optimal class of designs has been obtained. The lower bound so obtained is important in finding optimal designs. The unbiased estimates of variance components along with sampling distribution have been obtained following Henderson Method III. These parameters can be further used for obtaining the estimates of genetic parameters. The robustness of designs against missing observation using connectedness and efficiency criteria has been studied and a list of efficient robust designs for triallel and tetra-allele crosses has been tabulated. A list of robust and efficient designs with lower degree of fractionation is very much helpful for the breeders in situations of missing observation. Programs have been written in SAS [PROC IML] software for computing efficiency factor of the designs involving triallel crosses for estimating gca effects to investigate the robustness of designs against missing observation by calculating the canonical efficiency.



## Bioinformatics



Neeraj Budhlakoti

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Dr. Anil Rai

### *Title of the Thesis*

### **Development of robust methods for genomic selection**

Genomic selection is an advance method of breeding where genome-wide dense markers information is used to predict genetic merit of an individual in a breeding programme. In today's scenario genomic selection is a promising tool for improving genetic gain of individuals under study. Genomic selection is a form of marker-assisted selection in which genetic markers covering the whole genome are used to identify QTL which are in LD with at least one marker. Genomic selection predicts the breeding values of lines in a population by analyzing their phenotypes and high-density marker scores. Genomic selection process starts with building a statistical model from individuals having both genotypic and phenotypic data (i.e. training set), this model is further used for estimation GEBVs for individuals having only genotypic information. Individuals are then ranked on the basis of GEBVs and subsequently superior individuals are selected. Genomic selection procedures have proven useful in estimating breeding values and predicting phenotype with genome-wide molecular marker information. Number of parametric methods has been proposed to predict individual breeding values by modeling the relationship between individual genotype and phenotype. Normally in the method of estimation of breeding value for genomic selection, assumptions of the model (e.g. Normality, linearity, independence of explanatory variables) are violated which may provide false breeding value. It is also noticed that parametric methods only performs satisfactory when system under study have additive genetic architecture. However, some nonparametric methods have been developed to capture non additive (dominance & epistasis) variances, but these are generally fails to capture additive variances.

The idea behind this study is to identify best suitable model from parametric and nonparametric model under different genetic architecture. First, we have gone through various parametric models and evaluated their performance on real and simulated datasets. Under parametric models, we have studied most commonly used methods i.e. linear regression, RR, BLUP, GBLUP, LASSO, Bayesian. For nonparametric models, we have studied models like RKHS, SVM, NN and RF. It was observed from the results that for additive architecture, GBLUP performed quite well and among nonparametric methods, performance of SVM was found to be encouraging. Keeping these results in the mind, a robust model has been developed for genomic selection studies which can handle additive and epistatic effects simultaneously by minimizing their error



variance. Developed integrated model has been evaluated using the prediction accuracy and error variance. It has been found that our proposed model is either performing better or at par with the existing models. It has also been observed that our proposed model is robust to the diverse genetic architecture i.e. additive and epistatic. Apart from this, impact of outlier on genomic prediction accuracy has also been explored. In this study, a new efficient method using meta-analysis for outlier detection in genomic data has been proposed. It has been shown that by implementing efficient diagnostic measure for outlier detection, accuracy of genomic selection model can be improved. Comparative study has been made among various existing methods of outlier detection in high dimensional genomic data for their impact on accuracy of genomic estimated breeding value. It has been observed that our proposed method has outperformed among existing methods.



## Floriculture and Landscape Architecture



Aparna Veluru

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Dr. K. P. Singh

### *Title of the Thesis*

### **Morphological and molecular characterization of rose genotypes and assessment of a subset of genotypes for their performance under coconut plantations**

A study was carried out to analyse the diversity among 148 rose genotypes including modern cultivars of Indian, exotic origins and wild species using morphological and molecular markers inclusive of assessing the performance of some of these native cultivars under coconut plantation in tropical wet climatic region. Morphological and molecular characterization of rose genotypes was conducted at ICAR-IARI and ICAR-NBPGR, New Delhi. Morphological characterization was done in 148 rose genotypes using 59 morphological traits based on DUS test guidelines developed by PPV&FRA, India. DUS characteristic profiles were developed for all 148 genotypes and diversity among them were assessed using hierarchical cluster analysis. A total of eight different clusters were identified in the dendrogram with high characteristic uniformity. Cluster-I is identified with maximum number of genotypes 109, followed by cluster-III with 11 genotypes, cluster- II & VIII with 7 genotypes each, cluster-IV & VII with 5 genotypes each, cluster-V with 3 genotypes and cluster-VI with one genotype. Molecular characterization of roses was performed using SSR markers. Of 48 SSRs used, 30 markers exhibited polymorphism among all genotypes. Polymorphic Information Content (PIC) value of SSR markers varied from 0.08 (Rh50) to 0.8 (Rh58) with an average of  $0.5 \pm 0.2$  per marker. The observed number of alleles ( $N_a$ ) for different SSR loci in studied population varied from 1 (Rh 50) to 6 (Rh 48) with an average of  $2.9 \pm 1$  per locus. The Unweighted Pair Group Method with Arithmetic mean (UPGMA) dendrogram constructed using Dice similarity coefficients and Shan-function showed variability present among the cultivated and wild germplasm. Structure analysis based on microsatellite allelic data, partitioned 148 genotypes into four different subpopulations with some individual genotypes having genomic admixture. Modern Indian genotypes were classified under two different subpopulations I & II; exotic and wild species were identified under subpopulation III & IV. The  $F_{ST}$  values between different subpopulations varied from 0.03-0.2. Analysis of molecular variance (AMOVA) revealed 83.12% of genetic variation due to variance within the genotypes followed by significant levels of variation (10.42%) between the populations; least variance of 6.46% was noticed among individuals within groups.

An evaluation study was performed using 10 characterized rose genotypes under two types of coconut plantations i.e. 3 years and 52 years old plantation in tropical wet climatic region at ICAR-CPCRI,



Kasaragod, Kerala. The performance of characterized genotypes under both the plantations was assessed based on their growth and flowering. Amongst of all genotypes, better survival was noticed in Damask rose (98.37%), Rose Sherbet (91.07%), Pusa Arun (84.19%) and Arunima (67.39%). Between the plantations, superior growth was noticed in roses grown under young plantations (3 years) as compared to old coconut plantations (52 years). Intercropping was found to be beneficial for coconut and an increase in net yield of the palms were observed up to 22% during intercropping period.



## Fruit Science



Sunil Kumar

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**Chairperson** : Dr. O. P. Awasthi



Dr. O. P. Awasthi

### *Title of the Thesis*

### **Morphogenetic characterization of Kinnow mutants**

The present investigation was carried out at ICAR-IARI, New Delhi during 2016-2018. From the diverse mutated population of Kinnow mandarin, five-year-old putative mutants generated from varying doses of gamma irradiation (15, 20, 25 and 30 Gy) and EMS (0.05%, 0.1%, 0.2% and 0.5%) were selected for the study and compared with the wild type (WT) for various morphological, physio-biochemical and fruit quality traits. They were further characterized using SSR markers. Plant height and fruit yield were reduced by 49.65% and 65.91% in G-20 developed at 30 Gy. Compared to wild type (WT), leaf area was recorded maximum and minimum in G-6 and G-14 developed from 20 and 25 Gy. Photosynthetic pigments, chlorophyll *a* and *b* were degraded maximum in G-20 (30 Gy), while total phenol was stimulated in G-18-G-20 (30 Gray). Proline accumulation was higher in G-14 and G-15 and total soluble protein (TSP) in G-15 (25 Gy). Antioxidant enzymes (SOD, CAT and POX) and glutathione reductase (GR) were up-regulated maximum in the mutants generated from 30 Gy. Fruit weight, fruit size, PAL and PME activity were observed differently in mutants. The desired low seeded mutants G-6 and G-9 were obtained with an average of 7-8 seeds/fruit developed at 20 Gy as compared to 31 seeds/fruit in the wild type. The juice recovery per cent in these mutants had parallel values with the wild type. Furthermore, irradiation treatment enhanced IAA content by 188.78-247.23% in G-7-G-9, while 79.57-93.46% enhancement in ABA content was assayed in G-6 and G-7 developed at 20 Gy. Phenological traits in the EMS induced putative mutants exhibited stimulatory response of 10% in plant height in E-2 and E-5 (0.05% EMS) while it was inhibited by 25% in the mutants E-16 and E-17 created from 0.5% EMS. The plant height although was inhibited in E-16, the fruiting intensity as compared to WT was higher in the said mutant by almost two-fold. Almost 50% reduction in fruit yield was noted in mutants E-6 and E-8 (0.1% EMS). Chlorophyll pigments *a* and *b* were observed maximum in the mutants E-1 and E-14 developed from two contrasting doses of 0.05 and 0.2% EMS. The Photosynthetic rate was minimum in E-13 developed from 0.2% EMS. A correlated dose-dependent increase of almost two-fold was recorded in the total phenol, proline and total protein content in the mutants created from 0.2 and 0.5% EMS. The upregulated antioxidant enzyme activity was significantly higher in E-16 (0.5% EMS). The number of seeds < 15 seeds/fruit was indexed in the mutants E-16 and E-19. The phytohormones IAA and ABA were assayed maximum in E-18 (0.5% EMS). In an attempt to characterize the putative mutants, thirty-four SSR markers were screened for polymorphism of



which two were found informative. The findings of the present study revealed that the putative mutants exhibited much-needed variation in Kinnow mandarin with noble traits such as reduced plant height and less number of seeds/fruit (6-9) which can be utilized for the selection of desirable mutants or can be used in the future breeding programme.



## Genetics and Plant Breeding



Venkata R Prakash Reddy

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Dr. H. K. Dikshit

### *Title of the Thesis*

### **Association mapping for key traits influencing phosphorous uptake and utilization efficiency in mungbean (*Vigna radiata* L.)**

To dissect the genetic architecture of phosphorus use efficiency (PUE) in mungbean, a total of 195 diverse genotypes were evaluated for phosphorus (P) uptake and utilization efficiency traits using the hydroponic system at IARI, New Delhi. The total P uptake (TPU) and P utilization efficiency (PUtE) were ranged from 0.51 to 4.79 mg P/plant and 0.09 to 0.27 g DW/mg P, respectively under optimum P (OP) condition. Whereas these traits were ranged from 0.1 to 0.82 mg P/plant and 0.22 to 1.83 g DW/mg P respectively, under low P (LP) condition. Further, the genotypes PUSA 1333 and Pusa Vishal based on TPU and IPM 406-1 and MH 521 based on PUtE were found to be efficient genotypes under both OP and LP conditions. Among the studied traits, total root length, total root surface area, total root volume, root dry weight, shoot dry weight and total dry weight were explaining most of the variation under both OP and LP conditions and proved to be ideal traits for screening PUE in mungbean. From the total 195 genotypes, 144 genotypes were pooled based on the frequency distribution of studied traits for both molecular characterization and marker trait analysis. The study for the first time generated a large number of 76,160 genome wide SNPs including 55,634 chromosome based SNPs by employing next generation sequencing (NGS) based genotyping by sequencing (GBS) methodology. Population structure analysis revealed the presence of three subpopulations among the 144 genotypes. Further, high resolution linkage disequilibrium (LD) estimates ( $r^2$  value of 0.62) and LD decay (~50 kb physical distance) were observed in mungbean chromosomes. Association mapping analysis revealed that a total of 231 SNPs were shared by both GLM and MLM models associated with P uptake and utilization efficiency traits under different P regimes. Further, this study identified the 18 putative candidate genes including three potential candidate genes *VRAD11G08340*, *VRAD10G05520* and *VRAD10G10750* were found to be associated with nutrient uptake and root architectural development pathways. Moreover, two genes *VRAD11G08340* and *VRAD10G05520* showed significant variation in protein structure between native and mutated versions. The identified SNPs and candidate genes are powerful tools for PUE improvement in mungbean breeding programme.



## Microbiology



Vijaya Rani

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Dr. Rajeev Kaushik

### *Title of the Thesis*

### **Developing plant growth promoting and methane oxidizing microbial inoculants for irrigated rice**

Methane is an important greenhouse gas after carbon dioxide with a global warming potential of 28. CH<sub>4</sub> produced in the flooded paddy fields is released through aerenchyma and by the mechanisms of diffusion and ebullition at the soil-water interface. Methane-utilizing bacteria (MUB) inhabit the rice ecosystem and play an important role in reducing the overall CH<sub>4</sub> emission by using it for their energy and growth needs. We hypothesize that the use of MUB with plant growth promoting attributes as bio-inoculants in flooded paddy ecosystem can reduce CH<sub>4</sub> emission and improve plant growth and yield parameters. Hence, soil and rice plant samples were collected from the phyllosphere, rhizosphere, and non-rhizosphere of five rice-growing regions of India viz. Brahmaputra Valley-Assam (S1), Ernakulum-Kerala (S2), Aduthurai-Tamil Nadu (S3), Varanasi-Uttar Pradesh (S4), and Gaya-Bihar (S5) at the tillering stage and investigated for selecting efficient methane-oxidizing and plant growth-promoting bacteria. Out of 263 morphotypes purified from AMS agar, 123 showed naphthalene oxidation (an indicator of soluble methane monooxygenase activity) in NMS agar with CH<sub>4</sub> as sole C source by the development of purple-red color. Significantly higher number of isolates were isolated from lowland flooded paddy ecosystems of Aduthurai (33.33%) followed by Ernakulum (20.33%) and Brahmaputra valley (19.51%), as compared to upland irrigated regions of Gaya (17.07%) and Varanasi (8.94%). Among sub-samples, significantly higher isolates were found inhabiting the phyllosphere (58.54%) followed by non-rhizosphere (25.20%) and rhizosphere (15.45%). These 123 isolates were phylogenetically grouped into 13 bacterial and 2 yeast genera (*Meyerozyma*, and *Pichia*) and most isolates belonged to *Burkholderia* (62) followed by *Hyphomicrobium* (14), *Meyerozyma* (9), *Paenibacillus* (9), *Pseudomonas* (8), *Rahnella* (5), *Methylobacterium* (4), *Serratia* (4), *Paraburkholderia* (2) and 1 each of *Gordonia*, *Curtobacterium*, *Enterobacter*, *Rhodococcus*, *Pantoea* and *Pichia*. Out of 123 isolates, only 30 isolates belonging to 7 genera (*Hyphomicrobium*, *Burkholderia*, *Methylobacterium*, *Paenibacillus*, *Pseudomonas*, *Rahnella*, and *Meyerozyma*) showed significant growth on CH<sub>4</sub> as sole C source in 6 days. Based on kinetics of methane utilization studies, *M. oryzae* MNL7 showed CH<sub>4</sub> (ppm) utilization rate (-dS/dT) of 302.9±5.58 with a maximum specific growth rate ( $\mu_{max}$ ), maximum CH<sub>4</sub> utilization mg protein<sup>-1</sup> d<sup>-1</sup> ( $K_{max}$ ) and half-maximal growth rate ( $K_s$ ; mg CH<sub>4</sub> L<sup>-1</sup>) of 1.50±0.071, 12.65±0.13, and 1.92±0.092, respectively. Based on PGP attributes (N<sub>2</sub> fixation, IAA production and solubilization of P, K, and Zn), *Methylobacterium oryzae* MNL7, *Paenibacillus polymyxa* MaAL70, *Hyphomicrobium facile*



MaAL75, *Pseudomonas sp.* MNR81 and *Rahnella aquatilis* MaAL105 were selected for soil microcosm studies. *M. oryzae* MNL7 and *P. polymyxa* MaAL70 performed significantly better with 53.91% and 40.12% reduction in CH<sub>4</sub> flux, respectively. During field evaluation, the co-inoculation of MNL7 and MaAL70 led to a significant decrease in cumulative CH<sub>4</sub> emission by 12.03%, 11.46% and 6.93% when urea, DAP + urea, and FYM were used as N- source, respectively over uninoculated plots. In a second field experiment to evaluate the effect of different rice varieties (Pusa44, IR64, CRD310, and MTU1010) and consortium inoculation, Pusa44 and IR64 showed greater emission at 65 DAT, whereas CRD310 and MTU1010 showed significantly higher emission at 52 DAT. CH<sub>4</sub> emission was significantly higher in uninoculated plots, irrespective of the rice variety, over inoculated plots. Significant reduction in cumulative methane emission by 7.44%, 9.10%, 11.40%, and 9.82% was observed in Pusa44, IR64, CRD310, and MTU1010, respectively due to co-inoculation of *M. oryzae* MNL7 and *P. polymyxa* MaAL70 over their uninoculated control. The present investigation illustrated that methane utilizing bacteria can be important inputs for managing the overall emission of methane from the flooded paddy ecosystem and promoting the growth



## Molecular Biology and Biotechnology



Lianthanzauva

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Dr. Ramcharan Bhattacharya

### *Title of the Thesis*

### **Understanding mustard–aphid interaction for development of aphid–resistance**

Indian mustard, *Brassica juncea* is a major oil-yielding crop of India. Productivity of Indian mustard (*B. juncea*), is heavily constrained due to damage inflicted by mustard aphid, *Lipaphis erysimi*. There are more than 400 aphid species with different host range. Mustard aphid is a specialist aphid species, which infests rapeseed-mustard crops by colonizing rapidly through parthenogenetic reproduction. The adults and nymphs of the insect suck the phloem sap and completely devitalize the plants leading to huge loss in economic yield. In contrary, legume specific cowpea aphid, *Aphis craccivora* even if experimentally released on the mustard plants fails to build up population and eventually eliminated. In the present study, differential host-response of Indian mustard to two aphid species, *L. erysimi* which is successful insect-pest on Indian mustard and the other *A. craccivora*, which is unsuccessful on it, has been studied based on transcriptome analysis. The two aphid species showed differential feeding efficiencies on mustard as the host and it was evident by the difference in the amount of honeydew secreted by them while feeding. The leaf transcriptomes of infested and uninfested mustard plants treated individually with the two aphid species were captured in three libraries. Illumina platform with 2 x 150 paired-end chemistry was used for RNA-sequencing and the quality reads were assembled *de novo*. A comparative assessment of the differential gene expression in Indian mustard due to feeding by the two aphid species was carried out. The analysis empirically showed differential regulation of the defense related transcription factors, and the genes related to oxidative burst, phytohormone biosynthesis, secondary metabolite biosynthesis etc. A wholistic interpretation of the differentially expressed genes suggested more transcriptional reprogramming of the host by the successful insect-pests. Transcriptome data was further validated by qRT-PCR analysis. For ectopic expression and functional characterization of the selected candidate gene(s), virus vector mediated gene-expression was envisaged as a rapid method. Therefore, attempts were made for developing a virus vector based on the croton yellow vein mosaic virus (CYVMV) which had been demonstrated to infect *B. rapa*. The generated virus vector showed rearrangement of crucial DNA elements involved in the replication and systemic spread of the virus vector, which stopped its further use in *B. juncea*. In an effort to understand plant-aphid interaction in mustard as a host and non-host, out of the several differentially regulated genes, a sugar transporter *BjSWEET11* gene was further studied. The cDNA encoding *BjSWEET11*



under a CaMV35S promoter was transferred to *B. juncea* plants through *Agrobacterium*-mediated plant transformation. Several transgenic lines were confirmed for the integration and gene-expression of the transgene. The insect bioassay on the transgenic plants showed attenuating effect of the *BjSWEET11*-overexpression on the multiplication and population growth of mustard aphid. The result indicated potential involvement of this transporter gene in endogenous plant defense mechanism of Indian mustard.



## Plant Pathology



Darshan K

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Dr. Rashmi Aggarwal

### *Title of the Thesis*

### **Transcriptomic analysis of *Chaetomium globosum* Kunze for bioprospection of the antagonistic related gene(s)**

Nature has bestowed us with plenty of worthy microbes. Among them, *Chaetomium globosum* Kunze (Family: Chaetomiaceae) has been recognized as an internationally emerging biocontrol fungus. It mycoparasitizes various pathogens and produces antifungal metabolites to suppress the growth of many soil and seed-borne phyto-pathogens. A number of basic research articles have been published related to its antagonistic activity. However, molecular events and identification of genes involved in biosynthesis of secondary metabolite are not yet explored in *C. globosum*. Transcriptome data on *C. Globosum* strain Cg2 in interaction with pathogen *B. Sorokiniana* isolate BS112 generated through the IlluminaHiSeq platform (2×150 bp), which yielded of 20-22 million reads with 50-58% GC. Reference guided *de novo* assembly generated 45,582 transcripts with 27,957 unigenes. Transcriptome analysis displayed distinct expression profiles in the interaction (Cg2-BS112), out of which 6109 unique differentially expressed genes (DEGs) were observed. The predominant transcripts classified as genes involved in “catalytic activity” constituted 45.06%, of which 10.02% were associated with “hydrolyticactivity” (GO:0008152) and similarly, in the biological process, 29.18% of transcripts were involved in “metabolic activity” (GO:0004096; GO:0006979). Heat map and cluster categorization suggested an increase in the expression levels of genes encoding secondary metabolites and other hydrolytic CAZymes. The obtained RNA-seq data was validated by RT-qPCR data using 20 random lychosen genes, showing consistency with the RNA-seq results. For the first time development of polymorphic EST-SSR markers in *C. Globosum* with perfect repeats using the Illumina RNA-Seq data have been reported. Out of 27,957 unigenes investigated, 8,485 EST-SSR loci were mined. Of these, mononucleotide repeat motifs were most abundant (4382; 51.64%) followed by tri- nucleotides (3101; 36.54%), while penta and hexanucleotide repeats were the least, containing 46 (~0.28%) and 59 (0.35%) respectively. Out of these 8,485 EST-SSRs, a total of 50 primer pairs were designed and validated for polymorphism among 15 available *C. Globosum* isolates. Seventy-four alleles (2-4 alleles per locus) were detected from 22 polymorphic SSR markers. The mean polymorphic information content was 0.3929. Further to unravel the antagonistic mechanism of *C. globosum*, metabolomic profiling was done to identify associated antifungal volatile and non-volatile metabolites. The GC-MS data showed that the Cg2 strain produced a variety of antifungal secondary metabolites such as Octadecene trans-limonene oxide, dodecene, and octadecanoic acid, which may be involved in the antagonism. Similarly, UPLC-QToF-ESIMS analysis



of chloroform soluble fraction of *C. Globosum* (Cg2), *B. Sorokiniana* (BS112) and their combination, Cg2-BS112 led to identification of non-volatile metabolites. These metabolites were characterized as chaetomugilin A, D, E & F, chaetoviridin A, B & Ea nd chaetoglobosin Q & N. Thus, this work indicates that the biocontrol agent *C. Globosum* produces a number of compounds and causing inhibition of *B. sorokiniana*. Based on these findings, we infer that several mycoparasitism-related enzymes, secondary metabolites and antibiosis related genes were involved in antagonism of *C.globosum*.The obtained data will greatly enrich the current *C. globosum* genetic information and provide a good foundation for better understanding of the molecular mechanism of *C.globosum* against plant pathogens.



## Seed Science and Technology



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Dr. Sudhir Kumar Jain

### *Title of the Thesis*

### **Study on quality seed production in cucumber (*Cucumis sativus* L.)**

To address the problem of higher number of under developed or unfilled seeds, seed dormancy and sensitivity to micronutrients during cucumber quality seed production, my present study entitled “Study on quality seed production in cucumber (*Cucumis sativus* L.)” was carried out at ICAR–Indian Agricultural Research Institute, New Delhi. The targeted objectives were seed development & maturation; harvesting stages & post-harvest ripening, fruit load regulation, spatial effects of ovule within a fruit; and foliar application of Zn- & Fe-NPs on seed yield and quality. The investigations were conducted using two cucumber varieties PusaBarkha and PusaUday under two environments during two growing seasons viz summer-2019 & kharif-2019 under open field; and summer-2019 & winter-2019 under protected environments. Seed crops, with 200 plants (100 from each variety) in three replicates, were grown on raised beds following CRBD and/or FRBD. Five to ten flowers, from each plant were hand pollinated; fruits were harvested at periodic intervals, subjected to need based PHR; seeds were harvested manually and used. Plant growth, fruit and seed attributes were recorded targeted seed yield and quality.

Irrespective of varieties & seasons, variations for all the fruit & seed attributes, in general, were significant with respect to growing environments. With the advancement of seed development and maturation various fruit & seed attributes increased viz fruit & seed dimensions, seed fresh & dry weights, food reserves (TSP, total starch & oil contents); whereas, seed moisture content, TSS, ROS ( $H_2O_2$  &  $O_2^-$ ) and antioxidants (SOD, CAT & POX) decreased. Seeds attained germinability on 25 DFP; physiological maturity on 40 & 50 DFP; and harvest maturity on 45 & 60 DFP (5-10 days later to PM) under open field and protected environments, respectively. To obtain optimum seed yield with better seed quality, the fruits should be harvested and subjected to post-harvest ripening, either on 40 DFP+30-days PHR or 45 DFP+20-days PHR under open field, whereas either on 50 DFP+30-days PHR or 55 DFP+20-days PHR under protected environments, respectively. Retention of two fruits per plant may be recommended for practice as it gave higher seed yield without compromising seed quality. For achieving higher yield with better quality, seed should be harvested from middle and/or styler segments of a fruit. Foliar application of zinc and/or iron NPs with optimum doses [Zn-NPs ( $300mg\ l^{-1}$ ) and/or Fe-NPs ( $200mg\ l^{-1}$ ) resulted in higher plant growth, fruit development, seed attributes. viz longer vines, increased total chlorophyll in leaves, numbers of fruits per



plant, bold seeds, more numbers of seeds per fruit and seed yield [enhanced assimilate (except oil content) in seeds] with better quality (germination & vigour; higher activity of dehydrogenases, and lower EC, TSS & TSP from seed leachates; increased hydrolytic enzymes ( $\beta$ -amylase & protease); in turn rapid & higher seed germination; increased ROS ( $H_2O_2$  &  $O_2^{\cdot-}$ ) as well all three antioxidants (SOD, CAT, POX). However, higher doses of Fe-NPs ( $300\text{mg l}^{-1}$ ) showed negative/toxic effects on most of the studied parameters. NPs treatment for getting better seed quality under open field was more beneficial over protected environments (having optimum conditions).



## Soil Science and Agricultural Chemistry



Kiran Karthik Raj

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Dr. R. N. Pandey

### *Title of the Thesis*

### **Mobilization of soil iron to minimize iron deficiency chlorosis of soybean (*Glycine max* (L.) merr.) under ambient and elevated $\text{CO}_2$ and temperature conditions**

Climate change has negative impact on iron nutrition of soybean plants especially when grown in calcareous soil. The present study was envisaged to efficiently manage iron deficiency stress of soybean crop. The differential response and adaptation by different genotypes of soybean to iron-limiting stress were assessed in this research work. In first experiment, through hydroponic culture with modified Hoagland solution containing varying concentration of iron *viz.* Fe sufficient (+Fe, 25  $\mu\text{M}$  Fe-EDTA) and Fe deficient (-Fe, 2.5  $\mu\text{M}$  Fe-EDTA) levels, 50 genotypes of soybean were screened for iron efficiency. Relative performances of genotypes were compared using C-14 exudation and dry matter produced. Additionally, average performance with respect to total chlorophyll content, iron concentration in shoot, total dry matter produced and total root exudation were considered for better screening results. The genotypes were classified into four iron response categories; iron efficient and responsive (FeER), iron inefficient and responsive (FeIR), iron efficient and nonresponsive (FeENR) and iron inefficient and nonresponsive (FeINR) categories. NRC-45, IC-18734, J-231 and G-2132 were identified as representative genotypes for each of these categories, respectively. It was found that the relative abundance of oxalic (2.4 fold increase), citric (2.7 fold increase) and malic acid (2.5 fold increase) were found the root exudate of FeER genotype relative to that of FeINR under iron limiting (-Fe) condition. Extrusion of proton and ferric chelate reductase activity were significantly higher in FeER than FeIR genotype. Differences among the soybean genotypes to counteract iron deficiency stress suggests that intra-specific variability can be exploited to shape the future breeding programmes for decreased sensitivity to adverse condition and could address the emerging challenges of abiotic iron limiting stress. In the second experiment, a pot culture study was carried out in the glass house of National Phytotron Facility with soybean as test crop. In tandem with FeER genotype, the effectiveness of different soil amendments such as pyrite and by-product from the sugar industry, Sulphitation Press Mud (SPM), with various microbial combinations were assessed in twelve treatments for mobilizing iron from soil to plant, and to minimise iron deficiency chlorosis (IDC). Among twelve treatments compared in the second experiment, the treatment combination FeER + 12.5 mg  $\text{FeSO}_4$  + SPM + *Aspergillus niger* + AMF performed the best. This is attributed to the combined effect of low molecular weight organic acid produced by *Aspergillus niger* through decomposition of SPM, and by virtue of iron efficient genotype to secrete the same. Furthermore, greater exploited soil volume



facilitated by AMF (*Glomus mosseae* and *Glomus fasciculatum*) facilitates better absorption of the nutrient. A futuristic study was conducted, with the help of plant growth chambers in the third experiment, using soybean as the test crop. The interactive effect of a set of treatments with the ambient and elevated CO<sub>2</sub> and temperature conditions were gauged. The results from the third experiment distinctly revealed that elevated CO<sub>2</sub> and temperature could adversely affect plant nutrition. Environmental condition (variables were CO<sub>2</sub> and temperature) exerted significant impact on CaCO<sub>3</sub>, HCO<sub>3</sub><sup>-</sup> and DTPA extractable iron concentrations in soil. It was also observed that genotype x environment interaction (G x E) have significant effect on IDC. Native calcium carbonate was dissolved by the higher partial pressure of carbon dioxide (Pco<sub>2</sub>) under elevated CO<sub>2</sub> and temperature (e-[CO<sub>2</sub>+T]) condition, brings greater HCO<sub>3</sub><sup>-</sup> ion concentration and induces greater iron stress. This is attributed to the antagonistic interaction between Fe<sup>2+</sup> with HCO<sub>3</sub><sup>-</sup> ion. To combat the constraints in Fe nutrition, especially under e-[CO<sub>2</sub>+T], the iron efficient genotype of soybean exude more amount of low molecular weight organic acids. Furthermore, ferric chelate reductase (FCR) activity gets reduced by e-[CO<sub>2</sub>+T] through its effect by HCO<sub>3</sub><sup>-</sup> ion. The present study revealed that the synergistic effect produced by the combined application 12.5 mg FeSO<sub>4</sub> together with partly decomposed SPM with *Aspergillus niger* and composite culture of AMF (*G. mosseae* and *G. fasciculatum*) to an iron efficient genotype was more effective in controlling the IDC. Further, because of antagonistic interaction between Fe<sup>2+</sup> with HCO<sub>3</sub><sup>-</sup> ion results in greater iron stress under elevated condition compelled to modify the treatment as FeER + 16.25 mg FeSO<sub>4</sub> + SPM+ *Aspergillus niger* + AMF for better result. The research points out the need of taking up an integrated approach for the management of nutrient limiting stress viz. use of iron efficient and responsive genotypes, continuous supply of organic matter along with microbial inoculation, especially under climate change scenario.



## Vegetable Science



Saheb Pal

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Dr. Eguru Sreenivasa Rao

### *Title of the Thesis*

### **Mapping of Fusarium wilt resistance in watermelon (*Citrullus lanatus* (Thunb.) Matsum. and Nakai) germplasm and assessing their potential as rootstocks**

The present investigation was conducted to designate two selected virulent Indian *Fusarium oxysporum* f. sp. *niveum* (*Fon*) isolates into races, to identify stable source of resistance against these races, to study inheritance of resistance, to map resistance employing candidate-QTL and QTL-sequencing approach and to study the influence of the resistant accessions as rootstocks on yield and quality of grafted watermelon. The isolates collected from Chamrajanagar, Karnataka and Karnal, Haryana were designated as *Fon* races 1 and 2 respectively. The germplasm panel was screened twice for resistance against these races. 44 *Citrullus* sp., six bottle gourd and three *C. maxima* × *C. moschata* hybrids were resistant to *Fon* race 1 while 29 *Citrullus* sp., nine bottle gourd and three *C. maxima* × *C. moschata* hybrids were resistant to *Fon* race 2. Five resistant *Citrullus lanatus* accessions were crossed with a common susceptible parent (BIL-53) to develop six generations for each combination to study inheritance of resistance to *Fon* race 2. The resistance in IC0523047, EC794455 and EC759804 was governed by two major complementary dominant genes with involvement of modifying genetic factors. The segregating progenies of the other two resistant accessions (IIHR-9 and EC794421) did not follow any of the simple Mendelian/epistatic ratios tested, suggesting polygenic inheritance. Generation mean analysis detected epistasis only in BIL-53×EC794455 and BIL-53×EC759804. Allelism test indicated absence of allelic relationship between IIHR9 and IC0523047 for resistance. For validation of six InDel markers, reported by Li *et al.* (2017), located within a candidate QTL (*Fon*-1) governing resistance to *Fon* race 1, association analysis was carried out in a panel of 336 *Citrullus* sp. accessions. Among the six markers tested, four were significantly associated with resistance. InDel-4 showed most significant association and explained maximum variation, thus can be used for marker-assisted introgression of *Fon* race 1. Employing QTL-sequencing, resistance to *Fon* race 2 was mapped in a highly resistant *C. lanatus* accession EC794421. Two statistically significant genomic regions were identified each on chromosomes 1 and 7 which were further saturated with SSR and InDel markers. The markers *viz.*, BVWS02309 and BVWS01116 on chromosome 1 and BVWS00358 on chromosome 7 were most significantly associated (PVE=40.8%, 34% and 16.9% respectively) with resistance. Eighteen *Fon* resistant *Citrullus* sp. accessions, three hybrid squashes, two bottle gourd and one *C. maxima* accessions were evaluated as rootstocks for their root parameters and also the vigour, earliness, quality and yield upon grafting a susceptible commercial variety as scion onto these. The length and diameter of the rootstock



hypocotyl were found as an indicator of robustness of the root system. A significant influence of the rootstocks on different vigour, yield and quality traits of the scion was observed upon grafting. An increase of average fruit weight by 50.69%, 55.37% and 82.37% and yield per plant by 112.15%, 89.54% and 107.06% was observed in grafts onto RS-10, RS-11 and RS-18 respectively. These *Fon* resistant and best performing rootstocks can be deployed for environment-friendly management of Fusarium wilt disease of watermelon without compromising fruit yield and quality.





