64 YEARS
POST GRADUATE SCHOOL
1958-2022

Sixtieth Convocation

Significant Research Achievements of Post Graduate Students
2021-2022

Presented by

Professors of
Post Graduate School

February 6-11, 2022

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

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Seed Science and Technology	07	03
Total	**25**	**14**

Genetics and Plant Breeding

1

Prof. Vinod

The Division of Genetics is widely regarded as the "Seat of Green Revolution" in India. Division has been making significant contributions to basic, strategic and applied research in genetics and plant breeding. The Division has the mandate to conduct basic and strategic research for genetic enhancement of field crops; applied research/varietal development in various field crops; transfer of technologies developed by the Division; post-graduate teaching and research /human resource development; developing and strengthening collaborative linkages with national/international organizations in mutual areas of interest in research and post-graduate teaching. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Abiotic stress tolerance

Marker assisted pyramiding of QTLs governing reproductive stage drought tolerance into rice variety, Pusa 44

Pusa 44 is a popular high yielding rice cultivar in north-western India. However, it is highly sensitive to reproductive stage drought stress (RSDS) resulting yield losses upto 70 per cent. The receding water level in north-western India is one of the major concerns for sustaining cultivation of Pusa 44. Therefore, the present study entitled 'Marker Assisted Pyramiding of QTLs Governing Reproductive Stage Drought Tolerance into Rice Variety, Pusa 44' was carried out to pyramid QTLs for reproductive stage drought stress tolerance into Pusa 44 through Marker Assisted Selection and evaluation of the Pusa 44 *qDTY*NILs for physiological, biochemical, yield and yield components under reproductive stage drought stress. A modified marker-assisted backcrosses breeding strategy was adopted for introgressing *qDTY2.1*, *qDTY3.1*, *qDTY9.1* and *qDTY12.1* into Pusa 44, wherein *qDTY2.1* and *qDTY3.1*, were sourced from IR81896-B-B-195 and IR81896-B-B-142; *qDTY9.1* from IR87728-59-B-B and *qDTY12.1* from IR90019-22-28-2-B. The background selection was deferred till BC_3F_4 generation which could save considerable resources in time and other logistics involved in background selection. A total 123 NILs were developed by introgressing four QTLs in the background of Pusa 44 including 29 mono-QTL NILs, 44 di-QTL NILs and 54 tetra-QTL NILs in various combinations. The mono-QTL NILs include four *qDTY2.1* NILs, one *qDTY3.1* NIL, six *qDTY9.1* NILs and 18 *qDTY12.1* NILs with RPG recovery ranging from 86.6 to 98.6 %, 95.0 %, 87.9-96.7 % and 94.7-98.7 %, respectively. The di-QTL pyramided NILs include 20 NILs possessing *qDTY2.1+qDTY9.1*, and 20 possessing *qDTY3.1+qDTY12.1* with an RPG recovery ranging from 84.6 % to 95.3% and 92.8 % to 99.0 %, respectively. A total of 54 tetra-QTL pyramided NILs with all four QTLs, *qDTY2.1+qDTY3.1+qDTY9.1+qDTY12.1* with an RPG recovery ranging from 96.9% to 98.9 %. Physiologically, the improved NILs showed superior drought response as assessed through parameters such as leaf rolling score and membrane stability index. There was a significant reduction in grain yield under drought in all the parents and NILs than the yield under irrigated conditions. However, significant yield improvement was realized in the improved NILs over the recurrent parent, Pusa 44, under RSDS. The yield superiority of the improved lines was 1.7 times that of Pusa 44 for the mono-QTL NILs carrying *qDTY2.1*, 2.7 times for *qDTY3.1* NIL, 1.9 times for the *qDTY9.1* NILs and 2.8 times than Pusa 44 yield for *qDTY12.1* NILs. Among the di-QTL pyramids, yield advantage under drought over Pusa 44 was 2.2 times greater for *qDTY2.1*+*qDTY3.1* NILs, 1.8 times higher for *qDTY2.1*+*qDTY9.1* NILs and 1.5 times more among *qDTY3.1*+*qDTY12.1* NILs. Using the drought tolerance indicators of the improved NILs, a non-parametric approach using rank averages was used for the cumulative assessment, which could identify significantly stable and drought tolerant NILs. The pyramiding of genes/ QTLs can be accelerated through intercrossing of early generation backcross derived plants (BC_3F_2) rather than waiting for the development of NILs (BC_3F_6). Improved Pusa 44 *qDTY*NILs have been developed which can tolerate RSDS which after appropriate testing in national trials could be an appropriate replacement for the recurrent parent Pusa 44, in its area of adaptation. The improved Pusa 44 *qDTY*NILs possessing four QTLs in different combinations in the genetic background of Pusa 44 forms an important genetic resource for divulging the mechanisms of these QTLs and their interaction in conferring RSDS in rice. These Pusa 44 *qDTY*NILs can also be tested and released for cultivation in drought prone environments for improving rice productivity and production. The improved NILs can also act as donors for further rice cultivar development and improvement.

Assessing genetic variation and mapping of aluminium toxicity tolerance in rice (*Oryza sativa* L.)

Rice production in acid soils around the world is constrained with several soil factors, such as aluminium (Al) toxicity. Toxicity due to Al occurs when excess Al3+ ions are released in the soil solution. In India, Al toxicity is predominant in the northeast, particularly in the uplands, which has the largest proportion of acid soils than elsewhere. However, the northeast India is endowed with rich rice genetic diversity, where several native genotypes show excellent adaptation to local environments. These genotypes possess genetic adaptation to several constraints including excess soil Al. However, not much information is available on the diversity of Al tolerance in the native cultivars of the northeast India as well as the genetics. A study was undertaken to divulge the variability for tolerance to high Al, as well as mapping genomic regions controlling tolerance. Study involved 109 genotypes originating from India including the northeast that were constituents of the 3000 rice genome panel. Additionally, six cultivars were used to identify the critical Al concentration that differentiated tolerant genotypes from the sensitive ones. We could find that, among different traits, the root growth was the most significantly affected trait in rice seedlings. To standardize the reduction in root growth, we have used relative reduction in root length (RRRL) as the response paramters for determining Al toxicity tolerance. Among the various concentrations tested, we identified 60 mg L^{-1} as the critical level, which could significantly differentiate tolerant and sensitive genotypes. We have also investigated hematoxylin-staining score for differentiation of tolerance and sensitive classes through a root staining protocol. The staining, however, was found unreliable under high Al concentration, as several tolerant genotypes showed differential staining pattern at 60 mg L^{-1} and beyond. Further analysis on the variability of Al response among the germplasm panel indicated a distinct pattern among the genotypes. The tolerant and sensitive classes of genotypes were distinct and non-continuous indicating a significant influence of major genetic factors in conditioning the tolerance. Fifteen tolerant lines could be identified which constituted 9.2% of the panel used in the study, of which ten were native to northeast India. Using genome wide markers, we could stratify the population into two subpopulations that, however, did not show any pattern associated with Al tolerance. The genome-wide association study (GWAS) on traits such as root and shoot growth under the hydroponics screening, mapped fifteen significant marker trait associations (MTAs) distributed across chromosomes 1, 3, 4, 6, 7, 8 and 12. Among these, two MTAs on chromosome 3 and chromosome 8 showed significant influence on root length under Al stress as well as for RRRL. For both the MTAs, a relatively high percentage of variation explained was recorded over that of the root length under stress. This implied a major role for these MTAs in conditioning Al toxicity tolerance. No other common MTAs was found affecting more than one trait. Presence of several MTAs indicated presence of multiple mechanisms for Al toxicity response in rice. Further, no previous report on QTLs/ genes was found corresponding to the MTAs identified in this study, indicating the novelty of the MTAs. The marker-based survey of the major Al transporter gene, *NrAT1* among the panel indicated the presence of the gene among 75% of the tolerant genotypes, identifying it as the major contributing gene for tolerance. However, we could find genotypes that were devoid of *NrAT1* allele but showing tolerance and vice versa. This also indicated that there might be additional mechanisms other than *NrAT1* operating among some of the tolerant genotypes. The results of the current study suggest that *NrAT1* is a major candidate gene that can be recruited for introgression of Al toxicity tolerance in cultivars under development. Besides, integration of other genomic regions along with *NrAT1* could facilitate the development of cultivars with tolerance to high Al suitable for the Northeastern India.

Mapping genomic regions (QTLs) imparting salt stress tolerance in chickpea (*Cicer arietinum* L.)

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

Characterization and allele mining for drought tolerance from chickpea landraces

The chickpea productivity was hampered due to abiotic stresses and the drought stress is a major concern specifically terminal drought stress is the major contributor towards yield loss. The breeding for development of drought tolerant varieties in chickpea will be the primary aim of chickpea crop improvement. The landraces of chickpea will be the main reservoir for most of the economical important traits, the extensive phenotypic characterization and genotyping will help to identify the effective markers associated with the important traits and parallalley utilization of these landraces in pre breeding and crop improvement. The present investigation for characterization and allele mining for drought tolerance in chickpea landraces was carried out with the different objectives to screen chickpea genotypes for drought tolerance and identification of marker association for different traits. The 125 landraces collected from West Asia and North Africa (WANA) along with 25 released varieties in national system were evaluated at IARI and Dharwad. The 9 morphological traits were recorded for irrigated and rainfed condition at two locations and two seasons and 7 physiological traits were recorded under normal and drought condition at IARI, New Delhi. The one trait Drought Susceptibility Index (DSI) was calculated for both IARI and Dharwad location. The results from the combined ANOVA for morphological traits across the locations and seasons showed that the mean sum of square of genotypes x location interaction were significant for most of the trait studied, so that the studied genotypes had wide variability and the environmental influence on the fully expression potential of genotypes. The genotypes namely IG5856, PUSA72, IG5904, IG5849 and ICC4958 recorded the more grain yield under rainfed condition at both the location. The correlation between the morphological traits was significant between most of the traits and strong correlation was observed between SY and BY. The traits SY, NPB, NSB, NPP, 100SW, HI and BY had significant positive correlation among them. DSI was low for the genotypes IG5856, Pusa362, ICC4958, ICC92944 and RSG888, IG5904 at IARI, New Delhi, and PUSA72, ICC4958, ICCV10, RSG888, ILC866, IG5851B, IG5858, ILC5980, ILC0(Lativia) and IG5856 at dharwad location indicates these are drought tolerant genotypes. The box plot for all the morphological traits shows that the mean of all the traits decreased in rainfed condition compared to irrigated condition The results from the combined ANOVA for physiological traits in normal vs drought condition shows that the mean sum of square for all the 7 physiological traits was significant for normal vs drought condition. The genotypes IG5904, ICC4958 and IG5861 recorded higher RWC, the genotypes ILC8666, IG5861 and IG5856 were recorded higher MSI and the genotypes ICCV10 and ILC139 are recorded higher CTD indicated these were drought tolerant based on RWC, MSI and CTD. The positive correlation was observed among all the physiological traits. The box plot for physiological traits showed decrease in the mean of traits in all the traits except RL, however in some the genotypes longer RL was reported in drought condition. The stability analysis from AMMI was revealed that the GEI was portioned into three PC, the PC1 and PC2 (97.4%) explains the majority of the variability, the genotypes ILC184, IG5895 and IG5904 were stable genotypes based on the AMMI stability value (ASV) and the genotypes IG5856, PUSA72, IG5884 and IG5858 were stable and high yielding based on Yield Stability Index (YSI). The GGE biplot PC analysis PC1 and PC2 together explains 95.9% of variability. The total 6367 SNPs which are Minor Allele Frequency (MAF) of more than or equal to 0.05 were used for diversity, population and association analysis. The average PIC value of 0.25 and genetic distance of 0.33 was reported for these SNPs. The average linkage disequilibrium (LD) across the genome was 0.14 and average LD decay in the genome was of 225588 bp. The kinship between the individual genotypes varied from -0.52 to 2.07 and average genetic distance between the individual genotype was 0.31. The four sub populations were obtained based on the structure analysis from the 129 genotypes. The genome wide association studies for the morphological and physiological data with 6367 SNPs was carried out using FarmCPU, which consider both fixed and mixed model. The threshold p value to select the significant SNPs was bonferroni correction at p value 1. The total 63 significant SNPs reported to be associated with all morphological and physiological traits including DSI except NSB. The 7 SNPs reported to be associated with more than one trait may be these SNPs have pleiotropic effect. The total 23 SNPs was found to be significant for 100SW followed by 10 SNPs for SY and 7 SNPs for NPP and NPB. The two SNPs were reported for DSI. The total 12 SNPs reported for RL, SL, RDW and SDW. Eight SNPs were associated with both irrigated and rainfed condition, 33 for rainfed condition and 22 for irrigated condition alone Thirty-seven putative candidate genes were identified from the significant associated SNPs. Some of the genes like Guard Cell Hydrogen Peroxide-Resistant1 (GHR1) associated with DSI and NPP, E3 Ub ligase associated with SY, UDP-glycosyltransferase associated with BY, the LEA (Late embryonic abundant protein) with NPP and BY, PRP genes and GDSL esterase lipase protein with 100SW are known to be activated in drought stress condition. The gene like zinc finger BED domain-containing protein DAYSLEEPER-like, which is essential for plant development associated with 100SW and SY was essential for plant development. The allele diversity for CAP2 gene in the 7 selected genotypes from aforementioned 150 genotypes was studied. The total 15 SNPs (transition and transversion) were identified in the CAP2 and its 1000bp upstream promoter region, of which two SNPs sites at 669 and 83 upstream regions of CAP2 gene were parsimony informative sites. Four SNPs were indentified in CAP2 gene of which one SNP (C-T) was found in coding region of ICC4958 genotype, which makes the substitution of the amino acid Arginine (R) in the reference genotype by Tryptophan (W). The relative expression of CAP2 gene under stress condition was studied in these seven genotypes and the prominent expression was observed in the genotypes IG5856, ICC4958 and IG5861. The relative expression of CAP2 gene and morpho-physiological characterization of these genotypes showed the association. In summary the characterized drought tolerant genotypes and significant SNPs can be used in future breeding for developing drought tolerant varieties and also for improved yield.

Theme 2. Biotic stress tolerance

Comparative RNA-Seq analysis and antioxidant studies to understand the complex regulatory network of MYMIV resistance in mungbean (*Vigna radiata* (L.) R. Wilczek)

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

Inheritance of resistance to mungbean yellow mosaic virus in soybean

Soybean occupies first place in India as an edible oil seed crop with respect to area and production. The area of soybean is increasing year by year but the productivity still remains low. The three major constraints in soybean production in India are drought; weed infestation and location specific biotic stress (Lal and Sapra, 2013). A set of ninety-two advanced breeding lines developed from several diverse crosses were screened for resistance against Mungbean Yellow Mosaic Virus (MYMV) at the hot-spot. Out of 92 genotypes studied seven *Glycine max* (L.) Merrill and ten *Glycine soja* (Siebold and Zucc.) derived genotypes were found to be immune to the MYMV. These 92 advanced breeding lines along with the five checks were characterized for seven qualitative and nine quantitative traits. They were further grouped into six different clusters using K-means clustering method. The genotypes in cluster V and VI were highly diverse and can be used for developing heterotic crosses. Inheritance of resistance to MYMV was studied in the resistant parent SL 958. SL 958 was crossed with susceptible parent VLS 59. The segregation for resistance to MYMV in F2 population showed a goodness of fit to 3:1 susceptible ratio with probability of 0.28 at X2 (3:1) as 2.51 in the cross SL 958 x VLS 59. The viral genome was isolated from the susceptible genotype DS 1487 for cloning. The bipartite genome of Mungbean Yellow Mosaic India Virus isolated from infected soybean was successfully cloned and sequenced. The sequence comparison showed that the cloned gene sequence has 99% similarity to MYMV virus of Urdbean and Horsegram. Molecular markers (SSR markers) linked to MYMV resistance in soybean were also reported by different authors. Out of 10 SSR markers studied to see if these markers can distinguish the resistant and susceptible genotypes. The results show that they failed to distinguish the resistant and susceptible genotypes.

Characterization of dicoccum wheat germplasm using morphological and molecular markers and identification of leaf rust resistant germplasm

Emmer wheat (*Triricum dicoccum*), an annual, self-pollinated crop with tetraploid chromosomes (2n=4x=AABB=28) are the rich source of important nutritional parameters. Dicoccum germplasm conserved in the Indian national genebank is a potential source of several important traits and their characterization and evaluation will generate knowledge about the available genetic diversity, unique traits and the resistant source. In the present study, 192 dicoccum wheat accessions from the National Genebankwere assessed for their genetic diversity using agro-morphological traits and also characterized for leaf rust resistance. Subsequently, a subset of 96 accessions were selected using Powercore software for agro-morphological descriptors and passport data, and were characterized using 56 genomic microsatellite markers. The analysis of variance indicated the existence of sufficient genetic variation among accessions for all the characters studied in different locations. Based on pooled analysis, grain yield was positively and significantly correlated with DM, PDL, GS, GWS and TGW. On the basis of principal component analysis (PCA), first six PCs explained 77.638% cumulative variation based on 14 quantitative traits. Major contributing traits for PC1 were: GRS (0.801), SLS (0.680), SL (0.560) and GWS (0.538), GY (0.484), DM (0.453), GL (0.443), DSE (0.429), TGW (0.423). Accessions having high PC scores EC299240, EC11389, IC535070, IC535113, EC577960, IC138450, EC540809, EC540813, IC138474, EC299074, EC577404, IC534960 may be useful for emmer wheat improvement. Cluster analysis grouped the total 192 accessions into six clusters with Cluster I and VI being contrast for several traits which may be used in selection of diverse parents for crossing program. In the present study nineteen accessions were found to be very resistant at seedling stage against leaf rust disease pathotype 77-5. Molecular profiling of 96 diverse emmer accessions using 28 polymorphic SSR markers revealed a total of 93 polymorphic alleles and the highest PIC value (0.991) was observed for Xcfd20 marker followed by (0.985) for Xcfd13. Population structure as well as neighbour joining tree classified 96 diverse *dicoccum* accessions into two groups. We identified in this study donor germplasms for multiple traits such as IC551397 for GS, SL, GL and resistant to leaf rust; IC443708 for PH, SL, GLWR, GY; IC112083 for DM, DSE; EC609395 for GS, SLS, resistant to leaf rust that can be used for improvement of bread and durum wheat.

Theme 3. Quality traits improvement

Analysis of genetic variability for lipoxygenase activity and validation of *lipoxygenase 3* (*LOX3*) gene affecting retention of kernel tocopherols in maize during storage

Deficiency of vitamin-E or tocopherol results in several neurological and age-related disorders in humans. Though traditional maize is rich in total tocopherols, α-tocopherol, the most active form of vitamin-E is present in low concentration (6-8 µg/g). Utilization of maize mutants with favourable allele of vte4 gene led to the development and deployment of several α-tocopherol rich (16-19 µg/g) maize hybrids worldwide. However, degradation of tocopherols during post harvest storage substantially affects its efficacy as a tool for combating the adverse effects of micronutrient deficiency. In the present investigation, a diverse panel of vte4-based inbreds along with its wild type (VTE4) genotypes was analyzed to study genetic variation for retention of tocopherols during storage and effect of lipoxygenase (LOXs) on retention of tocopherols. Mean α-tocopherol among vte4-based inbreds reduced to 5.32 µg/g after a period of six months of storage from 21.36 µg/g in the freshly harvested kernels. In normal inbreds, it got reduced to 1.28 µg/g from the initial level of 11.60 µg/g at harvest. Retention of α-tocopherol in the vte4-based inbreds was 24.78% which was significantly better than the normal inbreds (11.06%). HKI323-PVE (45.44%), HKI1105-PVE (24.08%), HKI161-PVE (23.17%) and HKI1128-PVE (22.73%) were the promising α-tocopherol rich maize inbreds with better retention potential even after sixmonths of storage. Lipoxygenase activity in the two contrasting genotypes with differential retention for α-tocopherol viz. HKI323-PVE (10.03 µg/g after six months) and HKI193-1- PVE (3.71 µg/g after six months) showed a perfect negative correlation of specific activity of lipoxygenase enzyme with retention of α-tocopherol (r = -0.725). mRNA expression level of *LOX3* gene among these distinct genotypes showed contrasting trend over different storage intervals. The correlation between expression level of *LOX3* and retention potential for α-tocopherol was significant and negative (r = -0.826), revealing that higher expression of *LOX3* led to low retention of α-tocopherol during storage. The information generated in this study signifies the crucial effect of *LOX3* gene on retention of α-tocopherol. Promising genotypes with high retention of α-tocopherol, favourable *LOX3* allele and reduced lipoxygenase activity can be effectively utilized in the biofortification programme to develop α-tocopherol rich maize hybrids with higher retention during the post-harvest storage.

Studies on genetic variability and molecular characterization of diverse inbreds and genetics of resistant starch in maize (*Zea mays* L.)

Starch is a major energy reserve in higher plants and the most abundant carbohydrate next to cellulose. Starch fraction that is digested within 20 mins in human gut is called as readily digestible starch (RDS). Slowly digestible starch (SDS) takes 20-120 mins, while resistant starch (RS) takes >120 mins to digest. RS is resistant to enzymatic-hydrolysis in the small intestine (SI), and is fermentable by microflora in the colon. This incomplete digestion by human pancreatic amylase allows starch molecules to be cleaved in the colon by bacterial enzymes to produce short chain fatty acids (SCFA) particularly butyrate, resulting in promoting good colonic health and preventing colon-rectal cancer. RS significantly lowers down the glycaemic index (GI) in humans. The GI of traditional maize is 81, while the GI of high amylose maize conditioned by amylose extender1 (ae1) gene reduces GI to 44. Maize with a potential to grow in diverse environments serves a preferred choice for RS-based foods. So far there is no report on improvement of amylose and RS in maize India. Here, a set of 48 diverse maize inbreds were evaluated for amylose and RS at three locations (Bajaura, Delhi and Jhansi) during kharif-2020. These inbreds were further characterized by markers associated with *ae1* (*sbe2b*) and its modifier gene, *sbe1a*. 27 SNPs earlier identified to be linked to accumulation of amylose in maize were converted to PCR-based markers. These SNP-based markers were also used to characterize the inbreds varying for amylose and RS. Further, a set of 21 hybrids developed through 7 × 7 half diallel (Model-I, Method-IV) were evaluated at three locations (Delhi, Jhansi and Parbhani) during kharif-2020 for analyzing the genetics of accumulation of amylose and RS in maize kernels. The study revealed wide variation for amylose (1-66%) and RS (1-39%), with a mean of 28.9% and 9.9%, respectively among the diverse inbreds. Three inbreds viz., PMI-AML-145 (amylose: 50.4%, RS-20.9%), PMI-AML-147 (amylose: 64.5%, RS-38%) and PMI-AML-146 (amylose: 66.5%, RS-39.4%) were identified as the most promising for both amylose and RS. These novel lines can be used as donors in the breeding programme. In case of amylose and RS, genotypes contributed 94-99% of the total variance. Effect of environment (0.01-0.08%) and genotype × environment (G × E) interactions (1.56-0.27%) was negligible for amylose and RS. This suggested that amylose and RS were quite stable across locations. There was no correlation between total starch (TS) and amylose ($r = 0.14$). Similar trend was also observed between TS and RS ($r = 0.02$). This suggested that there may not be yield penalty by increasing amylose and RS in maize kernels. However, amylose was strongly correlated with RS ($r = 0.81$), thereby indicating that enhancement of amylose would lead to the enhanced accumulation of RS. Molecular analysis for ae1 (sbe2b), sbe1a and 18 QTLs generated 40 alleles with average major allele frequency of 0.84. The gene diversity, PIC and genetic dissimilarity was 0.23, 0.19 and 0.33, respectively. The markers grouped 48 genotypes into six major clusters. High amylose and RS lines were grouped into cluster-A and cluster-B, which can be useful in selecting parents for hybridization ensuring accumulation of favourable alleles into single genetic background. Principle coordinate analysis supported cluster analysis and the results were in congruence with the pedigree of the inbreds. Markers, *Sbe2b* and *Sbe1a* were correlated with amylose ($r = 0.37$, $r = 0.47$, respectively) and RS ($r = 48$, $r = 0.58$, respectively). Marker, MGU-HAM-6 (allele ‘A’) for sucrose transporter 6 (SUT6) gene was also correlated with RS ($r = 0.48$). RS among 21 hybrids varied from 15.8-23.9% with an average of 20.9%. The mean amylose among the experimental hybrids was 38.1%, with a range of 23.8-49.1%. However, check hybrids had significantly lower amylose (29.1%) and RS (2.3%). Higher amylose and RS was observed in PUSA-AML-H12 (49.1% and 23.9%), PUSA-AML-H18 (45.6% and 23.8%) and PUSA-AMLH16 (45.4% and 23.5%). PMI-AML-147 (3.48 and 1.09), PMI-AML-146 (1.41 and 0.48) and PMI-AML-149 (3.29 and 0.38) were the best general combiners for both amylose and RS. PUSA-AML-H1 (6.10 and 1.01) and PUSA-AML-H12 (2.84 and 0.59) were the best specific combiners for amylose and RS. Additive variance was predominant for amylose, while RS was influenced more by non-additive gene action. This is first report of genetic analysis of amylose and RS among maize inbreds in India.

Enrichment of sweet corn genotypes with provitamin A, lysine and tryptophan through marker-assisted introgression of *crtRB1* and *opaque2* alleles

Sweet corn has emerged as one of the most preferred vegetables worldwide due to its delicious taste and diverse uses in various soups and snacks items. However, traditional sweet corn is poor in nutritional quality due to low levels of provitamin-A (proA), lysine and tryptophan. In present study, two *shrunken2* (*sh2*)- based sweet corn hybrids viz., ASKH-1 (SWT-16 × SWT-17) and ASKH-2 (SWT-16 × SWT-18) were targeted for nutritional enrichment through marker-assisted introgression of favourable alleles of *βcarotene hydroxylase1* (*crtRB1*) and *opaque2* (*o2*). PMI-PV-5 and PMI-PV-8 were used as donor parents. Gene-based markers; umc1066 (SSR) and 3’TE-InDel were utilized for foreground selection of *o2* and *crtRB1*, respectively in BC_1F_1, BC_2F_1 and

BC_2F_2 generations. Background selection using 102-113 polymorphic SSRs recovered >90% genome of recurrent parents. Introgressed progenies possessed higher level of proA (18.87 μg/g), lysine (0.37%) and tryptophan (0.08%) compared to parental lines (proA: 3.04 μg/g, lysine: 0.19%, tryptophan: 0.05%). Reconstituted hybrids recorded 18.98 μg/g of proA with a maximum of 7.7-fold increase over original hybrids (3.12 μg/g). The lysine and tryptophan concentration in improved hybrids was 0.39% and 0.10% with an average enhancement of 1.71- and 1.79- fold, respectively over original versions (lysine: 0.23%, tryptophan: 0.06%). The average dehusked cob yield (11.82 t/ha) and brix (17.66%) of improved hybrids was at par with their original versions (dehusked cob yield: 11.27 t/ha, brix: 17.04%). The converted inbreds and hybrids also showed high degree of similarity for plant-, ear- and grain- characteristics to their respective original versions. These biofortified sweet corn hybrids with enhanced proA, lysine and tryptophan assume great significance in providing balanced nutrition. This is the first report to stack sh2, crtRB1 and o2 genes to improve nutritional quality in sweet corn. Evaluation of eighteen biofortified sweet corn hybrids at 20-, 24- and 28- days after pollination (DAP) under three sowing dates revealed significant influence of genotypes, sowing time, harvest time and their interactions on sweetness, lysine, tryptophan, β-carotene (BC), β-cryptoxanthin (BCX) and proA concentration. Decreasing trend of accumulation for lysine, tryptophan, BC, BCX and proA was observed at 20-, 24- and 28-DAP, respectively. However, mean brix attained the peak at 24-DAP followed by 20-DAP and lowest brix recorded at 28-DAP. Considering both nutrition and sweetness, 20-DAP was the best suitable time for harvesting of sweet corn ears. Later date of sowing recorded higher concentration of nutritional traits compared to earlier dates of sowing. We also analyzed the expression pattern of crtRB1 and o2 genes among introgressed and traditional sweet corn inbreds at 20-, 24- and 28-DAP. Biofortified sweet corn inbreds possessed significantly lower expression levels of crtRB1 (4.1-folds) and o2 (2.2-folds) compared to their wild type alleles in traditional sweet corn inbreds across DAPs. The expression of crtRB1 and o2 increased from 20-DAP to attain the highest peak at 24-DAP, and further decreased by 28-DAP. Lower expression of crtRB1 and o2 genes strongly correlated with the higher nutritional profiles (r= >0.70) during different stages of kernel development. This is the first report on expression of crtRB1 and o2 genes during kernel development in biofortified sweet corn. Additionally, introgressed sweet corn inbreds were analyzed for various seed vigour attributes. The o2- introgressedinbreds showed significantly lower germination and seed vigour than original inbreds, while *crtRB1*- and *o2+crtRB1*- introgressed inbreds recorded at par seed germination and vigour compared to original inbreds. Considering the seed vigour traits and nutritional quality, *o2+crtRB1*-based sweet corn was found ideal over *o2*- and *crtRB1*-based sweet corn genotypes.

Identification of quantitative trait loci and candidate genes associated with enhanced grain zinc and iron concentration in wheat (*Triticum aestivum* L.)

The development of biofortified wheat with greater levels of iron (Fe) and zinc (Zn) is considered a sustainable strategy for solution to the problem of micronutrient deficiency. The identification of genomic regions controlling the grain micronutrient concentration along with the linked markers provides a greater opportunity for precise transfer of the controlling segments in the breeding populations. The current study utilized both biparental population and association panel, mainly to identify the genomic regions associated with grain zinc and iron concentration. 190 recombinant inbred lines (RILs) from 'Kachu' × 'Zinc-Shakti' cross were phenotyped for grain Fe and Zn concentrations and phenological and agronomically important traits at Ciudad Obregon, Mexico in the 2017–2018, 2018–2019 and 2019–2020 growing seasons and Diversity Arrays Technology (DArT) molecular marker data were used to determine genomic regions controlling grain micronutrients and agronomic traits. We identified seven new pleiotropic quantitative trait loci (QTL) for grain Zn and Fe on chromosomes 1B, 1D, 2B, 6A and 7D. The stable pleiotropic QTL identified have expanded the diversity of QTL that could be used in breeding for wheat biofortification. Nine RILs with the best combination of pleiotropic QTL for Zn and Fe have been identified to be used in future crossing programs and to be screened in elite yield trials before releasing as biofortified varieties. In silico analysis revealed several candidate genes underlying QTL, including those belonging to the families of the transporters and kinases known to transport small peptides and minerals (thus assisting mineral uptake) and catalyzing phosphorylation processes, respectively. The Genome-Wide Association Studies (GWAS) panel consisted of 183 diverse genotypes that were evaluated during the 2019-20 crop season at IARI-New Delhi, IARIIndore and GBPUAT-Pantnagar for grain Fe and Zn, protein content, test weight and thousand kernel weight and genotyped with the Breeders' 35K Axiom Array. A total of 55 marker-trait associations (MTAs) were identified, of which four significant MTAs were identified for GFeC on chromosome 2B, 3A, 3B, 6A and two significant MTAs identified for GZnC on chromosomes 1A and 7B. The putative candidate genes found were F-box-like domain superfamily, zinc finger CCCH-type proteins, Serine-threonine/tyrosine-protein kinase, Histone deacetylase domain superfamily and SANT/Myb domain superfamily proteins among others.

Genetic and molecular analyses of cooking parameters in rice

Rice is one of the most important cereal crops feeding more than half of the total population across the world. Being a less expensive source of carbohydrates, it forms a major dietary source for the people especially in South and South East Asia. Instant cooked food is gaining popularity among the consumers worldwide. A large number of genes/ QTLs governing cooking quality traits have been mapped in rice and some of them have been cloned. However, there has been limited work on time needed for optimal cooking in rice. Boka Chaul, a landrace from lower Brahmaputra valley of Assam has a unique property of zero or no cooking for consumption. The present study was carried out with the objectives of characterizing the physical and biochemical parameters associated with cooking, to elucidate the inheritance and to attempt mapping of gene(s)/ QTLs governing cooking associated parameters in rice. In order to achieve the above objectives, three rice genotypes namely, Boka Chaul, Pusa Basmati 1121 (PB 1121) and Pusa Basmati 1509 (PB 1509) were used for standardization and assessment of differences in cooking parameters. For soaking time and cooking temperature, there was no variation among the three rice genotypes, as the optimum cooking and elongation was observed at 30 minutes of soaking and cooking at temperature of 100°C. The time taken for optimum cooking showed significant variation with Boka Chaul taking only seven minutes, while PB 1121 took eight minutes and PB 1509 took 13 minutes. Among the biochemical parameters, the alkali spreading value score was seven in all the genotypes, grouping them into low gelatinization temperature category. Boka Chaul and PB 1121 exhibited hard gel consistency while PB 1509 exhibited medium gel consistency. The amylose content of PB 1121 and PB 1509 were intermediate while that of Boka Chaul was marginally higher than both.Two crosses namely, Boka Chaul/ PB 1121 and Boka Chaul/ PB 1509 were advanced to F_2 generation and significant variation was observed in the segregating population for optimum cooking time of milled rice among the 187 F2 progenies from Boka Chaul/ PB 1121. Out of the 187 genotypes, 35 genotypes were optimally cooked in less than seven minutes, 61 genotypes between 7-8 minutes, 64 genotypes in eight minutes and 27 genotypes took more than eight minutes. The segregation of the F2 population did not fit into any ratio for monogenic or digenic segregation, and showed a near normal distribution indicating the complex nature of the inheritance for cooking time. The optimum cooking time was not necessarily associated with the cooked grain kernel length, since there were extra-long slender grains that cooked within 7 minutes of cooking at 100°C and there were shorter grains which took longer than eight minutes of cooking. Bulked segregant analysis with bulks of 15 genotypes (grains from F2 individuals) each exhibiting extreme contrast for cooking time (cooking time < 7 minutes and > 8 minutes), could not identify putative linkage with any of the 59 polymorphic SSRs. There is a need to develop RIL population which will enable multi-location phenotyping as well as sufficient samples for phenotyping to map the QTL(s) governing cooking time. Additionally, high density markers shall be employed for genotyping as the per cent polymorphism between Boka Chaul and the Basmati rice varieties were comparatively low. There is a need for in-depth studies to understand the basis of zero cooking property of the landrace, "Boka Chaul" through studies integrating genetic, biochemical, genomic and metabolomic tools.

Theme 4. Genetics of miscellaneous traits

Studies on morphological and molecular characterization of mutant lines of wheat

Mutant lines developed through gamma irradiation of two popular varieties, HD 3086 and HD 3118 were studied for phenotypic variation in M_3 and M_4 generation and characterized at morphological and molecular level. 250 mutant lines were identified in M_3 generation in field with mutant phenotype for morphological and, agronomic traits. The selected mutants were planted with 4 check varieties in timely and late sown condition in augmented design and phenotypic variation was observed for days to heading (DH), plant height (PH), glaucousness (GL), SPAD chlorophyll content, Flag leaf area (FLA), spike length (SL), spike weight (SW), number of spikelets per spike (NS), grain yield (GY), thousand grain weight (TGW) and awn/awnless traits. Anova displayed significant difference for GL, PH, SL, NS and TGW in timely sown condition and for GL, DH, PH, SPAD, SW, GY and TGW in late sown condition. GL, PH, SW and GY were positively correlated with TGW under timely sown condition and GY is positively correlated with TGW under late sown condition. Mutant lines showed an overall increase in GL score in late sown condition suggesting the role of glaucousness in adaptation to heat stress. Mutant lines with short/ no awns had low stress tolerance index, higher plant height and lower grain yield under stress condition indicating the presence of awns may be beneficial to heat stress environments. Evaluation of mutant lines for leaf rust race 77-9 and for yellow rust races 238S119 and 110S84 revealed 9 leaf rust resistant lines and 4 highly resistant lines to yellow rust race. Mutant lines with specific traits were genotyped with gene specific markers for adaptation traits such as vernalization, photoperiod requirement, plant height and, glaucousness. None of the markers for vernalization, photoperiodism and reduced height used in this study showed polymorphism indicating there is no mutation in these genomic regions. Mutants lines for non-glaucousness showed absence of DMC gene specific marker depicting there may be deletion mutation at this locus. Mutant lines with reduced/no awns revealed polymorphism at 5A gene locus indicating a 25bp known deletion at this locus and the deletion was confirmed by sequencing of PCR amplicons. A few selected mutants for leaf rust, yellow rust, glaucousness and awnless traits were used for SNP genotyping using 35K SNP chip revealing 0.04 to 1.6% polymorphism between selected mutants and parent HD 3086. Neighbour joining analysis on the basis of 35K SNP markers revealed leaf rust and yellow rust resistant lines forming one cluster suggesting some common alleles for rust resistance. SNP genotyping indicated a number of point mutations were induced that may be putatively linked to economically important traits. The identified lines may be used as donor in breeding programmes and represent an excellent material for basic genetic studies in future.

Development of non-necrotic backcross derived lines of wheat varieties HD2967 and HD2733

Hybrid necrosis in wheat occurs because of two dominant complementary genes, *Ne1* and *Ne2*located on chromosomes 5BL and 2BS respectively. When one variety carries *Ne1* and the other variety *Ne2*, hybrid necrosis occurs at F_1 stage resulting in death of the F_1 plant. Two high yielding wheat varieties, HD2967 and HD2733 which often used in crossing programs either to develop a new variety or to introgress some useful genes, produced hybrid necrosis in some of the crosses resulting in failure of development of F_1 plants. So, a programme was initiated to preclude the necrosis genes from the parental lines. To remove the necrosis gene present in these varieties, first we have to know the necrosis genes present in them. For this three markers *Xbarc74* (co-dominant and linked to *Ne1*), *Xwgrc3146* (dominant and co-segregating with *Ne1*) and *Xbarc55* (co-dominant and linked to *Ne2*) were used in marker validation. Both the markers *Xbarc74* and *Xwgrc3146* identified the presence of Ne1 gene in wheat varieties, HD2967 and HD2733 along with positive check C306. Recessive allele of *Ne1*i.e *ne1* found in wheat varieties HD2932, HD3059 and negative checks Agra Local and NI5439. The marker *Xbarc55* amplified a different size of band in HD2967, HD2733 and HD2932 corresponding to positive check Sonalika while equal size of band was produced in wheat cultivar Parula. This means all these varieties, HD2967, HD2733 and HD2932 do not carry *Ne2* gene while Parula carries *Ne2*. As the varieties, HD2967 and HD2733 carries only *Ne1*, marker assisted backcrossing was used to replace dominant *Ne1* with recessive ne1 by using HD2932 as donor parent. Parental polymorphism survey between DP and RPs identified 47 polymorphic markers each out of 642 markers used. While some of the polymorphic markers were common between both the parental sets, most of them are different. Foreground selection in BC_1F_2 generation identified plants with *ne1*genein homozygous (*ne1ne1*) and heterozygous (*Ne1ne1*) state. Background selection in these plants identified a plant with 85.10% and 84.78% of RPG in HD2967 and HD2733 respectively. Foreground selection was also carried in BC_2F_1 generations of two varieties and plants with heterozygote ne1 were identified. In BC_2F_1generation, 95.75% and 93.47% of RPG was recovered in HD2967 and HD2733 respectively. These backcrosses derived lined were also selfed and backcrossed to produce BC_2F_2 and BC_3F_1 generations respectively. Background selection in BC_2F_2 and BC_3F_1 generations will further increase the RPG and help in identification of homozygous (*ne1ne1*) NILs in BC_2F_2 generation. Homozygous NILs once identified can be used in any crossing programme without producing hybrid necrosis at F_1 stage.

Mapping quantitative trait loci for stay greenness and its component traits associated with nitrogen use efficiency in rice

To ensure food security for the future, contemporary rice breeding must harness novel secondary traits linked to higher productivity. Functional stay greenness (FSG) is one such secondary trait, characterized by delayed senescence during the reproductive stage, connected to higher grain yield and related to nitrogen (N) use. Pusastay green 16 (PSG 16) is a novel stay green mutant that appeared in a breeding population which showed true to type breeding in the subsequent generations and showed higher grain yield. Study of the inheritance pattern of the stay green behaviour in PSG16, by crossing with two non-stay green parents Pusa 677 and Pusa 44 indicated a major gene inheritance in the F_2 generation. The trait was found associated with the measure of total chlorophyll content (TCC) at the physiological maturity stage. The relationship of TCC to other agronomic traits, in the segregating populations of the cross, from F_2-F_5, showed a consistent association with grain yield, suggesting the functional property of the stay green trait. However, TCC showed a quantitative inheritance pattern. Additional investigations on the inheritance pattern and gene actions for the TCC revealed significant additive and dominant gene actions. On an individual gene basis, the dominance superseded the additive component, thereby signifying the class variation observed under the goodness of fit test. However, a large interaction component with additive × additive gene action could be identified in trait expression. Therefore, the inheritance of stay green trait was complex and deviated from the simple additive dominance pattern. A careful breeding procedure involving intermating, sib-mating and recurrent selection may be needed to utilize the trait in crop improvement. The causative loci need to be mapped for further understanding of the stay green behaviour of PSG16, along with in-depth physiological characterization for the functionality of the trait. PSG16 and Pusa 677 along with two checks (Nidhi and Rasi) were screened under hydroponics and field level with differential N regimes for studying various parameters viz., seedling growth, crop growth rate, total protein content and nitrogen use efficiency 109 (NUE) parameters. Among parents, PSG16 outperformed for all NUE parameters viz., agronomic NUE, physiological NUE, N harvest index, grain yield efficiency index, N recovery efficiency, and N assimilation efficiency. Among the checks, Nidhi, the high NUE line well performed for all NUE parameters. Hence PSG16 could be utilized as donor for stay green trait and high NUE line to integrate in rice breeding programme to increase grain yield under low N input conditions. We have evaluated a RIL population derived from Pusa 677/ PSG16 to understand the genetics of the FSG trait in a mutant, PSG16. Evaluated under two N regimes along with checks RILs showed significant variation for agronomic traits and N use. Grouped based on the stay green expression RILs showed significant variation for leaf chlorophyll content, flowering time, and yield components. A total of 104 polymorphic markers spanning all 12 chromosomes created a total linkage map of 1910.8 cM. Mapping of influential genomic regions using quantitative trait loci (QTL) mapping identified a major QTL on chromosome 1 associated with chlorophyll content and flowering time. Of the six major QTLs identified, four colocalized were found consistent across different N regimes. Of the remaining two QTLs, one was associated with grain number and located on chromosome 7, while another on chromosome 6, was found linked to N harvest index and spikelet fertility. Based on the segregation pattern we conclude that PSG16 has a clear advantage in grain yield as well as having better N use efficiency, particularly related to N assimilation. However, the genetic control of stay green trait and N use was not found to be direct. The novel trait of PSG16 could be advantageous in deciphering multiple stress tolerance in rice.

Genetic investigation on the allelic distribution of wide compatibility gene in rice (*Oryza sativa* L.)

A set of 967 rice gemplasms consisting of 297 IRG (International Rice Germplasm) lines, 180 *tropical japonicas* and 490 other rice germplasms (mostly released varieties) were screened for *S5* locus possessing *neutral (S5-n)*, *indica (S5-i)* and *japonica (S5-i)* alleles using PCR based functional markers namely S5-InDel, IASP2 and JASP1, respectively. Among them, 171 (17.68%) lines were found homozygous *S5-n* allele possessing a band size of 281 bp, 656 (67.84%) lines were identified as homozygous for *S5-i* allele with a band size of 527 bp and 140 (14.48%) lines we identified as homozygous for *S5-j* allele with a band size of 325 bp. Out of 171 wide compatible varieties, a subset of 123 lines were selected and characterized at three different locations for twelve morphological traits. Three WCVs had higher spikelet fertility (%) namely, N77, Dular, N82 and N112. Five wide compatible varieties were found to have yield per plant more than 30 gm and performed promising with higher yield potential namely, N44, N77, N62, N60. Further, these 123 wide compatible varieties including Dular and Nagina 22 were subjected for diversity assessment based on morphological traits. Cluster based analysis revealed two clusters, wherein, 60% of the wide compatible varieties have been grouped in cluster I along with Dular and Nagina 22, whereas cluster II was represented by 40% of the wide compatible varieties. Both the clusters had variable proportion of *indica* and *japonica* types. Further, 92 wide compatible varieties were selected from 123 WCVs based on seed availability and flowering duration. These 92 WCVs were screened using 90 micro-satellite markers to know the molecular diversity. Molecular markerbased Population structure revealed two populations consisting of 49 genotypes in population I (POP1) and 31genotypes in population II (POP2) and 16 genotypes were classified as admixture. Further, a total of 164 inter sub-specific hybrids were developed utilizing 41 selected wide compatible varieties crossed with two *indica* and two *japonica* genotypes namely, Pusa44, IR64, TPJ29 and TPJ52. These hybrids were grown for multi-location evaluation in three different environments and it was found majority of the hybrids having excellent spikelet fertility percentage with an average of 70.53 %. With the findings of our study, we conclude the potentiality of identified WCVs and also it showed the utility of PCR based functional marker (InDel S5) in quick and precisely identification of wide compatible varieties. These identified superior wide compatible varieties can further be used as a novel source of WC gene and will be utilized for marker assisted incorporation of *neutral* allele into elite rice varieties and development of inter sub-specific hybrids.

Inheritance and validation of markers for kernel row number in tropical maize (*Zea mays* L.)

Grain yield in maize is a complex trait, determined by many component traits. However, kernel row number (KRN) is a major component with high heritability among the other yield component traits. But the genetic information on KRN traits in tropical germplasm is meager. This study was conducted to understand the number of genes controlling KRN and its inheritance pattern in tropical maize. Bulked segregant analysis approach was used to identify putative markers linked to the trait. Two F_2 populations *viz*., population I (AI 505 × AI 542) and population II (AI 505 × AI 541) was evaluated for yield and yield components during *Kharif*- 2020 at IARI, New Delhi. The KRN data of both the F_2 individuals from both populations were fit to a gene model as explained by the classical work of E.M. East, on tobacco. The population I having 232 F_2 individuals exhibited one individual with a high KRN parental phenotype which was approximately equal to one in 256 i.e. $1/4^4$. Similarly, population II having 250 F_2 individuals exhibited 17 individuals with a high KRN parental phenotype which was approximately equal to one in 16 i.e. $1/4^2$. The result was again endorsed by Wright and Castle's estimator implying that 4 and 2 factors determine KRN component in population I and population II respectively. There was a significant positive correlation between KRN and ear diameter, kernel number per row, and grain yield. Hence, this can be a key selection trait for inbred line improvement followed by genetic enhancement of hybrid *per se*. A set of 69 SSR QTL-based markers linked to the KRN trait was used in assessing the parental polymorphism between high and low KRN parents, of which 23 markers were found to be polymorphic. Of the 23 polymorphic markers, nine were found to be polymorphic between the high and low KRN bulks. These nine markers were used to validate the QTL for the KRN trait. A putative QTL was identified on chromosome 2 with 10.24 and 18.26 as LOD and PVE (%), respectively with flanking markers bnlg 1017 and bnlg 1017. Further fine mapping of the identified QTL may give insight into the linked markers followed by the genes responsible for KRN in tropical maize.

Genetic analysis and identification of loci governing prolificacy in "Sikkim Primitive" - a novel landrace of maize in India

Presence of multiple ears per plant also known as 'prolificacy' holds immense promise in developing high yielding baby corn hybrids. 'Sikkim Primitive' is a unique Indian maize landrace known for possessing 5-9 ears per plant. So far, the genetics and molecular understanding of prolificacy in 'Sikkim Primitive' has not been deciphered. Here, systematic analysis indicated the prominence of epistatic gene action in regulating prolificacy in 'Sikkim Primitive'. Presence of negative additive × additive [i] gene effects depicted the reducing effect of one of the parents over prolificacy. A major gene block was found to be responsible for prolificacy in 'Sikkim Primitive'. QTL mapping identified a major QTL, named as 'qProl-SP-8.05' explaining 31.7% phenotypic variation using $F_{2:3}$ population of MGUSP101 × HKI1128. This QTL was also validated in $F_{2:3}$ individuals of MGUSP101 × UMI1200. A 6 bp insertion in tb1 gene (located at 420 bp downstream of coding sequence) specific to all teosinte accessions was identified and validated using a newly designed PCR marker. All maize tb1 mRNA and protein were found to possess 1101 bp and 366 amino acids. TB1 protein was found to have highly conserved TCP and R motif. Genomic characterization of 'Sikkim Primitive' and diverse maize inbreds revealed that variation unique to MGUSP101 was found in coding region of branching related genes viz., *ramosa3* and *Zeaxanthinepoxidase1*. The polygalacturonate 4-alphagalacturonosyltransferase activity was a significant gene ontology (GO) term associated with genes harboring high impact mutations unique to 'Sikkim Primitive'. This gene is related to pectin biosynthesis and related pathway. In 'qProl-SP-8.05' region on chromosome-8, a frameshift mutation was found in *Zm00001eb365210* encoding a *glycosyltransferase* gene which is also involved in pectin related pathways. The present study thus conclusively provided a clear understanding of inheritance the locus involved of prolificacy in 'Sikkim Primitive'. The information thus assumes practical significance in breeding superior baby corn hybrids.

Genetics and interrelationships of time of flowering and stem growth habits in chickpea (*Cicer arietinum* L.)

Time of flowering and stem growth habit are the two important plant architectural traits desirable for improving adaptation of chickpea and its grain yield potential under cool long-duration environments of northern Indo-Gangetic plains. An understanding of the inheritance of flowering time and semi-determinacy in new found sources having the best combination of earliness and architectural traits would facilitate breeding of chickpea varieties better adapted to such environments. The present study was to understand genetics of time of flowering and stem growth habit in early flowering and podding genotypes and study of interrelationships to know the effect of flowering time and stem growth habit on pod and seed traits. Three parents, namely BGD72 (IDT, Late, Desi), BG1054 (SDT, Early, Kabuli) and BG1044 (SDT, Early, Desi) and F_1, F_2 and $F_{2:3}$ of three crosses (BGD72 x BG1054; BGD72 x BG1044 and BG1044 x BG1054 were evaluated for flowering time, stem growth habit (IDT &SDT) and productivity related traits at the Division of Genetics, ICAR-IARI, New Delhi during rabi 2019-20 and 2020-21. The study of F_1 s and segregation pattern in F_2 s and F_3 progenies of BGD72 (Late) x BG1054 (Early) and BGD72 (Late) x BG1044 (Early) showed that late flowering was dominant and followed 3 Late:1 Early suggesting early flowering in BG1044 and BG1054 was governed by a single recessive gene each. The F_1 plants of BG1044 (Early) x BG1054 (Early) were early and showed no segregation for flowering time in F_2 and F_3 demonstrating that BG1044 and BG1054 might be carrying the same gene for early flowering. The study of F 1 s and segregation pattern in F_2 s and F_3 progenies of BGD72 (IDT) x BG1054 (SDT), BGD72 (IDT) x BG1044 (SDT) suggested that indeterminate growth was dominant and followed 3IDT: 1SDT indicating semi-determinacy in BG1044 and BG1054 was controlled by a single gene in each. The F_1 plants of BG1044 (SDT) x BG1054 (SDT) were semi-determinate and showed no segregation for stem growth habit in F_2 and F_3 suggesting that BG1044 and BG1054 carried the same gene for semi-determinacy. Time of flowering showed significant negative correlation with seed yield per plant in the F_2 of BGD72 (IDT Desi Late) x BG1044 (SDT Desi Early) suggesting the possibility of combining earliness and greater seed yield through selection. Hybridization between indeterminate desi and semi-determinate kabuli parents followed by careful selection of semi-determinate recombinants with more number of pods in F_2 is expected to result in simultaneous improvement of earliness (early flowering and podding) as well as seed yield in chickpea.

Genetic analysis of plant height in [(*Cajanus cajan* (L.) Millsp.)]

Pigeonpea is often cross-pollinated crop belonging to papilionaceae. It is an essential pulse crop and a major source of protein in Indian agriculture and in India known as 'Arhar' or 'Tur', which is typically used to make dhal. Green pods are eaten as vegetables, dried pod husk and seed are fed to cows, and straw is utilized as fuel and shelter. Plant height plays a vital role in reducing crop losses by making crop lodging tolerant and efficient crop management which reduces yield loss by pest and disease. The current study was made to understand the genetic nature of plant height and to identify the putative SNPs associated with the dwarf trait in F_2 through BSA. Two contrasting parents for plant height i.e, ICP 14459, a dwarf line, and ICP 10509, a tall line, were used as parents to develop populations. F_1 from the cross between these two parents were analyzed and a chi-square test was performed in F_2 to know the inheritance and genetic nature of the dwarf trait and it was found that a single homozygous recessive gene controlled the dwarf trait. Bulk segregant analysis followed by SNP genotyping with 62k SNP chip was done to find out the putatively linked SNPs to the dwarf trait. The genotyping using the already known 28264 SNPs resulted in a total of 5,749 polymorphic markers between the parents. Out of these, only 84 SNPs were found to be polymorphic between the parents and both bulk and were distributed on all 11 chromosomes. Through the annotation analysis, we shortlisted three loci that might play an important role in determining plant height. In our investigation, only one probe with probe id AX-165343046 was found to be genic in nature. In pigeonpea, it was discovered in the coding region of LOC109808376, which is ABC transporter B family member 11. For any definitive conclusion, the results of this investigation require the development of PCR-based markers for potential SNPs found using BSA, as well as validation. These markers can also be employed in marker-assisted plant breeding to transfer dwarfing and other desirable agronomic traits for better resource management and crop husbandry.

Genetic studies and molecular mapping of seed viability in soybean [*Glycine max* (L). Merrill]

Soybean (*Glycine max* L. Merrill, 2n=40) is the numero uno oilseed crop in India. It contains 40-45% quality protein and 18-20% health-friendly oil besides several essential nutritional elements. Because of its ever-increasing popularity in food, feed, cosmetics, pharmaceutical and some other production industries, the demand for soybean has been increasing tremendously; however, the production and supplies hardly meeting the demand. Among other factors, shortage of quality seeds has been affecting soybean production significantly. Loss of seed viability during ambient storage critically affects seed quality and supply. It is therefore important to understand genetic control of the trait for its effective improvement through breeding. In this study, an attempt was made to understand the genetics of seed viability and map the associated genomic regions with SSR markers. For this purpose, five cultivated soybean genotypes (EC1023, EC105790, G-2651, UPSL-34, and UPSl-736) with high seed viability (i.e. more than 90% germination after one year of ambient storage) were crossed with three genotypes (VL5-61, PK-1243, MACS-565) having poor viability (i.e. less than 60% germination after one year of ambient storage). The F1 seeds obtained from three crosses viz., EC1023 x VL561, UPSL736 x PK1243 and UPSL736 x MACS565 were tested and true hybrids were advanced to the subsequent generations individually. The F2:3 seeds of the cross EC1023 x VL5-61 along with the parental genotypes were subjected to accelerated ageing under the optimized conditions of 410C and ~100% RH for 72 hours followed by germination test. The germination of the seeds of EC1023 and VL5-61 after accelerated ageing was 40% and 14%, respectively, while the same for the F2:3 seeds ranged from 4.16% to 71.42% with an average of 17.31%. The continuous distribution of germination in the F2:3 seeds indicated that the seed viability is controlled by many genes or quantitative trait loci (QTL). Germination (%) was positively and significantly correlated with average seedling length (r=0.78) and seedling dry weight (r=0.83). Parental polymorphism studied with 506 SSR markers indicated it to 20.35%. The distribution of the polymorphism was not uniform across the chromosomes; Chr. 15 had 46.15% polymorphism as against 15.78% on Chr. 3 and 4. The software for inclusive composite interval mapping mapped 8 QTL for seed viability viz., qSv-6.1 and qSv-6.2, qSv-7.1, qSv-8.1 and qSv-8.2, qSv-10.1, qSv-13.1, and qSv-17.1 on Chr. 6, 7, 8, 10, 13 and 17, respectively. The phenotypic variation explained (PVE) by the QTL ranged from 1.97-11.10% with LOD ranging from 2.53 to 4.07. Two QTL viz., qSv-7.1 (PVE=11.10%) and qSv13.1 (PVE=11.08%) appeared to be major QTLs for seed viability. All but qSv8.2 appeared to be novel QTL. For 100-seed weight 2 QTLs viz., qHSW-5.1 (PVE=10.70%) and qHSW-17.1 (PVE=19.86%) were mapped on Chr. 5 and Chr.17, respectively; both were major QTL. The QTL for seed viability (qSv-17.1) and hundred seed weight (qHSW-17.1) overlapped on Chr. 17 in the marker region Satt301-Sat_326. The mapped QTLs were validated in 40 interspecific RILs with varying level of seed viability. The germination in ambient stored seeds found to be comparable with that of the accelerated ageing seeds. The SSR marker Satt538 linked to the QTL qSv8.2 could successfully (70%) separate the highly viable RILs from the poor-viable RILs. Similarly, SSR markers Sat_316 and Sat_173 were 80-85% successful in separating the high and poor viable RILs. The information on genetics of seed viability and QTLs and markers identified in this study will pave the way for developing genotypes with enhanced seed viability through molecular breeding.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Shalma Maman	21293	M.Sc.	Analysis of genetic variability for lipoxygenase activity and validation of lipoxygenase 3 (LOX3) gene affecting retention of kernel tocopherols in maize during storage	Dr. Vignesh M.
2.	Shashidhar B R	21294	M.Sc.	Studies on genetic variability and molecular characterization of diverse inbreds and genetics of resistant starch in maize (*Zea mays* L.)	Dr. Firoz Hossain
3.	Uttarayan Dasgupta	21295	M.Sc.	Comparative RNA-Seq analysis and antioxidant studies to understand the complex regulatory network of MYMIV resistance in mungbean (*Vigna radiata* (L.) R. Wilczek)	Dr. Gyan Prakash Mishra
4.	Revanth Ragul A	21296	M.Sc.	Genetic and molecular analyses of cooking parameters in rice	Dr. Gopala Krishnan S.
5.	Pavan Kumar Naik	21297	M.Sc.	Studies on morphological and molecular characterization of mutant lines of wheat	Dr. Neelu Jain
6.	Baby S V	21298	M.Sc.	Development of non necrotic backcross derived lines of wheat varieties HD2967 and HD2733	Dr. Niharika Mallick
7.	Jatin Tanwar	21299	M.Sc.	Characterization of *dicoccum* wheat germplasm using morphological and molecular markers and identification of leaf rust resistant germplasm	Dr. Jyoti Kumari
8.	Purnima Ray	21300	M.Sc.	Inheritance of resistance to mungbean yellow mosaic virus in soybean	Dr. Sanjay Kumar Lal
9.	Jayanth Kallugudi	50049	M.Sc.	A genetic investigation on the allelic distribution of wide compatible gene in rice (*Oryza sativa* L.)	Dr. Prolay Kumar Bhowmick
10.	Ashish Bhatt	50050	M.Sc.	Assessing genetic variation and mapping of aluminium toxicity tolerance in rice (*Oryza sativa* L.)	Dr. K. K. Vinod
11.	Tejaswini Navalli	60049	M.Sc.	Genetics and interrelationships of time of flowering and stem growth habits in chickpea (*Cicer arietinum* L.)	Dr. Venkatraman Hegde

12.	Sahana Police Patil	60050	M.Sc.	Inheritance and validation of markers for kernel row number in tropical maize (*Zea mays* L.)	Dr. Raveendra N Gadag
13.	Raju Gopal Gadiwaddar	60051	M.Sc.	Genetic Analysis of plant height in [*Cajanus cajan* (L.) Millsp.]	Dr. Kumar Durgesh
14.	Brijesh Kumar Mehta	10612	Ph.D.	Enrichment of sweet corn genotypes with provitamin A, lysine and tryptophan through marker-assisted introgression of crtRB1 and opaque2 alleles	Dr. Firoz Hossain
15.	Neeraj Kumar	10613	Ph.D.	Mapping genomic regions (QTLs) imparting salt stress tolerance in chickpea (*Cicer arietinum* L.)	Dr. C. Bharadwaj
16.	Nitish Ranjan Prakash	10819	Ph.D.	Genetic analysis and identification of loci governing prolificacy in “Sikkim Primitive” - a novel landrace of maize in India	Dr. Firoz Hossain
17.	Manisha Saini	10823	Ph.D.	Genetic studies and molecular mapping of seed viability in soybean [*Glycine max* (L). Merrill]	Dr. Akshay Talukdar
18.	Harish D	10922	Ph.D.	Characterization and allele mining for drought tolerance from chickpea landraces	Dr. C. Bharadwaj
19.	Archana R	11055	Ph.D.	Mapping quantitative trait loci for stay greenness and its component traits associated with nitrogen use efficiency in rice	Dr. K. K. Vinod
20.	Rathan N.D.	11056	Ph.D.	Identification of quantitative trait loci and candidate genes associated with enhanced grain zinc and iron concentration in wheat (*Triticum aestivum* L.)	Dr. Anju M. Singh
21.	Kyaw Swar Oo	11147	Ph.D.	Marker assisted pyramiding of QTLs governing reproductive stage drought tolerance into rice variety, Pusa 44	Dr. A. K. Singh

Plant Genetic Resources

2

Prof. Veena Gupta

The National Bureau of Plant Genetic Resources (NBPGR) has played a pivitol role in the improvement of various crop plants and diversification and development of agriculture in India through germplasm introduction from various institutes/organizations located in foreign countries and germplasm collection from within the country and conservation thereof. The main activities of the institute are to plan, organize, conduct and coordinate exploration and collection of indigenous and exotic plant genetic resources; to undertake introduction, exchangeand quarantine of plant genetic resources; characterize, evaluate, document and conserve crop genetic resourcesand promote their use; to develop information network on plant genetic resources; to conduct research, undertaketeaching and training, develop guidelines and create public awareness on plant genetic resources. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Diversity assessment for insect-pest resistance

Assessment of genetic diversity and differential reaction of black gram (*Vigna mungo*) germplasm to pulse beetle (*Callosobruchus maculates*)

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

Genetic diversity analysis of wild brinjal germplasm of primary gene pool (*Solanum insanum* L. and *Solanum incanum* L.) and their evaluation for brinjal fruit and shoot borer (*Leucinodes orbonalis* Guen.) resistance

Wild brinjal (*S. incanum* and *S. insanum*) germplasm from primary genepool possesses wide variation with better adaptation to new environment. The present investigation was done with the objective to study the morphological and molecular diversity in wild brinjal germplasm of primary genepool through agro-morphological descriptors and molecular markers. The twelve qualitative descriptors had shown the presence of all the descriptors' states. The nine qualitative descriptors had shown the Shannon Diversity Index (H') value≥0.40 indicating presence of substantial diversity in these descriptors. Significant differences in accessions and checks were observed for all the descriptors except days to 50% flowering in checks. The values of PCV%, GCV%, ECV% and heritability% were estimated. The coefficient of variation observed at phenotypic level for 26 descriptors were high when compared with the genotypic coefficient of variation and error coefficient of variation but in days to 50% flowering the value of ECV is more than PCV and GCV which means environment or location effect is there for this descriptor. The mean performance of all the accessions for 27 descriptors with their mean, standard error, standard deviation and CD at 5% were calculated and few promising accessions were identified which showed superiority over the best check. Days to 50% flowering recorded highest number of significant correlation coefficient with other descriptors. The Ward's Cluster analysis has given a clear cut separation of accessions and checks. Accessions are grouped in five clusters and checks in one separate cluster. Among five clusters of accessions, two clusters are exclusively for *Solanum incanum* which also signifies the clear cut separation of 91 wild species from *S. incanum*. In another three clusters, both the wild species (*S. incanum* and *S. insanum*) were included but grouped as per passport information. PCA analysis has been done to know the relative contribution of each descriptor to the total variability. Eigen value >1 was considered for calculating the relative contribution in this study. There are six principal components (PC1 to PC6) contributed total 78.65% of variance. Molecular diversity analysis using 20 SSR primers exhibited polymorphism for the entire set of 72 accessions, at two or more number of the SSR loci. The number of alleles scored for each marker varied from 2 to 4 alleles. Polymorphism Information Content (PIC) also calculated where values ranged from 0.16 to 2.7 with an average of 1.44. In present study, the values of heterozygosity (or Gene diversity) ranged from 0.07 to a maximum value of 0.49 for polymorphic loci with an average of 0.37 heterozygosity. Four major groups were shown by all 72 accessions in cluster analysis viz., cluster I with 33 accessions and the cluster II with 30 accessions and the cluster III consists of 8 accessions and the cluster IV consists of 1 accession. No distinct separation of wild species of brinjal, and cultivated varieties based on molecular characterization was seen. Molecular markers can detect a lot of variability within the *S. incanum* and *S. insanum* accessions and also the cultivated varieties *S. melongena* used as checks used in the study. Evaluation of wild brinjal (*Solanum insanum* and *Solanum incanum*) germplasm for brinjal fruit and shoot borer (*Leucinodes orbonalis* Guen.) resistance was carried out at natural field condition. Seven promising accessions viz. IC256077, IC546046, IC426469, IC421461, IC421202 and IC541210 of *S. incanum* and IC599705 from *S. insanum* were identified superior to best check.

Theme 2. Diversity assessment for abiotic stresses

Unraveling physiological and molecular mechanism of terminal-heat stress tolerance in bread wheat (*Triticum aestivum* L.) germplasm

Bread wheat (*Triticum aestivum* L.) is grown in sub-tropical and tropical areas globally and as such exposed to high temperature during grain filling period (GFP). Global warming has further affected its production and productivity in heat-stressed (HS) environments. We examined the effect of heat-stress on 31 morpho-physiological and yield-related traits in 96 bread wheat accessions grown under non-stressed (NS) and HS environments. Late sowing decreased crop growth and GFP, and as a result reduced 26 morpho-physiological and yield-related traits. The reduction in the traits was severe in susceptible accessions than the tolerant. Physiological traits like early ground cover, chlorophyll fluorescence (CF), CTD, NDVI, plant waxiness (PW) and leaf rolling (LR) showed higher expression in the tolerant accessions under heat-stress. Grain length/width ratio enhanced under heat-stress. Ultrastructural changes in endosperm and aleurone cells of matured grains studied using scanning electron microscope revealed that the reduction of size and density of large starch granules is the major cause of yield and TGW decrease in the heat-stress susceptible lines. Plot yield associated positively with its contributing traits namely GFP, yield/plant, grains/spike, grain weight/spike, grain width, plant biomass and harvest index under both NS and HS environments, and with CF, LR and PW only under heatstress. The molecular analysis using microsatellite markers revealed the presence of high level of genetic variation in the germplasm. The 25 primer-pairs amplified 263 alleles with 98.1% polymorphism. In total 35 unique alleles and 47 rare alleles were identified. These unique and rare alleles could be used in DNA fingerprinting and genotype differentiation. The mean number of observed alleles, effective alleles, PIC and Shannon's information index were 10.52, 6.19, 0.69 and 1.99 per locus, respectively. The expected heterozygosity ranged from 0.50 to 0.89 with an average of 0.8 and revealed the presence of high molecular diversity in the germplasm. Wright's fixation index (FST) value of 0.15 indicated the moderate level of genetic differentiation in bread wheat germplasm. Dice's coefficients of similarity varied from 0.14 to 0.86 with mean of 0.34. UPGMA dendrogram grouped 96 accessions into 6 major clusters. However, structure analysis revealed three sub-populations in the germplasm. Seven genespecific primers amplified PCR products in 96 accessions indicated the absence of amplicons length polymorphism. The most stable and high-yielding accessions namely IC566223, IC128454, IC335792, EC576707, IC535176, IC529207, IC446713 and IC416019 were identified as climate-smart germplasm lines. Germplasm lines possessing desirable traits were selected as potential parents for the development of bi-parent and multi-parent populations.

Theme 3.Taxonomic studies in plant genetic resources

Cytogenetic and molecular studies to reveal taxonomic status of *Trichosanthes cucumerina* complex

Trichosanthes is one of the largest genera of family Cucurbitaceae (also known "gourd family") andamong this genus *Trichosanthes cucumerina* L. is the most significant cultivated group not only as vegetable but also its important medicinal and nutritious properties. Mainly it has two species under cultivation i.e., *Trichosanthes dioica* (pointed guard) and *Trichosanthes cucumerina* var. *anguina* (snake guard). Taxonomic validation of some of the National Genebank accessions with *Trichosanthes* species status was done to authenticate the species status. The present study used cytological and nuclear ITS sequence to establish different taxonomic status under *T. cucumerina*complex. Total 35 accessions of non designated *Trichosanthes cucumerina* accessions were collected from National Gene Bank of ICAR- NBPGR. Chromosome number (2n=2x=22.) and relative genomic content (2.00 pg) through flow cytometry helped in ruling out the possibilities of species contamination of polyploid species *T. Cucumeriodes*.Phylogenetic analysis based on nuclear ITS sequence of 13 accession showed different taxonomic status of accession. Multiple sequence pairwise alignment of ITS sequences, four major deletions were observed for all the accessions but the accession number IC 265569 (T11), IC 550288 (T25), and IC 549866 (T37) showed insertion in three major regions. Phylogenetic tree constructed with authenticated samples and *Trichosanthes* accessions based on UPGMA of nuclear ITS sequences, segregate the sample accessions into three groups, 10 accessions formed a separate cluster and defines as *Trichosanthes cucumerina* var. *cucumerina* species. Accession number, IC 265569 (T11), IC 550288 (T25) formed separate cluster and maybe more closely associated with the *Trichosanthes nervifolia*, while the accession number IC 549866 (T37) form the third cluster, in between the *Trichosanthes cucumerina* var. *Anguina* and *Trichosanthes nervifolia*. IC 549866 (T37) was previously identified as *Trichosanthes cucumerina* var. *sublobata*, but can be assumed that this accession may be a natural hybrid between *Trichosanthes cucumerina* var. *Anguina* and *Trichosanthes nervifolia* or it may be belongs to the genus *Trichosanthes brevibracteata*. Generation of 55 ITS sequence from more accessions along with diagnostic morphological characters will further be taken to acertain these findings.

Theme 4. Conservation protocol development

Cryopreservation of *Fragaria vesca* L. shoot tips and virus elimination through cryotherapy

Cryopreservation protocol standardisation and efficiency of cryotherapy for virus elimination in *Fragaria vesca* (IC319113) cultures was investigated for efficient cryo-conservation of the species. Standardization of cryopreservation protocol included selection of multiplication media, preculture medium andduration, and PVS2 treatment duration. Murashige and Skoog media supplemented with different concentrations of sucrose viz., 0.3M, 0.5M and 1M for 24 hr and 48 hr duration were used forpreculture. PVS2 treatment duration was standardized by treating shoot tips with PVS2 fordifferent durations like 20min, 30min, 60min and 90min. Out of these, preculture for 24 hrs on 0.3M sucrose medium and 30min PVS2 treatment duration was optimized. Before cryotherapy, 30 samples of *in vitro* cultures of *F. vesca* were tested for four associated viruses namely arabismosaic virus (ArMV), raspberry bushy dwarf virus (RBDV), strawberry mild yellow edge virus (SMYEV) and raspberry ringspot virus (RpRSV) using polyclonal antisera for respective virusesusing DAS-ELISA. Out of thirty samples tested, it was found that 100% cultures were free fromArMV, RBDV and SMYEV and 90% cultures were free from RpRSV. Subsequently, shoot tipsof 10% positive samples were cryopreserved by V-cryoplate method using earlier standardizedsteps. Cryopreserved shoot tips yielded maximum 63.33% regrowth. Post-cryotherapy, 30 plantsgenerated out of 60 cryopreserved shoot tips were tested by DAS-ELISA and representativesamples by RT-PCR for RpRSV. Success rate of cryotherapy was 96.67% for elimination of RpRSV. The present study demonstrated that cryotherapy can be used as a potential technique forvirus elimination.

Theme 5. PGR characterization

Marker-assisted assessment of genetic redundancy in selected maize germplasm collection

The National Genebank at ICAR-National Bureau of Plant Genetic Resources conserves one of the largest collections of maize germplasm, which comprises of indigenous maize diversity collected from throughout the country. A major collection is from the north eastern hill region, from where recent exploration missions have added large number of populations with unknown identity. The large collection size of such populations hampers their effective utilization since in maize, concerted efforts are required to address the genetic bottlenecks of heterogeneous groups. Hence, the present study was undertaken to assess the extent of redundancy, through use of passport, morphological and molecular characterization data, in a selected set of 24 maize populations collected from four northern districts of Mizoram. The experiments involved 30 morphological descriptors and 93 microsatellite markers for an extensive analysis of multiple parameters. The analysis could identify redundant sets within genetic clusters, through integration of geographic, morphological and molecular data and from within 24 accessions, 17 accessions were marked for bulking, which would bring down the conservation size from 24 accessions to 13 accessions. The study also proposed an exploration strategy for mimban maize populations, that within a district, samples of collected from comparable altitude, having synchronized flowering behaviour and cob size should be pooled and submitted as single accession. Further application of this information in maize populations from other regions and also in other crop groups that are conserved in NGB, is envisaged.

Genetic characterization and allele mining of quality traits in maize (*Zea mays* L.) landraces from Himalayan Regions of India

Maize (*Zea mays* L.) is an important cereal crop with multiple uses as food, feed, fodder, fuel and biofuel. Phenotypic characterization of newly collected germplasm is essential for selecting genetically diverse lines for maize breeding. We characterized 99 landrace germplasm accessions collected from India's maize diversity hotspots located in North-Eastern Himalayan (NEH) and North-Western Himalayan (NWH) regions using 30 morphological traits and 25 highly polymorphic SSR markers. Landrace accessions were evaluated in field experiment in an augmented block design along with 4 checks. The high extent of phenotypic variation was observed both in plant and ear traits. Very high positive correlations were estimated between flowering traits (days to tasseling, silking) and maturity, and between plant height and ear height. Boxplot analysis indicated that maize accessions from NEH region displayed comparatively high phenotypic diversity for plant traits, while the accessions from NWH region showed the highest variation for ear and kernel traits. Analysis of principal component showed two principal components describing 88.24% of total variation. Plant height, ear height, ear length and tassel branching, days to 50% tasseling, days to 50% silking, days to 80% maturity were the most discriminatory traits. Cluster analysis grouped all 99 landrace accessions into eight clusters. Present study was also conducted to assess genetic diversity of 99 maize landrace accessions using 25 SSR (Simple Sequence Repeat) markers and to characterize the land race accessions using gene specific markers *crt*RB1, *lcy*E and *o*2 quality genes. A total number of 257 SSR alleles were amplified among these landrace accessions. The number of alleles per marker ranged from 3 to 22 with an average of average of 10.8 alleles per microsatellite. The High polymorphic information content (PIC) value indicated the presence of high level of genetic variation in maize landrace accessions evaluated in this study. Both phenotypic and SSR analysis showed significant genetic diversity. Gene specific marker linked to the *crt*RB1 gene had a considerable effect on enhancing β-carotene content in maize. In *crt*RB1 favorable allele 2 (600 bp) was identified in four landrace accessions (two each) from accession of Himachal Pradesh (NWH) and Nagaland (NEH). Maize landrace accessions displaying desirable (favorable) allele could be converted into homozygous inbred line by selecting favorable allele in background for further utilization in crop improvement programme.

Agro-morphological, nutritional and molecular diversity analysis of grain type chenopod germplasm

The genus *Chenopodium* (family: Chenopodiaceae) includes about 250 species in which 21 species occur in India and cultivated for use as vegetable and for grains. *Chenopodium quinoa* a native of the Andes and *Chenopodium album* is a native of Europe and Western Asia is an important food sourcedue to its complete nutritional characteristics. *Chenopodium* species have aptitude to produce high-protein grains under ecologically extreme conditions makes it important for the diversification of agriculture as in high-altitude regions of the Himalayas and North Indian Plains. It is rich in the essential amino acid lysine, making it a more complete protein diet and does not contain gluten, so it can be eaten by people who have celiac disease as well as by those who are allergic to wheat. The high-quality oil and rich in fibre and minerals like iron, phosphorus, potassium, zinc and magnesium, as well as Vitamin E and B-complex. In present study, 60 selected accessions comprising of 5 different species were studied for agro-morphological characterization for two consecutive seasons 2017-18 to 2018-19 in augmented block design for 9 qualitative and 8 quantitative traits. These parameters show good range of variation for days to 50% flowering (38-113 days), days to 80% maturity (73-179 days), plant height (30-331 cm), Leaf length (3.5-19 cm), Leaf width (2.6-19.7 cm), panicle length (10-69 cm), 1000 seed weight (0.3- 1.8 g) and seed yield per plant (5.07-65.0g). Correlation studies revealed that all the parameters positively correlated to the yield and principal component analysis showed that two components contribute for total variance of 94.5%. Cluster analysis grouped all the accessions into four major cluster (I to IV) which consists of 24, 4, 11, and 19 accessions respectively. Biochemical parameters which shows the ranges between moisture content (8.3 – 11%), ash content (1.3 – 4.0%), protein content (10.4 - 18.3%), fat content (2.6 – 6.8%), total sugars content (2.4 – 4.5%), total starch content (46.4 – 62.3%), total carbohydrates content (62 – 74.5%), total dietary fibre (5.8 – 13.3%), and total phenols content (105-205 mg/100g). Correlation studies revealed that moisture, starch and carbohydrates are positively correlated each other and negatively correlated to protein, fat and ash. Principal component analysis showed that three components contribute for total variance of 83.1% and cluster analysis grouped all the accessions into four major cluster (I to IV) which consists of 4, 10, 9, and 37 accessions respectively. Molecular genetic diversity using 53 SSR primers ranged the number of alleles from 1 to 10 with the average of 4.7 alleles per marker and PIC ranged from 0.476 to 0.997 with the average of 0.783 per marker followed by cluster dendrogram grouped into five groups (I to V) which consists of 41, 3, 6, 3, and 7 accessions respectively and lynch pairwise distance matrix revealed that closely related accessions (IC0588891 and IC0588899, distance=0.000) and highly diversed accessions (IC0583584 and IC0363733, distance= 0.809).Under the study, some of the indigenous (IC-0107263,0109731 0258332, 0415405, IC0611818, and 0617316) and exotic (EC-0359445, 0359448, 0359449, 0507746, 0507747, and 0507749) lines showing promising results for both morphological and biochemical parameters have been identified for use in *Chenopodium* crop improvement.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the Student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Sandip Kumar Panigrahi	21321	M.Sc.	Assessment of genetic diversity and differential reaction of black gram (*Vigna mungo*) germplasm to pulse beetle (*Callosobruchus maculatus*)	Dr. Kavita Gupta
2.	Subham Deb	21322	M.Sc.	Cytogenetic and molecular studies to reveal taxonomic status of *Trichosanthes cucumerina* complex	Dr. S. Rajkumar
3.	Mallikarjun Biradar	21323	M.Sc.	Marker-assisted assessment of genetic redundancy in selected maize germplasm collection	Dr. Sherry R. Jacob
4.	Praveen Gumachanamardi	21325	M.Sc.	Cryopreservation of *Fragaria vesca* L. shoot tips and virus elimination through cryotherapy	Dr. Sandhya Gupta
5.	Nagaraj Naik D.	21375	M.Sc.	Genetic diversity analysis of wild brinjal germplasm of primary gene pool (*Solanum insanum* L. and *Solanum incanum* L.) and their evaluation for brinjal fruit and shoot borer (*Leucinodes orbonalis* Guen.) resistance	Dr. K.K. Gangopadhyay
6.	Anil Patidar	10508	Ph.D.	Unraveling physiological and molecular mechanism of terminal-heat stress tolerance in bread wheat (*Triticum aestivum* L.) germplasm	Dr. Mahesh C. Yadav
7.	Hari Prasath S.	10851	Ph.D.	Agro-morphological, nutritional and molecular diversity analysis of grain type chenopod germplasm	Dr. Veena Gupta
8.	Mr. Jagdish Goyanka	10853	Ph.D.	Genetic characterization and allele mining of quality traits in maize (*Zea mays* L.) landraces from Himalayan Regions of India	Dr. Mahesh C. Yadav

Seed Science and Technology

3

Prof. Monika A. Joshi

The Division of Seed Science and Technology provides leadership in maintenance breeding, seed production, certification, quality evaluation, storage, physiology, pathology, variety identification, genetic purity evaluation and DUS testing for plant variety protection, development of seed quality assessment procedures and human resource development. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Seed production technology

Standardisation of seed production technology of sponge gourd hybrid: Pusa Shrestha

The present study was undertaken to standardise the hybrid seed production technology of Pusa Shrestha. The parental lines; DSG-43 and DSG31 were sown in kharif 2020 and spring-summer 2021 under insect proof net house to study the plant growth, flowering behaviour, seed yield and quality parameters in relation to hybrid seed production. In addition, pollen viability and stigma receptivity studies, use of PGRs for modification of sex expression in female parental line of the hybrid and studies on optimization of the planting ratio of parental lines for hybrid seed production were also undertaken. The results showed that higher vegetative growth, fruit and seed yield was observed in kharif season whereas higher seed quality was obtained in spring-summer season. Among the parental lines; the male parent; DSG-31 performed better than female parent; DSG-43 for vegetative growth and yield traits. Pollen viability and stigma receptivity was influenced by weather conditions in both the seasons. The study showed that pollination should be undertaken between 6 to 10 am for higher fruit setting and seed yield in both seasons. Seed storage studies indicated good storability of sponge gourd seeds up to 6 months under ambient storage conditions. The plant growth regulators improved vegetative growth (vine length, number of branches), sex expression (induction of flowers at lower nodes, more flowers, higher sex ratio), fruit traits (number of fruits per plant, fruit weight, fruit length, fruit width), and seed yield (number and weight of seeds) and quality (germination and seed vigour) and had positive effect in both the seasons. Among growth regulators, GA3 applied @ 150 ppm was best followed by NAA @ 150 ppm and Ethrel @ 200 ppm for improving vegetative growth, flowering behaviour, sex ratio, fruit traits, seed yield and quality traits. The Maleic Hydrazide @ 300 ppm had detrimental effect on the studied traits. Application of growth regulators at 2-3 leaf stage + 4-5 leaf stage (S2) and 2-3 leaf stage + 4-5 leaf stage + 7-8 leaf stage (S3) was most effective and the application at 2-3 leaf stage (S1) was lesser effective in influencing the studied traits. A planting ratio of 4:1(female: male) was found optimum for hybrid seed production of Pusa Shrestha under Delhi condition

Effect of planting geometry and micronutrient application on seed yield and quality of parthenocarpic gynoecious cucumber variety, Pusa Parthenocarpic Cucumber- 6

The present study was undertaken to study the effect of planting geometry and micronutrient application on seed yield and quality of the first public sector parthenocarpic gynoecious cucumber variety Pusa Parthenocarpic

Cucumber-6 released by ICAR- IARI, New Delhi.. The experiment was conducted under naturally ventilated polyhouse and three plant spacings (100 cm x 30 cm; 100x 45cm; 100 cm x 60 cm) were compared during Kharif 2020 and Spring-summer season 2021. In addition, conventional and nano formulations of micronutrients, zinc and boron were used at different concentrations for foliar spray on seedlings at three different stages viz., SA1 (Vegetative stage @ 15 DAT); SA2 (Reproductive stage @ 22-25 DAT); SA3 (SA1+SA2). The results exhibited that wider plant spacing of 100 cm x 45 cm and 100 cm x 60 cm proved to be superior, though both were statistically at par with respect to vegetative growth parameters (vine length, number of nodes and number of days taken to first flowering), fruit attributes (fruit length, girth and weight), seed yield traits (number of seeds per fruit, hundred seed weight and seed yield per vine), seed quality traits (germination, seedling length and dry weight, vigour indices and electrical conductivity). Further, the seed production season had a profound influence on the seed yield and quality attributes. The seed produced during the Spring-summer exhibited superiority in terms of vegetative growth, seed yield and quality traits. Among various treatments, T11 (Nano formulation of Zn + B @ 1 ml l-1) was significantly better as compared to other treatments with respect to vegetative growth, seed yield as well as quality attributes. The foliar spray at two stages; vegetative and reproductive stages (SA3) was most effective in enhancing the traits under study. It can be concluded that planting geometry of 100 cm x 45 cm, along with two stage spray of Zn + B Nano formulation @ 1ml l-1 was effective for optimizing seed yield and quality in Pusa Parthenocarpic Cucumber-6.

Theme 2. Seed quality assurance

Effect of salinity stress on seed yield and seed quality parameters in soybean (*Glycine max* L.)

In lieu of the salinity stress which severely impacts soybean crop growth and productivity, the identification of genotypes which are tolerant to salinity stress is the need of the hour. Hence, the present study was conducted for 156 genotypes, comprising of one year stored seed of 150 germplasm accessions which included 42 black seeded, 105 yellow seeded and 3 brown seeded accessions; and six freshly harvested varieties with the primary objective to evaluate the effect of salinity stress on seed yield and seed quality parameters in soybean. For seed quality evaluation in the laboratory, the petri plate method wherein 2.5ml of NaCl solution was added every alternate day was found to be better and more practical in approach as compared to between paper method. All the 156 genotypes were evaluated at four levels wherein distilled water was used as control (0 dS/m) in addition to three salinity levels viz. 3 dS/m, 6 dS/m and 9 dS/m. For the black seeded accessions, the mean value of germination reduced from 75.52 % at control to 67.82% at 3dS/m which further reduced to 52.78% and 36.47% at 6 dS/m and 9 dS/m, respectively. Similar trend was recorded for both yellow and brown seeded accessions and also for all other seed quality traits, though the reduction in seed quality parameters was more pronounced for yellow and brown accessions. Lower salinity levels (3 dS/m), in certain cases, recorded enhanced seed quality parameters, thereby, indicating that NaCl acted as a nutrient at lower salinity levels which helped them to tolerate and perform better due to various adaptive mechanisms. For freshly harvested varieties, the germination percentage was recorded to be 91.66% at 0 dS/m which decreased to 86.66% at 3 dS/m; and further declined to 66.66% and 45% at 6 dS/m and 9 dS/m, respectively. Similar trend was recorded for other seed quality parameters as well. The correlation values of all the seed quality parameters with salt tolerance index (STI), which was calculated based on the seedling dry weight (8 days old seedling), was used for selection of highly tolerant, moderately tolerant and highly susceptible genotypes from the material under investigation. Accordingly salinity levels of 3dS/m for yellow group and 6dS/m for black and released varieties were selected. All three brown genotypes were at par with respect to STI and no categorization could be made. The pot culture experiment conducted in 20 selected genotypes to evaluate the effect of salinity stress on morphological, seed yield and contributing traits, revealed that at higher salinity levels, all the characters such as number of branches per plant, number of pods per plant, total biomass per plant, seed yield per plant, germination percentage along with both seed vigour indices decreased significantly over control. The findings of pot culture further validated the categorization of genotypes into respective tolerant/susceptible groups. Amongst the released varieties, Pusa 9712 and Pusa 12 were found to be highly tolerant and varieties SL 1074 and SL 958 were found to be highly susceptible. Similarly, highly tolerant/ susceptible genotypes were identified amongst each of the black and yellow seeded accessions. Further, black seeded accessions were observed to have better salinity tolerance as compared to yellow seeded accessions.

Theme 3. Seed quality enhancement

Effect of nanoparticles on seed quality and storability in paddy (O*ryza sativa* L.)

The present study was conducted on paddy variety Pusa Basmati 1509 during the year 2020-21 wherein the seeds were dry and wet dressed with each of nano and bulk forms of zinc oxide, titanium oxide and silicon dioxide @ 50, 100, 250, 500 and 750ppm along with the two controls i.e., untreated and treated with recommended PoP (Thiram treated @2g/Kg of seeds. Treated seeds were stored in different packaging material i.e., polythene and cloth bag under ambient room conditions upto six months to study the storability of different nanoparticles seed treatments. Highest radicle emergence (95.3%) and highest germination percent (94.7%) was recorded for seeds treated with dry nano ZnO@250ppm and dry bulk ZnO@50ppm, respectively. Seeds treated with dry nano TiO2 (500ppm) recorded lowest abnormal seedling percent (2.3%). Highest seedling vigour index I (6129) was reported for dry bulk ZnO@250ppm. Highest total dehydrogenase activity (0.766) was reported in dry bulk ZnO @ 500ppm as compared to both the controls whereas significantly lowest moisture content (7.9%) was observed in thiram @ 2g/kg as compared to untreated seed. Lowest total pathogen infection (8.3%) and *Penicillium sp*. infection (1%) was observed in seed treated with dry bulk ZnO @ 750ppm and significantly lowest *Rhizopus sp*. infection (3%) and lowest *Aspergillus sp.* infection (2.3%) was observed in seed treated with dry bulk ZnO @ 500ppm and dry nano ZnO @ 50ppm, respectively. Results of storage studies of treated seeds along with the two controls up to 6 month period of storage illustrated that after six months of storage, highest germination percentage (86.8%) was recorded for dry bulk Zno @ 50ppm in polythene bag than cloth bag as compared to both the controls. Highest seedling emergence (84.06%) was recorded for thiram @ 2gm/kg in polythene bag as compared to control. The dry bulk ZnO @ 50ppm significantly improved germination percentage while numerically improved field emergence was observed in seed treated with dry nano ZnO @ 250ppm. In line with the initial enhancement, the retention of germination above IMSCS was also noticed in seeds treated with dry bulk ZnO @ 50ppm when stored in polythene bags.

Effect of nanoparticles on seed quality, yield attributes and storability in chickpea (C*icer arietinum* L.)

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

Theme 4. Seed biology

Studies on the basis of phenol colour reaction in seeds of wheat (*Triticum* spp.)

Phenol colour reaction in wheat is a very important genetic parameter for grouping wheat varieties in seed testing and variety identification. But this character is non uniform across varieties and different wild species. The genome from which gene for phenol colour reaction originates is studied well. PPO activity in the different colour groups remains unclear. So, to validate the origin of the gene and to understand the biochemical basis of phenol colour an investigation was made. An experiment was conducted to evaluate 57 wheat genotypes for phenol colour through ISTA approved method during 2019-20. The total phenol content and PPO activity was estimated in the genotypes as well. Inter- and intra-earhead phenol content in a variety was studied. Variation among grains located in different positions in an earhead was found. Non-significant difference among different earheads of a plant was found. In wild species, species with “AA” genome showed higher phenol content and other intermediates like L-DOPA, pyrocatechol and tyrosinase, than other genomes while other diploid genotypes i.e., “DD” or “GG” showed very low PPO activity. In the fresh and old seed lots of cultivated species, PPO activity was slightly increased in one year old lot while in wild species, no significant difference in one year old lot was observed indicating that PPO gene remained conserved and hence is not affected by storage period. The results of study indicated that phenol colour is a distinguishing trait to characterize wheat cultivars and its biochemical basis help determine the amount of PPO activity in seeds. This can be used to trace the origin of gene responsible for phenol colour and as an indicator to identify a desirable variety in different wheat based processing industries.

Studies on seed quality parameters in relation to biochemical composition in Indian quality mustard

In lieu of the limited information available on correlation between biochemical composition and seed quality parameters for Indian quality mustard, developed by breeders with low erucic acid and glucosinolate content; the present study was conducted on thirty genotypes comprising of eight conventional genotypes, eight single zero genotypes and fourteen double zero genotypes. Significant difference was recorded for germination percentage and seed vigour indices of conventional, single zero and doubles zero genotypes. Highest germination percentage was found in conventional genotypes (90.2%), followed by single zero genotypes (83.8%), and double zero genotypes (71.4%). Higher germination percentage, seed vigourindices and higher protein content was recorded for freshly harvested seeds as compared to controlled deteriorated seeds. Mean protein content was more in single zero genotypes (24.8%) followed by conventional genotypes (22.8%) and double zero genotypes (22.3%). Palmitic and stearic acid content were found to be highest in conventional genotypes, (12.4%), followed by single zero (9.7%) and double zero genotypes (8.5%). Similar trend was observed in other fatty acid like oleic acid content, linoleic acid, eicosenoic acid and erucic acid content. Fatty acid composition significantly varied among the treatments. On the other hand, chlorophyll content was found to be low in conventional genotypes (15.7 ppm), but higher chlorophyll content were found in double zero (23.2 ppm) and single zero genotypes (22.2 ppm). Maximum glucosinolates content were observed in conventional genotypes (55.5 µmol/g) and single zero genotypes (48.8 µmol/g) followed by double zero genotypes (14.5 µmol/g). Simillar trend was observed in sinapine content and phenol content in different types of mustard. Non extractable proanthocyanidin was found highest in conventional genotypes (33.7 µg cyanidin eq / g), followed by single zero (31.6 µg cyanidin eq / g) and double zero genotypes (27.4 (µg cyanidin eq / g). Extractable proanthocyanidin were recorded similar in conventional genotypes (11.9 µg cyanidin eq / g), double zero genotypes (11.6 µg cyanidin eq / g) and single zero (11.0 µg cyanidin eq / g) genoytpes. In conclusion, the conventional genotypes and single zero genotypes were better in terms of seed quality parameters which were positively correlated with high protein content, fatty acids, sinapine, glucosinolates, proanthocyanidin, phenol and lowest chlorophyll content. The increased content of the above compounds possibly regulates the water uptake by seed leading to less imbibitional damage and decreased seed leachates. The protein and glucosinolates provides nitrogen and sulphur source to the growing seedlings while fatty acids act as energy source. All these regulate the physiological quality of the seeds.

Theme 5. Seed pathology

Development of eco-friendly management strategies against seed discolouration for quality seed production in paddy

The present study was carried out to assess the effect of seed discolouration on seed quality parameters in terms of physio-chemical changes of seeds in various rice cultivars, to find the best bio control agent for the management of seed discolouration of paddy and morphological and molecular identification of seed discolouration causing fungi. Based on standard blotter method and agar plate method, six major and three minor pathogens associated seed discolouration were isolated. Among the identified pathogens, *Alternaria alternata* and *Fusarium equiseti* were seen in 80% of the surveyed area. A higher number of seed discolouration causing fungi were recorded in Delhi (7 pathogens). Based on cultural characters of seed discolouration causing fungi, phylogenetic tree was constructed. Species which were similar in morphological character came under one cluster whereas different clusters were formed for different species. Out of 42 isolates that are used for morphological characterization, 24 representative isolates were used for sequencing. For sequence confirmation, each isolate was analysed in the nucleotide BLAST search tool in the NCBI site which showed significant similarity with their corresponding fungal isolates. ITS and β-tubulin based phylogenetic analysis was performed which showed clear cut cluster formation of six groups. Analysis of ITS and β-tubulin based pairwise sequence identity showed an average of 99.16% - 99.95% sequence similarity among different groups of fungal isolates. Significant reduction in seed quality parameters was recorded for discoloured seeds compared to healthy seeds. Similarly, starch (5.3- 37.6%) and protein (1.6-46.2%) content also reduced significantly, whereas, an increase in total antioxidant (3.3-37.1%) and total phenol content (0.58-26.03%) were seen in discoloured seeds, as compared to healthy seeds. Under dual culture assay, maximum percent inhibition was recorded in *Trichoderma viride* (66.62%) followed by *T. harzianum* (65.93%) whereas, minimum in *Talaromyces flavus* (33.68 %) on the 7th day of incubation. Under field conditions, a combination of seed treatment, seedling dip and the spray of *T. viride* performed better for all plant growth and seed quality parameters in cultivars Pusa Sugandh-5 (PS-5) and Pusa-44 (P-44) as compared to control.

Study of *Fusarium oxysporum* f. *sp. lentis* on seed quality, its detection and development of wilt management strategy for quality seed production in lentil

Lentil (*Lens Culinaris* Medik.) commonly known as Masur, is an important pulse crop in India. The main constraints responsible for the low yield of lentil are the availability of poor quality seeds, diseases, insects and abiotic stresses. Among the diseases the wilt disease of lentil, caused by the soil and seed-borne fungus *Fusarium oxysporum* Schlecht f.sp. *lentis* (Fol) is one of the most severe and prominent disease of lentil. The present study was taken up to study the effect of Fol on seed quality, to assess the genetic diversity existing among the Fol population originating from different states of India by using RAPD markers, to develop Fol specific diagnostic scar marker and its management. Survey and surveillance were carried out and infected & healthy seed samples were collected from major lentil growing states. Seed health testing methods were carried out, it revealed the infection percentage ranges from 40 to 55% in Fol infected seed samples. In morphological studies, the isolates exhibited variability in colony color, growth rate and conidia size. Pink colony (18 isolates) was more common as compared to reddish (12 isolates) and Whitish (10 isolates). In colony growth rate compact mycelial growth was predominant (33 isolates) over cottony growth (7 isolates). The microconidia size varied from 6.3-10.8 × 2.04-5.26 µm whereas, macroconidia size varied from 10.78-39.01 × 2.4-5.60µm. Seed quality parameters were studied and a significant reduction in the germination percentage (48.78 %), seedling length (16.70 %), and seedling vigour (882), whereas an increase in electrical conductivity (EC) (93.14µS cm^{-1} g^{-1}) was observed in Fol infected seeds as compared to healthy seeds. In molecular characterization six RAPD primers produced 46 bands with 94.92% polymorphism. Primers OPN-12, OPE-14, OPS-30 and OPN-18 showed the highest polymorphism and proved suitable for genetic diversity analysis. A primer OPI-18 which produced a monomorphic band specific only to Fol isolates was used to develop SCAR marker. The SCAR marker SCAR FOL 1 (F and R) was developed from the amplified fragment of Fol by OPI-18 RAPD marker. SCAR FOL 1 (F and R) specifically amplified DNA of Fol isolates at 353 bp and did not amplify DNA of any of the negative controls.

Impact of sheath rot of paddy caused by *Sarocladium oryzae* on seed quality, its diversity and development of management strategy

Sheath rot caused by *Sarocladium oryzae* (Sawada) is an important seed-borne fungal disease of paddy which is becoming a major concern to the rice farmers in our country. In the present investigation, the impact of *Sarocladium oryzae* on seed quality, variability of *Sarocladium oryzae* using gene-specific markers, the development SCAR marker for quick identification and management strategy for sheath rot of paddy using both chemical and biological treatments has been studied. The examination of sheath rot infected seeds shows that the fungi *Sarocladium oryzae* is frequently associated with four other fungi namely *Fusarium moniliforme, Bipolaris oryzae, Curvularia lunata and Alternaria alternata.* The examination of paddy seeds infected with *Sarocladium oryzae*, which have been collected from 16 states and 2 union territories showed a severe reduction in seed germination and vigor when compared to healthy seeds collected from respective places. The mean germination percentages recorded from healthy panicles were 77% and the panicles affected by Sheath rot of Paddy recorded a mean germination percentage of 57.8%. Low vigour index1 was found with seeds infected with sheath rot, with the mean vigor index 797, compared to the mean vigor index of 1714 for healthy seeds. The variability in *Sarocladium oryzae* was examined using gene-targeted markers like SCOT (Start codon targeted polymorphism) and CBDP (CAAT box-derived polymorphism) and only the 19 SCOT out of 35 and 19 CBDP primers out of 25 showed scorable and reproducible amplification. The cluster analysis of both SCOT and CBDP primers showed that the isolates from the same agro-climatic region fit into the same cluster. The SCAR marker for identification of *Sarocladium* *oryzae* has been designed from RAPD primers, the monomorphic band obtained from OPM9 was eluted, purified, cloned in pGEM-T Easy vector and sequenced. Primers were designed with sequence information using Primer3 software. The marker was validated against the isolates of the pathogen collected from different locations of India and also found that it was non-specific to other fungi like *Fusraium moniliforme, Bipolaris oryzae, Curvularia lunata and Alternaria alternata.* The studies on management strategy against sheath rot of paddy revealed that Seed treatment with Carboxin (37.5%) + Thiram (37.5%) @2.5 gm/kg seed was found at par with Carbendazim (12%) + Mancozeb (63%) @2.5 gm/kg seed. Among bioagents, the seed treatment with *Pseudomonas flourescens* @10 gm/kg seed was found very effective in reducing the disease severity of sheath rot in paddy.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Vikram Patil	21348	M.Sc.	Effect of salinity stress on seed yield and seed quality parameters in soybean (*Glycine max* L.)	Dr. Monika A. Joshi
2.	Payal Mathur	21349	M.Sc.	Studies on the basis of phenol colour reaction in seeds of wheat (*Triticum* spp.)	Dr. S. K. Chakrabarty
3.	Sushma M.K.	21350	M.Sc.	Effect of nanoparticles on seed quality, yield attributes and storability in chickpea (*Cicer arietinum* L.)	Dr. S. K. Yadav
4.	Samudrala V. Mounika	21351	M.Sc.	Effect of planting geometry and micronutrient application on seed yield and quality of parthenocarpic gynoecious cucumber variety, Pusa Parthenocarpic Cucumber- 6	Dr. Sandeep K. Lal
5.	Mallana	21352	M.Sc.	Standardisation of seed production technology of sponge gourd hybrid: Pusa Shrestha	Dr. Vinod K. Pandita
6.	Bhanu Verma	21353	M.Sc.	Effect of nanoparticles on seed quality and storability in paddy (*Oryza sativa* L.)	Dr. S. K. Yadav
7.	Rashmita	21354	M.Sc.	Studies on seed quality parameters in relation to biochemical composition in Indian quality mustard	Dr. Sangita Yadav
8.	Venkatesha MG	10669	Ph.D.	Impact of sheath rot of paddy caused by *Sarocladium oryzae* on seed quality, its diversity and development of management strategy	Dr. Atul Kumar
9.	Praveen S. Patted	10881	Ph.D.	Development of eco-friendly management strategies against seed discolouration for quality seed production in paddy	Dr. Atul Kumar
10.	Sunil Jadhav	11117	Ph.D.	Study of *Fusarium oxysporum f. sp. lentis* on seed quality, its detection and development of wilt management strategy for quality seed production in lentil	Dr. Atul Kumar

School of
Crop Protection

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Agricultural Chemicals	06	01
Entomology	08	09
Nematology	05	03
Plant Pathology	10	06
Total	**29**	**19**

Agricultural Chemicals

4

Prof. Neera Singh

The Division of Agricultural Chemicals has proved a trendsetter in planning and execution of basic and applied research of national importance in multifarious domains of development, formulation and safety aspects of agrochemicals *viz.,* pesticides and pesticide adjuvants, superabsorbent hydrogels and composites, nitrification inhibitors, hybridizing agents, nutraceuticals, plant growth regulators, smart agro-inputs delivery systems, nanoproducts, new analytical methods for pesticide residues, etc. The mandates of the Division are the development of agrochemicals from natural and synthetic resources; agrochemical formulation, research and development; safety evaluation of plant protection schedules on agricultural crops; develop human resource of excellence. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Development of agrochemicals and formulations

Bioprospecting and insecticidal properties of *Zanthoxylum alatum* seeds

Bioactive volatile and non-volatile phytochemicals of *Zanthoxylum alatum* seeds were chemically profiled and evaluated for acaricidal activity against female adults of *Tetranychus urticae* and *Spodoptera frugiperda*. Monoterpene constituents accounted for 99.25% of oil and linalool (49.94%) was identified as most abundant constituent. Conventional solid liquid extraction (CSLE) using hexane, dichloromethane (DCM), ethyl acetate (EtOAc), methanol (MeOH) and water gave corresponding yield of 4.28%, 3.06%, 2.92%, 3.86 and 2.86%, respectively. Analysis of hexane extract revealed twelve volatile components, accounting 98.49% of extract; linalool (57.01%) and DL-limonene (33.72%) were most abundant. Acaricidal activity showed higher efficacy of essential oil (LC_{50} 127.9 µg mL^{-1}) and hexane extract (LC_{50} 142.7 µg mL^{-1}) against *T. urticae* after 48 h. The essential oil and hexane extract were reformulated separately to prepare nano-emulsions. Acaricidal activity of the nano-emulsions of essential oil and hexane extract exhibited LC_{50} of 103.4 and 111.7 µg mL^{-1} after 48 h, respectively. Further, nano-emulsion of essential oil was found to be effective against *S. frugiperda* with LC_{50} of 13.6 µg mL^{-1} after 48 h. Additionally, nanoemulsions of oil and hexane extract possessed AFI of 89.38% and 92.62% antifeedant activity against *S. frugiperda* after 24 h at 2500 µg mL^{-1} concentration.

Development and evaluation of azole based nanofungicide formulations for management of phytopathogenic fungi in maize

The current research describes the development of nanofungicide formulations of tebuconazole, fluconazole, bifonazole, isoconazole nitrate, ketoconazole, and itraconazole for enhancing crop production and reducing losses due to various fungal pathogens. The nanoformulations of pure azole compounds were prepared using polyethyleneglycol-200 and 300. Dilution and thermal stability was confirmed by following CIPAC guidelines. Transmission electron microscopy (TEM) investigations revealed the particle size of the developed nanoformulations was in the range of 1–100 nm. Nanoformulation exhibited remarkable *in vitro* antifungal efficacy with ED_{50} of 1.63

to 30.28 µg mL^{-1} against *Rhizoctonia solani*, *Macrophomina phaseolina*, *Sclerotium rolfsii* and *Aspergillus flavus*. *In vivo* study against *R. solani* in maize revealed that nanoformulations (100 ppm) were effective in controlling the Banded leaf and sheath blight disease with percent disease index values of 33.33 - 48.14% as compared to inoculated control having percent disease index value of 77.77% resulting in higher yields as compared to the inoculated control. Present study revealed that the prepared nanofungicide formulations have the potential to be used for the effective management of important fungal pathogens in maize.

Controlled release products enriched with bioactive principles of natural origin for management of stored grain pest problem in double zero mustard seeds-development and evaluation

Bio-prospect and bioinsecticidal potential of mustard essential oil (MEO) in combination with other essential oils and the defatted oilseed cake against the two stored grain insect pests of PDZM 31 was evaluated. Sustained vapor release sachet product (VP) formulations were prepared utilizing the indigenously available carriers and plant based bioactives having insect fumigant and/or killing properties, for enhancing storage life of double zero mustard seeds. MEO hydrodistilled from four *B. juncea* varieties (PM 28, PM 30, Pusa Jagannath and Pusa Karishma) was found to contain 2-pentenenitrile (95.1-81.6%), 5-cyano-1-pentene (0.1-2.5%), allyl isothiocyanate (0.4-4.1%) and 1-butene-4-isothiocyanate (0.1-13.4%) as the major constituents. Profiling of glucosinolates in defatted seed cakes by QToF- UPLC-ESIMS revealed presence of 7 glucosinolates and sinapic acid. Fourteen commercially available EOs, along with 4 mustard EOs were screened *in vitro* for fumigant toxicity against *T. castaneum* and *C. cephalonica* established that EOs of *M. communis*, *A. sativum*, and *B. juncea* (all varieties) showed toxicity potential against both test insects. Molecular docking of nine major constituents of these EOs revealed *in silico* mode of action of their bioactive constituents. Different combinations of three EOs (CEO1-CEO4) were evaluated to achieve composition with maximum fumigation toxicity and with multiple modes of action. CEO 4 found most effective was transformed into VP sachets. Bioefficacy of prepared VP sachet formulation assessed under closed container storage conditions demonstrated 100% mortality of insect populations and no population build-up was observed in any of the formulation treated container upto 6 months of study. After 5 months of storage, seed quality assessment of stored seeds established no adverse effects of formulation on germination and seed vigour. The findings of the present study will be further scaled up as novel biofumigant product and application technology for green management of stored grains.

Development and assessment of alkaloid(s) based formulation for thrips management

A study was conducted to understand the effects of alkaloids against thrips, and to develop a safe and effective controlled release formulation for its management. Seven alkaloids namely, atropine, cinchonine, noscapine, piperine, reserpine, strychnine and tropinone were screened against *Thrips palmi* by both *in silico* and *in vitro* approaches. Molecular docking studies of the alkaloids against four target proteins of *T. palmi*, namely, HSP70, EnoPh, CathB and CysP undoubtedly established tropinone as the best putative inhibitor. Bioassay of tropinone by leaf dip method revealed its LC_{50} values as 1262.6 and 734.9 µg mL^{-1} at 24 and 48 h, respectively. Based on the results, tropinone was selected for development of its controlled release formulation by encapsulating it in cross-linked chitosan matrix. Cross-linking of chitosan was carried out separately by three diisocyanates namely, hexamethylene diisocyanate (HMDI), tolylene-2,4-diisocyanate (TDI) and isophorone diisocyanate (IPDI) at three different stoichiometric ratios. All the formulations were characterized by rheometry, FT-IR spectroscopy and scanning electron microscopy. Encapsulation efficiency and loading capacity varied from 24.23 to 80.11% and 2.94 to 6.49%, respectively in the formulations. Fitting of release data to Korsmeyer-Peppas model suggested diffusion controlled release of tropinone from the formulations with highest $t_{1/2}$ of 9.23 days. The superior formulation was found to have prolonged effect against *T. palmi* as compared to commercial acetamiprid formulation in a pot experiment.

Theme 2. Assessment and management of contaminants in agricultural produce and in the environment

Bioremediation of aliphatic and poly aromatic hydrocarbons (PAHs) from oil contaminated soil using microbial consortia

Seventeen bacteria and 3 fungi isolated from the crude oil contaminated soil were evaluated to degrade aliphatic hydrocarbon in the crude oil (1%) and PAHs mixture (naphthalene, fluorene, phenanthrene, anthracene and pyrene) in medium, without and with Tween-80 (0.1%). *Pseudomonas* sp. A3, and *Bacillus amyloliquefaciens* A9 and *Aspergillus sydowii* AK20 were identified as the best aliphatic hydrocarbon degrader, whereas, *Kocuria rosea* AK4 and *Aspergillus sydowii* AK20 were the best PAH degrader. Tween-80, in general, affected degradation of aliphatic hydrocarbons/PAHs by bacteria, effect on fungal degradation was non-significant. Consortium of *Pseudomonas* sp.+*Bacillus amyloliquefaciens* and *Aspergillus sydowii* degraded total petroleum hydrocarbon (TPH) in crude oil in naturally contaminated (25% oil) loamy soil (Assam) with half-life ($t_{1/2}$) of 47.5 d (bacterial consortium) and $t_{1/2}$ 58.2 d (fungus) as compared to $t_{1/2}$ 135.9 d in uninoculated control soil. Bio-formulations of these microbes/consortium were at par with the free cultures in degrading TPH and PAH. Inoculation of soil with crude oil/PAHs degrading microbes increased microbial diversity and nitrogen activity in soil and negated the effect of contaminants.

Synthesis and assessment of pesticide removal potential of magnetite based composites from water

Composites (18) of magnetite with biopolymers including chitosan, starch, hydroxyethyl starch, CMC and microcrystalline cellulose, beta cyclodextrin, normal bentonite, nano organobentonite (with surface modification), graphene oxides, and activated carbon were prepared and used for removal of twelve selected pesticides from fortified and natural water samples. A multiresidue LC-MS/MS method was standardized for simultaneous detection of selected pesticides. Limit of detection and limit of quantification of the method was 0.005 μg mL^{-1} and 0.01 μg mL^{-1}, respectively. Optimised method gave recoveries in the range of 81.87-96.96% (0.5 μg mL^{-1}), 82.82-99.3% (0.1 μg mL^{-1}) and 84.56-96.17% (0.01 μg mL^{-1}). Pesticide removal efficiency of the prepared composites ranged from ~38% to ~100%. Among the biopolymers, magnetite-chitosan beads (MAG 2) showed ~70-99% sorption of fipronil, chlorantraniliprole, and azoxystrobin and all neonicotinoids, but thiacloprid and clothianidin. MPC CNC (MAG 6) showed sorption efficiency of ~75-90%. Amidst the clays, DMDA based complex (MAG 15) showed almost 99-100% sorption of all the pesticides, while activated carbon magnetite composite showed 100% sorption of all pesticides. Ten milligram of sorbent, 4 h contact time, 5 mL of solution (1 μg mL^{-1}), pH >7 and 25ºC were identified as parameters for optimum removal. Efficient regeneration of composites was achieved using methanol and ultrasonication. Two best performing adsorbents, magnetite-DMDA (MAG 15) and magnetite-activated charcoal (MAG 18), were used to remove pesticides from both fortified and unfortified tubewell water samples collected from IARI fields and Yamuna river water. Both the composites showed more than 90-100% sorption of pesticides in the unfortified natural water samples while, in fortified water, the range of sorption varied from 60-100% for magnetite-DMDA (MAG 15) and 82-100% for magnetite charcoal (MAG 18) composites.

Evaluation of matrix effect on pesticide residue estimation in crop group 27 & 28 (Herbs and Spices)

Modified QuEChERS extraction and cleanup method was optimized for trace level detection and quantification of 100 pesticides using UPLC-MS/MS and validated on coriander leaves, curry leaves (representative crops in crop group 027 *i.e*., Herbs), cumin seed, cardamom and ginger (representative crops of crop group 028 *i.e*., Spices) and performance evaluated in their respective member crops (mint leaves, tejpata leaves, fenugreek seed and tamarind, respectively). Water soaking prior to extraction was found effective in analysis of pesticides from cumin seed, cardamom and ginger matrix. The dilution effect of extracting solvent (acetonitrile) was much effective in reduction of matrix effect in coriander leaf, curry leaf, cumin seed and cardamom matrix, while it was not that much effective in case of ginger matrix. Use of anhy $MgSO_4$, PSA and GCB was found most effective as clean up agent for coriander matrix and anhy $MgSO_4$, PSA and C-18 for curry leaf, cumin seed, cardamom, and ginger matrix. The optimized method for coriander, curry leaves and cardamom performed equally good or even better in mint leaves, tejpata leaves and far better in tamarind, respectively and thus can be utilized effectively for member crops. Whereas the optimized method for cumin showed relatively poor performance for fenugreek and thus on residue estimation point of view, reconsideration is required to consider cumin seed as representative crop to decide upon the residue content in fenugreek seeds.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Anirban Sil	21201	M.Sc.	Synthesis and assessment of pesticide removal potential of magnetite based composites from water	Dr. Suman Gupta
2.	Ranjeet Kumar	21202	M.Sc.	Bioprospecting and insecticidal properties of *Zanthoxylum alatum* seeds	Dr. Aditi Kundu
3.	Shyam Kumar Gupta	21203	M.Sc.	Development and assessment of alkaloid(s) based formulation for thrips management	Dr. Anirban Dutta
4.	Renu Saini	21204	M.Sc.	Development and evaluation of azole based nanofungicide formulations for management of phytopathogenic fungi in maize	Dr. Rajesh Kumar
5.	Biswajit Horijan	21205	M.Sc.	Controlled release products enriched with bioactive principles of natural origin for management of stored grain pest problem in double zero mustard seeds-development and evaluation	Dr. Anupama Singh
6.	Sumit Shekhar	21370	M.Sc.	Evaluation of matrix effect on pesticide residue estimation in crop group 27 & 28 (Herbs and Spices)	Dr. Tirthankar Banerjee
7.	Ashish Khandelwal	10223	Ph.D.	Bioremediation of aliphatic and poly aromatic hydrocarbons (PAHs) from oil contaminated soil using microbial consortia	Dr. Neera Singh

Entomology

5

Prof. Debjani Dey

The Division of Entomology has pioneered in investigations in insect systematics and economic entomology *vis-a-vis* important crop pests. National Pusa Collections (NPC) serves as a national repository for insect pests of crops. The Division has been the pioneer in basic and applied research frontiers in agricultural entomology to offer effective pest management solutions to the country in the past several decades with rich haul of expertise in insect biosystematics. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Insect systematics

Taxonomic studies on tribe Crabronini (Hymenoptera: Crabronidae: Crabroninae)

A group of solitary predatory wasps commonly called as the Sand wasps (Hymenoptera: Crabronidae) are represented by over 200 genera with more than 9000 species worldwide. These wasps are brightly coloured and fast moving. Family Crabronini includes 8 subfamilies and 25 tribes. The most diverse, tribe Crabronini is cosmopolitan with over 1500 species under 47 genera. Studies on Indian Crabronid fauna is till today inadequate. Hence, the present studies were undertaken to comprehensively analyse the status of the Indian fauna. Extensive explorations for collection of these wasps were undertaken in North Indian states of Delhi, Haryana, Rajasthan, Punjab and Uttarakhand. The study also included old sphecid collections of National Pusa Collection, Division of Entomology, ICAR-IARI, New Delhi; National Forest Insect Collections, Forest Research Institute& Zoological Survey of India, North Regional Centre, Dehradun. An up-to-date annotated checklist of the Indian species was compiled comprising of 88 species under 13 genera. All synonyms and distribution records were included along with 22 new locality records. The study included 39 species under 10 genera. Twelve species new to science were described under genera *viz*., *Crossocerus* (5), *Ectemnius* (4), *Piyuma* (1) and *Rhopalum* (2). The male of *Ectemnius insignis* was described for the first time. The holotype location was corrected for *Crabro flavoniger*. Several new characters including genitalia, 65 coloured plates with >275 photographs have been included in the study. Diagnostic keys for the genera and species studied have been complied. NPC has been augmented with 200+ identified specimens of 39 species, holotypes and paratypes of all 12 new species. A phylogenetic tree constructed through maximum parsimony (MP) analysis based on 59 characters for genera and 212 characters for species with PAUP*4.0b10 indicated that all 13 genera of tribe Crabronini formed different clades but shared a common ancestor and hence were paraphyletic. The present studies thus have substantially augmented our knowledge of not only species diversity but also their phylogenetic relationships.

Taxonomic studies on microlepidoptera of Pusa campus, New Delhi

Order Lepidoptera, one of the largest insect orders comprises of both macrolepidoptera and microlepidoptera. Microlepidoptera includes smaller moths with wingspan ranging from 5-20 mm and are economically important due to their role as pests of food and cash crops. Additionally, they also act as pollinators and ecological indicators.

Limited studies have examined the regional moth diversity, especially of a thickly populated and a fast growing metropolitan city like Delhi. Based on extensive light trap collections and examination of specimens of National Pusa Collection, ICAR-Indian Agricultural Research Institute, biosystematic studies on micromoths of Pusa campus, New Delhi were undertaken A checklist comprising of 331 species of moths belonging to 32 families and 14 superfamilies from Delhi along with their synonyms was compiled. Perusal of the checklist indicated superfamily Noctuioidea to be most diverse represented by 164 species accounting for 49.5% of all the moths followed by superfamily Pyraloidea with 62 species representing 18.4% of the moths. Further Family Erebidae, the most dominant family was represented by 95 species. 37 species of microlepidoptera belonging to 8 families under 7 diverse superfamilies could be recorded from Pusa campus. Biology of 4 species was studied and 37 species were diagnosed/redescribed with emphasis on several new characters accompanied by 195 illustrations.

Theme 2. Insect pest management: HPR and climate change

Climate change impact assessment and ecological engineering studies on brown planthopper, *Nilaparvata lugens*

The impact of elevated temperature (Ambient+30°C) + elevated CO_2 (600±25 ppm), elevated CO_2 (600±25 ppm) and elevated Ozone (O_3) (60±5 ppb) on BPH *Nilaparvata lugens* (Stal.) and rice variety Pusa Basmati 1121 was studied in Free Air Temperature Enrichment (FATE) during Kharif 2020. Elevated CO_2 had positive effect on all the biological parameters of BPH. It had higher multiplication rate with higher nymphal and brachypterous female leading to higher BPH population (114.6±6.2 BPH/hill) at peak incidence compared to ambient control (41.2±4.4 BPH/hill). Fecundity and egg mass per female was higher in elevated CO_2 conditions. The sucking rate of BPH female as governed by honey dew excreted by females in elevated CO_2 conditions was higher than ambient control. Nymphal duration and adult longevity significantly decreased under elevated CO_2, eventually reducing the BPH developmental period as compared to control. Plant growth and development parameters positively affected by elevated CO_2. The yield parameters were negatively affected by elevated CO_2 conditions compared to ambient condition after BPH infestation. Similarly, under elevated temperature + elevated CO_2 conditions, BPH population was higher than ambient control. Interactive effect of elevated temperature + CO_2 also positively enhanced the plant growth and yield parameters in uninfested conditions. Despite this, BPH infestation caused heavy reduction in grain yield when compared to ambient control. Under elevated temperature + CO_2, photosynthetic rate, transpiration rate, water use efficiency and intercellular CO_2 concentration were found to be lower than or at par with the ambient control. It suggests that, the positive effect of elevated CO_2 is negated by elevated temperature. It exhibits that, elevated temperature and CO_2 in combination increases the yield losses by BPH in rice. On the other hand, elevated ozone reduced the multiplication rate and abundance of BPH population in the rice crop. The peak BPH population in ozone was lower as compared to peak population in ambient control. Fecundity was also recorded lower than ambient control and observed as 108.4±6.0 eggs/female and 135.6±3.7 eggs/female in September and October, respectively. Honey dew excreted was also found to be much lower than ambient conditions. Under elevated ozone, nymphal duration significantly increased over ambient control in both the months. It suggests that, poor nutritional quality of the plants under elevated ozone delays the nymphal development. Elevated ozone also negatively affected the plant growth and reproductive parameters of rice, as the plant height, tillers, length of panicle, total number of grains, grain yield and 1000 seed weight of the grain significantly reduced. BPH infestation further aggravated the negative effects of ozone and drastically reduced the yield parameters of rice. The changes in biochemicals like protein, total soluble sugar and phenol content as well as the activity of protective enzymes such as catalase, peroxidase and SOD in rice plant and BPH in FATE was also recorded. Protein content in the rice plants grown under elevated CO_2 and elevated ozone significantly decreased, BPH infestation further reduced the plant protein. Plants grown under stressed conditions of elevated temperature+CO_2, elevated CO_2 and elevated ozone had higher phenol content than the plants grown under ambient environmental. Total sugar content in the rice plants grown under elevated $CO_2$and elevated temperature+CO_2 significantly enhanced. Catalase enzyme activity in elevated CO_2 and ozone was higher than ambient control in uninfested plants and further it increased after BPH infestation. Peroxidase activity increased after BPH infestation in elevated temperature+ CO_2, elevated CO_2 and ambient control. Highest SOD activity was reported in plants grown under elevated CO_2 (1.73±0.10 U/ml) while it was found lower in elevated temperature+ CO_2 (1.55±0.07 U/ml) and elevated ozone (1.34±0.13 U/ml) as compared to ambient control. In general, enzyme activity was reported higher in plants grown under stress conditions like elevated temperature+ CO_2, elevated CO_2 and elevated ozone than ambient conditions. With changing climate scenario, a higher BPH population will aggravate crop losses in future and elevated ozone aggravate more yield losses than ambient conditions. Effect of ecological engineering on incidence of rice pests and abundance of natural enemies was studied with rice variety Pusa Basmati 1121 during Kharif 2019 and 2020. In the ecologically engineered rice plots, planted with mixture of crops and flowers, mean BPH population per hill was found to be significantly reduced in Kharif 2019 (6.3±2.5) as well as in kharif 2020 (9.4±3.6) as compared to control rice plots (9.8±3.9 and 14.4±5.1) in respective seasons. Furthermore, the activity of natural enemies like spider, mirid bug and rove beetle was highest in rice fields planted with crops like sesamum, sunflower and soybean Rice yield enhanced in plots planted with crops+flowers during Kharif 2019 (5.60±0.24 tons/ha) and Kharif 2020 (5.27±0.06 tons/ha) as compared to control rice plots (3.99±0.20 tons/ha and 4.27±0.06 tons/ha). Treatments with crops plant alone and flowers plants alone also recorded significantly higher yield than control plots in both the kharif seasons. It also reduces the incidence of rice pests, particularly the BPH, and enhances the rice grain yield.

Impact of climate change on brown planthopper (BPH) population with off season survival and host plant resistance perspective

Off season survival of BPH was investigated on the weeds and alternate host plants. However, no trace of BPH survival was found in Delhi region during the off season. Field visit to Maruteru revealed that BPH is surviving on the rice plants in the month of January-February. Early transplanting of rice and light trap catches revealed that BPH reappeared during the first fortnight of July. DNA from BPH samples of thirteen locations were isolated and mtCOI region was amplified post DNA isolation. Accession numbers were obtained from NCBI. Phylogenetic analysis revelaed no clustering and high degree of homogeneity between the geographically distinct populations. Hence exact source of immigration of BPH to Delhi region could not be arrived in the present study. Correlation between the annual peaks of BPH, *Nilaparvata lugens* trap catches and the weather parameters viz. maximum and minimum temperature (Tmax and Tmin), rainfall (RF), morning and evening relative humidity (RH1 and RH2) sunshine hour (SSH) and windspeed (WS) were explored individually for rice areas of Ludhiana (Punjab), Pattambi (Kerala), Chinsurah (West Bengal), and Karjat (Maharashtra). Regression model was developed by using the peaks of the trap catches and the weather parameters and the weather-based model was satisfactorily validated for these regions with R2=0.83, 0.87, 0.76 and 0.86 for Ludhiana, Maruteru, Chinsurah and Karjat respectively. The peak BPH trap catches had shown significant relationship with Tmax, Tmin, RH1, RH2, Rainfall, wind speed of standard meteorological weeks (SMW) of September in Ludhiana and Pattambi locations and SSH of SMWs of August and October for Ludhiana and Pattambi respectively. For Chinsurah BPH trap catches, significant relation was found with Tmax, Rainfall, SSH of SMWs of September month, RH1 and RH2 of SMWs of July and Tmin of SMW of August. Similarly, for Karjat, the peak of BPH trap catch had shown significant relation with Tmax, RH1, RH2, SSH of SMW of October, Tmin of SMW of August, RF of SMW of July. Through stepwise regression method, the most relevant weather parameters in Ludhinana were found to be Tmax, Tmin, RF and WS, whereas for Pattambi were Tmax, RH1, Rainfall and SSH. The most relevant weather factors for Chinsurah were Tmax, RF, RH1 and RH2. Impact of elevated CO2 (570±25 ppm) on BPH, *Nilaparvata lugens* on rice cultivars viz. TN1, PTB 33, Rathu Heenathi, RP 2068-18-3-5, Chinsaba, Swarnalatha and T-12 was studied in OTCs during kharif 2019 and 2020. Elevated CO2 had positive impact on the biology of BPH. It had aggravated the multiplication rate with increased number of nymphs, males and brachypterous females in all the cultivars leading to higher population during both the experiments. The fecundity per female and honeydew excretion got increased, dult and nymphal longevity significantly decreased under increased CO_2 conditions. Plant growth and yield attributes viz. number of tillers, 1000 seed weight and seed yield got positively influenced by the elevated CO_2 conditions in BPH un-infested condition. The results indicate that the yield determining factors were severely affected under elevated CO_2 than ambient levels under infested conditions in all the cultivars. The changes in the level of biochemical constituents like total phenols and total protein content and the activity of protective enzymes viz. peroxidases and catalases in the rice plants of seven different cultivars was analysed in OTC conditions. Protein content of the rice cultivars grown under elevated CO_2 conditions was found to be significantly reduced. Rice plants grown under elevated CO_2 had increased phenol content and the activity of total phenols increased further after BPH infestation in all the cultivars. Among the protective enzymes, the activity of catalase was found to be increased under elevated CO_2 conditions in all the rice cultivars which further increased after BPH feeding. The activity of peroxidase increased after feeding in both ambient and elevated CO_2 conditions, but there was significant reduction of this enzyme was observed in elevated CO_2 levels within BPH un-infested and infested conditions. Under climate change conditions, increased BPH population will lead to increased feeding and thus breakdown of plant resistance. Moreover, decrease in protective enzyme like peroxidase under elevated CO_2 conditions will compromise the resistance level of rice cultivars against BPH.

Studies on host plant resistance against rice brown planthopper *Nilaparvata lugens* (Stål) with climate change perspective

Brown planthopper (BPH), *Nilaparvata lugens* (Stål) (Homoptera: Delphacidae) is one of the major pests of rice, which causes huge yield losses every year throughout tropical, subtropical, and temperate areas of Asia. In most rice-growing areas, the management of this pest is through chemical insecticides. In order to minimize the use of insecticides, the development and use of economically viable and ecologically sound alternatives are needed. Thus, this study was aimed at identifying resistant sources in test rice genotypes viz., CR2711, ISM38, IRGC104646, CR3006-8-2, ARC10894, ARC7229, PTB33, and susceptible check TN1. The tolerance study revealed all the test genotypes to be more tolerant than TN1. Seedbox scoring study revealed the genotypes viz., CR2711, ISM38, IRGC104646, CR3006-8-2, ARC10894, ARC7229, and PTB33 to be resistant to BPH with significantly low damage score (1.30–3.07). Also, significantly lower honeydew excretion area (31.58–43.97 mm^2), nymphal survival (51.6–63.98%), and growth index (2.44–3.62) were recorded in resistant genotypes compared to TN1. Biochemical analysis revealed a higher level of soluble phenolics and peroxidase in all the resistant test genotypes than TN1. The study resulted in the quantification of genotypes, ARC10894 and ARC7229 as new BPH resistance sources that can be used in resistance breeding. Further the effect of elevated CO2 and silicon on the sucking behavior of the rice BPH was investigated under 'Open Top Chamber' (OTC) facility. Silicon amendment enhanced the activity of defensive antioxidant enzymes viz., CAT, SOD, and POD in plants at certain times following BPH infestation than those without Si amendment. Observed Intensified silicification in leaf sheath of Si amended plants was observed under both ambient and elevated CO_2. The sucking behaviour of BPH was affected by the Si amendment and was evident both under elevated and ambient CO_2 conditions. The Si amendment reduced the honeydew excretion, which was indicative of a reduction in BPH feeding. Accumulation of callose in the sieve tube of rice leaf sheath in response to BPH feeding was found to be responsible for reduced honeydew excretion. Molecular studies revealed the dynamic expression of callose synthase-encoding gene (OsGSL1) and callose hydrolase (Gns5) genes that revealed higher callose deposition in Si amended plants compared to those without Si amendment, and. It was found to be the main reason for reduced feeding or lower honeydew excretion by BPH in Si amended plants. Overall, the study revealed ARC10894 and ARC7229 as new BPH resistance sources that can be used in resistance breeding and also proved Si amendment as the ecologically sound potential alternative for the management of BPH under climate change conditions.

Identification and characterization of *Brassica juncea* L. (Czern&Coss) genotypes for different mechanisms of resistance to aphid, *Lipaphis erysimi* (Kaltenbach)

Studies conducted on thirty pheno-morphologically diverse *Brassica juncea* genotypes to understand the physico-chemical defense systems against mustard aphid, *Lipaphis erysimi* indicated significant differences among the plant traits. Traits like point to first branch, siliqua length and total siliquae per plant were found significantly but negatively, while total number of siliquae per plant, point to first siliqua on the main shoot and seeds per siliqua were positively associated with aphid resistance index. Genotypes *viz.*, RBJ 11, RBJ 77, RBJ 49, NPJ 161, PDZ 6, Pusa 119-1-3, Pusa 119-1-2, PM 30, PM 25, TN 3, GP 454, RLC 3 and Kranti had significantly lower, while Rohini, IC 355399, EC 61-9-2-2-2, RP 11-2-1-3-1, EC 62-46-1 and NRCHB 101 had higher number of aphids, *L. erysimi,* both under natural and artificial infestation. Total nymphal period was longer on genotypes, EC 62-46-1, PusaTarak, PM 30, RH 749, RP 7-3-2-21, PDZM 31, NRCHB 101, YSG, TS 18-5124, TN 3 and RP 11-2-1-3-1, and shorter on EC 61-9-2-2-2, Rohini and Kranti, indicating higher level of tolerance against *L. erysimi*. Total developmental period was longer, and fecundity and survival lower on Kranti, RLC 3, NPJ 50, GP 454, Rohini and IC 355399 as compared to the other test *B. juncea* genotypes, except in a few cases. Genotypes viz. PM 30, RH 749, PDZ 6, Pusa 119-1-3, Pusa 119-1-1 and Kranti were found with least leaf and bud preference, lower aphid multiplication rate and population build-up on different plant parts.Different biochemical compounds including enzymes and macronutrients differed significantly in the test *B. juncea* genotypes. There was significant increase in amounts of starch, sugar, protein, phenol, antioxidant, FRAP and tannins, while glucosinolates and plant pigments decreased in response to damage by *L. erysimi* in all the plant parts of test *B. juncea* genotypes. The activity of all the test defense enzymes and amounts of macronutrients were also found to increase in response to damage by *L. erysimi* in all the plant parts of test *B. juncea* genotypes. Genotypes *viz.*, RLC 3, IC 355399, Rohini, GP 454, NPJ 50, TS 18-5124 and Kranti had higher amounts of total antioxidants, tannins, phenols and FRAP, and resulted in adverse effects on the reproductive period, fecundity and survival of *L. erysimi*. Low sugar and lipid contents combined with higher protein, starch, phenol, antioxidant, FRAP and tannin content in RLC 3 and Kranti was found to impart tolerance against *L. erysimi*. Furthermore, high lipid content, and low phenol, antioxidant, FRAP and tannin contents in RBJ 11, RBJ 77, RBJ 49, NPJ 161, PDZ 6, EC 62-46-1 and Pusa 119-1-3 had enhanced aphid preference on these genotypes. Moreover, the mean percent change in different biomolecules, defense enzymes and macronutrients in different plant parts were variable among different *B. juncea* genotypes, indicating differential response against mustard aphid, *L. erysimi*. Thus, RLC 3, IC 355399, Rohini, GP 454, NPJ 50, TS 18-5124 and Kranti had higher amounts of constitutive and enzyme induced defense compounds, resulted in adverse effects on the reproductive period, fecundity and survival of *L. erysimi*, thus can be used in *Brassica* improvement program.

Studies on biological and biochemical interaction between *Lipaphis erysimi* (Kaltenbach) and *Brassica juncea* L.

Studies conducted on 13 *Brassica juncea* genotypes with varying levels of seed glucosinolates to understand the biochemical defense system against mustard aphid, *Lipaphis erysimi* revealed significant differences. The total nymphal, total developmental and reproductive periods were significantly shorter, and the host preference, fecundity, survival, population build-up, multiplication rate and resistance indices of *L. erysimi* was higher on the leaves, buds and siliquae of *B. juncea* genotypes PDZ 12, RLC 3, PDZ 1 and Heera, while reverse was the case with Giriraj, RH 749, Pusa Bold and Varuna. These findings suggest that *B. juncea* genotypes such as Varuna, Pusa Bold, Giriraj and RH 749 increase the developmental and reproductive duration, and had detrimental effect on fecundity and survival of *L. erysimi*, therefore can be of use in mustard improvement program. Further, the biochemical constituents *viz.*, total proteins, total sugars, total lipids, total antioxidants, total phenols, total tannins, ascorbic oxidase, ascorbic peroxidase, catalase, myrosinase, phenyl ammonia lyase and tyrosine ammonia lyase significantly varied in all the test plant parts of *B. juncea* genotypes, under healthy and damaged conditions. These constitutive and aphid-induced biochemical constituents across all the plant parts were significantly higher in Giriraj, RH 749, Pusa Bold and Varuna, and lower in PDZ 12, RLC 3, PDZ 1 and Heera, while reverse was the case with total glucosinolates. There was significant and positive association of aphid damage-induced total lipids, total phenols, total tannins and total glucosinolates with total nymphal, total developmental and reproductive periods, while association was negative with reference to host preference, fecundity and survival of *L. erysimi*. The ascorbate peroxidase, phenyl ammonia lyase and tyrosine ammonia lyase had significant and positive association with host preference, fecundity and survival, and negative association with total nymphal, total developmental and reproductive periods of *L. erysimi*. All the test biochemical constituents across plant parts contributed to 99.3 to 100.0% variability in host preference and biological performance of *L. erysimi* on the test *B. juncea* genotypes. However, total phenols, total tannins, total glucosinolates, ascorbate oxidase, ascorbate peroxidase and tyrosine ammonia lyase explained 79.2 to 99.8% variability in host preference and biological performance of aphids on the test mustard genotypes, suggesting that these biochemical constituents regulate plant defense in *B. juncea* against *L. erysimi*, and can be used for characterization of biochemical mechanisms of resistance in rapeseed-mustard against aphids.

Theme 3. Insect physiology

Investigations on role of gut microbes in *Bacillus thuringiensis* toxicity against pink bollworm, *Pectinophora gossypiella* (Saunders)

Introduction of transgenic Bt cotton, BGI in 2003 and BGII in 2006, revolutionised cotton production in India. However, pink bollworm *Pectinophora gossypiella* started and continued to damage cotton bolls within few years of introduction of Bt cotton. Resistance development to transgenic Bt cotton was unexpected and it severely hampered the benefit of Bt cotton technology. Gut bacteria are known to play a significant role in various functions in their insect host. Therefore in the present study, role of gut microbes in Bt efficacy was studied. Removal of the gut bacteria was done through the use of antibiotics. Culturable midgut bacteria of pink bollworm larvae collected from eight different geographical locations of central and southern India and unculturable midgut bacteria of pink bollworm population from Khandwa in Madhya Pradesh were isolated and identified. 16S rRNA based survey of culturable bacteria of *P. gossypiella* indicated a higher bacterial diversity associated with populations from Adilabad and Khandwa. Gut bacterial diversity was higher in male (21) compared to female (16). *Enterococcus casseliflavus*, *Enterobacter hormaechei* subsp. *xiangfangensis* and *Bacillus cereus* were common in both the sexes. *Paenochrobactrum glaciei* was isolated from insect gut for the first time. Distinct difference was recorded in the values of Shannon and Simpson diversity indices, ChaoI and ACE richness estimates in male and female populations. The alpha diversity analysis showed that the gut bacteria of male were diverse and rich as compared to that of female. Further, beta diversity analysis indicated that the gut bacterial communities of both larval groups were unique from each other. These findings are the maiden report on sex-based variation in gut bacteria in

Pectinophora gossypiella larvae. Metagenomic analysis of unculturable midgut bacteria targeting 16S rRNA V3-V4 region revealed that, Proteobacteria, Firmicutes, and Actinobacteria were the predominant phyla in the midgut of pink bollworm. Candidate phyla OD1 (Parcubacteria) and TM7 (Saccharibacteria) were reported from the gut of male pink bollworm but not from female. Taxonomic to phenotypic mapping revealed that, these gut bacteria play vital role in many metabolic and physiological activities of pink bollworm and these potential roles of gut bacteria also varied with the sex. Role of gut bacteria in Bt efficacy was studied using commercial formulation of Bt (DiPel®) and Cry1Ac and Cry2Ab toxins. They were evaluated using five concentrations against five-day old larvae of *Pectinophora gossypiella* with and without antibiotics (which removed the gut bacteria) by diet incorporation method. Lowest median lethal concentration (LC_{50}) was recorded in Cry2Ab (1.49 µg/gm of diet) followed by Cry1Ac (2.54 µg/gm of diet) and DiPel® (3.63 µg/gm of diet) without the antibiotics (AB). Whereas, highest LC_{50} (9.38 µg/gm of diet) was recorded in DiPel® + AB (chloramphenicol and tetracycline at 50 µg/gm of diet each) followed by Cry1Ac + AB (4.73 µg/gm of diet) and Cry2Ab + AB (3.66 µg/gm of diet). These results indicated that DiPel® as well as both the Cry toxins along with antibiotics were less toxic to larvae of *Pectinophora gossypiella* thereby indicating that gut bacteria potentially affect the susceptibility to *Bacillus thuringiensis*.

Colonization of entomopathogenic bacteria in brinjal plant and interaction with brinjal shoot and fruit borer, *Leucinodes orbonalis* (Lepidoptera: Crambidae)

Brinjal shoot and fruit borer (BSFB), *Leucinodes orbonalis* (Guenée) (Lepidoptera: Crambidae) attacks brinjal right from vegetative stage to final harvest stage. Recently its attack has also been reported at nursery stage. *Bacillus thuringiensis* (*Bt*) is the only entomopathogenic bacterium which has been explored for insect pest management programs. In view of the limitations for the use of *Bt* at field level, and resistance development in the pests due to transgenic *Bt* crops, development of a novel management technique to combat the pest besides searching for a potential entomopathogenic *Bacillus* spp. against *L. orbonalis* is essential. Hence the current studies were undertaken.In vitro bioassays of *L.orbonalis* with native *Bacillus thuringiensis* strains (17) *Bacillus subtilis* (5), *Bacillus pumilus* (2), *Bacillus atrophaeus* (1) and *Bacillus amyloliquifaciens* (1) along with reference strain i.e. *B.thuringiensis kurstaki* HD1 in spore crystal form at a single concentration of 10 µg g-1 of diet against neonates of *L.orbonalis* using diet incorporation method .After 7th day of treatment, the highest mortality was observed in *B. thuringiensis* reference strain HD1 (100%) followed by 96% (VKK-13 and VKK-BB2) and 80% (VKK-BB1) mortality with native *Bt* strains. Moreover, endophytic bacteria *Bacillus atrophaeus*, VKK-6OL and *B. subtilis* strain attained 68% and 52% mortality respectively. Virulence bioassays with shortlisted *Bacillus* strains indicated that median lethal concentration (LC50) of Btk HD1 (LC50=0.49 µg/g of diet) and BtVKK-BB2 (LC50=0.59 µg/g of diet) were found significant with lower LC50 values. Further, 25 *Bacillus* spp. including *Bt* isolates, two native Bt strains (VKK-BB2 and VKK-13) and two brinjal seed endophytic *Bacillus safensis* strains (BSEB-6 and BSEB-9) along with reference *Bt* (*Btk* strain HD-1) could record above 50% mortality. Other *Bt* strains, VKK-ENT 1(48.15%) and VKK-BB1 (40.74%) and neem leaf endophyte, *Bacillus subtilis* VKK-1OL exhibited 40.74 % mortality in the neonates of *L. orbonalis*. Three potential entomopathogenic *B. thuringiensis* strains (*Bt* VKK-BB2, *Bt* VKK-13 and reference *Bt*, *Btk*-HD1) were inoculated to brinjal seed separately via seed treatment, soil application to the seedlings and foliar spray at single concentration at 1x 108 CFU/ml in pot culture experiments. After reisolation of *Bt* colonies from leaf tissue the colonies were subjected to morphological and molecular approaches to confirm the endophytic ability of respective *Bt* strains. During quantification of colonies of respective *Bt* strains reisolated from leaves on 3rd day and 10th day after inoculation from soil application and foliar spray higher colonies were recovered on 3rd DAI. In case of seed treatment, *Bt* colonies could survive up to 30th DAI. Among the *Bt* strains, the native *Bt* strain VKK-BB2 was found to be potential colonizer with the highest recovery in all three inoculation methods. GFP tagging of *Bt* strain VKK-BB2 was carried out and confirmed the green fluorescence under Confocal Laser Scanning Microscope (CLSM). Inoculation of GFP tagged *Bt* VKK-BB2 to brinjal by three inoculation methods were comparable with *Bt* VKK-BB2 without tagging. Bright fluorescence signals were visualized in stem and leaf sections by using CLSM in all inoculation methods at single dose. Soil application + Foliar spray twice per week showed green fluorescence up to 15th DAI which suggested inoculum concentration and inoculation method influences the colonization ability in brinjal seedling. Bioassays of *L.orbonalis* were conducted with leaves collected from inoculated brinjal and uninoculated brinjal plants. Reference *Bt*, *Btk*- HDI showed the highest mortality (44.44%) in soil application + foliar spray treatment followed by native *Bt* strain VKK-BB2 (42.96%) in the same inoculation method. This is the first report on endophytic ability of entomopathogenic *Bt* in brinjal and its effect on larval herbivory.

Dynamics of endosymbiont interaction in *Bemisia tabaci*

Bemisia tabaci (Gennadius) (Aleyrodidae: Hemiptera: Insecta) is a cosmopolitan polyphagous, one among the most devastating insect pests of the twentieth century. *B. tabaci* is reported to harbor a primary endosymbiont, *Portiera aleyrodidarum* and seven other secondary endosymbionts *viz.*, *Arsenophonus, Cardinium, Fritschea, Hamiltonella, Hemipteriphilus, Rickettsia,* and *Wolbachia*. The present investigation was carried out to study the temporal, spatial and the host plant influence on the dynamics of endosymbionts in major genetic groups of *B. tabaci* in India. The study also reveals the differences in the biology of Asian genotypes of *B. tabaci*. The one such vital aspect of the study was to reveal the endophyte and endosymbiont interactions between *B. tabaci* and its host plants using culture dependant methods as well as availing metagenomic profiling and bacterial transformation approaches.

Portiera present in all the four population (New Delhi, Indore, Sri Ganganagar and Coimbatore) with its constant frequencies and association irrespective of spatial, temporal and host plant influence. Among the secondary endosymbionts, *Arsenophonus* found prevalent in all the four populations under study. The average infection frequencies of *Arsenophonus* in New Delhi population was observed to be 100%, 100% and 72.5% during 2017, 2018 and 2019 respectively. *Wolbachia* shows an average of 61%, 54.16% and 12.5% in terms of infection frequencies during 2017, 2018 and 2019 respectively where it shows a decreasing trend in the infection frequencies temporally. Even the spatial and host plant influence observed with low infections of *Wolbachia* when compared to *Arsenophonus* and *Rickettsia*. The trends in the infection frequencies of *Rickettsia* were in the average of 67%, 65% and 5.25% respectively during 2017, 2018 and 2019. The total developmental time from egg to adult was lowest in Asia II7 genotype and highest in Asia II5 genotype whereas developmental duration of the egg found shortest in Asia II7 and longest in Asia II5. The total developmental duration of nymph found to be highest in Asia II5 and lowest in Asia II7. The highest adult longevity was observed in Asia II5 and lowest in Asia II1 Indore. The mean fecundity was highest in Asia II7. Asia II1 Sri Ganganagar females recorded highest life expectancy, highest finite rate of increase, highest intrinsic rate of increase and shortest mean generation time. The results of the culture dependant approach in Asia II 5 reveals the presence of 5 genera with 19 bacterial species. Similarly, Asia II 7 contained 6 genera with 18 bacterial species. Cotton yielded a total of four genera with 22 species of bacterial strains, while tomato yielded four genera among twenty species of bacterial strains. *Bacillus* (*Proteobacteria*) is prevalent in both tomato and cotton. The common bacterial determinants upon successful transformation were confirmed for their florescence behavior using plate culture technique, PCR amplification with specific primers and confocal microscopy. The rhizosphere treatment of gfp tagged bacterial solution on cotton and tomato upon 10 days of treatment confirms the colonization of those specific tagged bacteria in the endogenous tissues of both cotton and tomato leaves. The release and confinement of whiteflies on bacterized plants for 7 days and further examination of those confined whiteflies using plate culture technique, PCR amplification with specific primers and confocal microscopy confirms the uptake and transmission of tagged bacteria from plants to whiteflies and their successful colonization in whitefly tissues. The study confirms the horizontal transmission pathway of micro biota between the plants and insects especially in the cotton-*B. tabaci* system.

Characterization of gut bacteria of Italian honey bee *Apis mellifera* (Apidae: Hymenoptera)

A study was conducted to explore the diversity of gut bacteria in the forager and hive bees of *A. mellifera* through culture dependent approaches by microbial isolation coupled with generic characterization using 16S ribosomal RNA probes and culture independent approaches like phospholipid fatty acid (PLFA) analysis and next generation sequencing on Illumina MiSeq platform. Additionally, biochemical studies were carried out to screen the cellulolytic, hemicellulolytic, lipolytic, pectinolytic and invertase activities of gut bacterial isolates. A total of 51 and 32 aerobic gut bacteria were found associated with forager and hive bees of *A. mellifera* respectively. The bacterial isolates from forager bee belonged to three Phyla: Firmicutes : 59 % of isolates (*Aneurinibacillus, Bacillus, Clostridium, Lysinibacillus, Paenibacillus*); Proteobacteria 37 % (*Cedecea, Enterobacter, Klebsiella, Ochrobactrum, Pantoea, Salmonella, Serratia, Stenotrophomonas, Xanthomonas*) whereas, in the hive bees Firmicutes (*Bacillus, Clostridium, Enterococcus, Lactobacillus, Lysinibacillus*) accounted for majority of the isolates (65 %) followed by Proteobacteria (*Enterobacter, Klebsiella, Pseudomonas, Serratia*) constituted 26 % of the isolates and Actinobacteria (*Microbacterium, Streptomyces*) accounted for the rest. Overall, greater bacterial diversity was observed in forager bees compared to hive bees. And within forager bee, hindgut supported greater diversity in terms of genera and species. Where as in hive bees, both the fore gut and midgut harbour diverse bacterial genera. Metagenomics analysis revealed that a complex community of bacteria comprising of Proteobacteria, Firmicutes, Actinobacteria and Bacteriodetes, Cyanobacteria are associated with the hive bees Burkholderiales, Enterobacteriales, Pseudomonadales, Lactobacilliales, Neisseriales, Bifidiobacteriales, Rhizobiales Rhodospirillales, Pasteurellales are common to both. Streptophyta, Xanthomonadales and Caulobacterales are unique to the hive bees, while, Flavobacterales are unique to foragers. A total of 22 and 11 isolates from forager and hive bees respectively possessed cellulolytic ability with specific activity of cellulose was ranging between 0.388 U/mg to 1.493 U/mg in forager bee and 0.47 U/mg to 1.38 U/mg in the hive bees. All the 81 gut bacterial isolates from *A. mellifera* showed lipolytic activity in the range of 0.166 U/mg to 2.509 U/mg. The pectinolytic activity of the gut bacterial isolates was estimated to be in the range of 0.012 U/mg to 3.693 U/mg in forager and hive bees. Fifty-one gut bacterial isolates showed invertase activity (0.010 U/mg to 6.062 U/mg). Demonstration of high activity of the above indicates that these gut bacterial isolates may probably aid in digestion of pollen and processing of nectar in *A. mellifera* bees.

Changes in transcriptome of whitefly (*Bemisia tabaci* Gennadius) associated with begomovirus infection

Chilli leaf curl disease caused by chilli leaf curl virus (ChiLCV, *Begomovirus*) a major constraint in chilli production globally is transmitted by Silverleaf whitefly (*Bemisia tabaci*, Hemiptera: Aleyrodidae) in a persistent circulative manner. Insecticides are commonly used for vector control for managing the disease. Understanding the molecular interactions between ChiLCV and *B. tabaci* and interrupting the interrelationship is a promising approach or as an alternative to hazardous pesticides. Transcriptome analysis of *B. tabaci* at an early stage of ChiLCV infection showed differential expression of 80 (29 upregulated and 51 downregulated) genes. The highest numbers of differentially expressed genes are categorized under molecular functions, followed by cellular components and biological processes. KEGG pathway analysis of differentially expressed genes showed that the genes are involved in functions like metabolism, signaling pathways, cellular processes, and organismal systems. Regulation of key DEGs such as carboxypeptidases, dual specificity protein phosphate, dynein, fasciclin 2, inhibin beta chain, replication factor, and Tob1 protein involved in receptor binding, viral accumulation, apoptosis, intracellular trafficking, cellular signaling, and endocytosis might favour the virus infection and circulation in *B. tabaci.* The present study increases our understanding of the networks of molecular interactions between ChiLCV and *B. tabaci.* The candidate genes involved in the key physiological process and ChiLCV transmission by *B. tabaci* would be novel targets for sustainable management of the *B. tabaci*-begomovirus complex.

Identification of *Thrips palmi* genes responsive to tospovirus infection

Thrips palmi (Thysanoptera: Thripidae), a common vector for tospovirus in the Asia-Pacific region transmits groundnut bud necrosis virus (GBNV, family *Tospoviridae*, order *Bunyavirales*) in a persistent-propagative manner. GBNV causes up to 90 percent yield losses in groundnut, tomato, and potato. Understanding the molecular interactions between thrips and GBNV and interrupting the interrelationship is a promising approach for the management of the virus-vector complex. The comparative transcriptome of *T. palmi* in response to GBNV infection showed 2,365 differentially expressed transcripts with comparable numbers up- (1384) and downregulated (981). Expression of the putative genes in response to GBNV infection was validated by qRT-PCR. Differential modulation of carbohydrate, energy, and nucleotide metabolism, as well as receptor signaling, and endocytotic pathways were identified. GBNV infection led to modulation of genes associated with host immune response like dynamin-1-like, hsp70, PFAS, spag6, serpin, and UHRF1-binding protein 1. Regulations of genes such as ABC transporter, arrestin, cuticular proteins, CYP, endocuticle structural glycoprotein, GABA receptor, laccase, nephrin, myrosinase 1-like, proteoglycan 4-like, and tyrosine kinases were also identified. Expression of several genes of *T. palmi* was conserved between GBNV and capsicum chlorosis virus (another tospovirus) infection but distinct to tomato spotted wilt virus infection in *Frankliniella occidentalis*. The majority of DEGs are involved in innate immunity, cellular signaling, membrane transport, intracellular transport, endocytosis, and cellular integrity that might facilitate the virus invasion and multiplication in *T. palmi*. The study provides an understanding of networks of molecular interactions between *T. palmi* and GBNV and suggests potential genetic targets for generic pest control.

Studies on physiological responses of *Spodoptera litura* exposed to short and long-term thermal stress

Tobacco cutworm, *Spodoptera litura* (Fabricius) (Lepidoptera: Noctuidae) is one of the most destructive polyphagous insect pests of 112 species of plants. Temperature is one of the most significant abiotic factors influencing an organism's nature, physiology, life history, distribution, abundance etc. Shorter periods of extremely high temperature, known as thermal stress are expected to become extensive and severe in the near future as a result of global warming. Effects of the thermal stress vary according to the life stage of the insect exposed because changes in the physiological responses to the temperature are subject to change during development. The physiological responses of short and long-term thermal stress on various developmental stages [27ºC – control, 42ºC 4hours single and multiple (2, 4, 2 and 2 days for egg, larva, pupa and adults respectively) stress, 46ºC 1hour single stress and multiple (2, 4, 2 and 2 days for egg, larva, pupa and adults respectively) stress] of *S. litura* were evaluated by recording survival rate, maturation success, female ratio, longevity, size and weight of male and female adults, GSI, eupyrene sperm count and reproductive fitness parameters comprises pre-oviposition, oviposition, post-oviposition period, total fecundity, mating success, mating frequency and fertility percent in adults emerging from the stressed stages. Observed values varied for all the parameters between treatments. Other than pre-oviposition and post-oviposition period the thermal stress exposure had significant influence on all other parameters studied. The increase in temperature and frequency of exposure caused a reduction in most of the biological and reproductive fitness parameters. The female ratio increased due to thermal stress at higher temperatures compared to control. The metabolic responses like water content (%), protein, carbohydrates and glycogen contents (µg/mg) of male and female adults of *S. litura* emerged from stressed egg and larva were studied. The results revealed that the water content reduced significantly in both male and female adults under thermal stress. The protein, carbohydrates and glycogen content increased many times in the stressed adults compared to control. 46 ºC 1-hour multiple stress considered to be the most impactful treatment as insects exhibited the least performance for all the parameters. The early developmental stages like egg and larva were the most susceptible stages to thermal stress.

Investigations on impact of thermal stress on reproductive physiology of *Spodoptera frugiperda*

The growth, survival, and development of insects are highly influenced by various biotic and abiotic factors. Temperature is one of the most important abiotic factors affecting the distribution, abundance, survival, development and reproduction of insects. The heat stress imposed on insects result in two types of effects, lethal results in immediate mortality and sub-lethal affects survival and overall fitness. Studies were conducted on the sub-lethal effects of a single hot event (42^{o}C) for three different durations (2, 4, and 6h) on the reproductive traits that are susceptible to heat stress in fall armyworm, *Spodoptera frugiperda* (J.E.Smith) (Lepidoptera: Noctuidae), a polyphagous lepidopteran pest causing economic loss to more than 353 plant species belonging to 76 families**.** Though there was no immediate mortality recorded across all stress treatments, a trade-off between thermo tolerance and reproductive performance was evident. The reproductive traits like mating success, mating frequency, pre-oviposition, oviposition and post-oviposition period, total fecundity and hatching percent was significantly affected upon heat shock with increase in duration, particularly through paternal effects. The heat shock provoked a hormesis effect in stressed females by enhancing fecundity and highest number of eggs was recorded in the stressed female combination of 6h stress. Further carry-over effects of parental stress in F_1 progenies hampered their developmental attributes *viz.,* larval duration, larval weight, pupal duration, pupal weight, percent pupal formation and percent adult emergence. The vital reproductive traits, gonadosomatic index and eupyrene sperm production were also highly affected in the off springs and the effect amplified with increase in exposure duration. Sex-specific expression of heat responsive gene (*Sf-hsp70* and *Sf-SOD*) indicated its role in heat resistance. Down regulation of *Vg* gene in male and female adults with increased exposure duration highly impacted the oocyte development in *S. frugiperda*. Results suggest that a single hot event can also have detrimental effects on reproductive fitness of fall armyworm especially through paternal effects.

Theme 4. Toxicological studies

Toxicity variations of insecticides against cotton whitefly *Bemisia tabaci* (Genn.)

Toxicological studies on cotton whitefly, *Bemisia tabaci* (Genn), an insect-pest causing significant economic losses on a global scale indicated significant variations in the susceptibility levels among various populations collected from different cotton growing regions of India *viz.*, Amravati (Maharashtra), Guntur (Andhra Pradesh), Hisar (Haryana), Indore (Madhya Pradesh), Ludhiana (Punjab), New Delhi (Delhi) and Sriganganagar (Rajasthan) along with the lab susceptible strain collected from Subabul, *Leucaena leucocephala* wild host of *B. tabaci*, were subjected to stage specific bioassays considering the most susceptible stage for each against insecticides *viz.*, fipronil, flonicamid, pyriproxyfen, buprofezin and spiromesifen following IRAC susceptibility test methods. Populations from Sriganganagar, Amravati and Ludhiana recorded higher LC50 values for all the test insecticides and exhibited moderate to high level of resistance to flonicamid and fipronil; populations from New Delhi, Indore, Guntur and Hisar exhibited varying levels of susceptibility (susceptible, low to moderate resistance) towards the different test insecticides. All the populations were found susceptible to pyriproxyfen and buprofezin whereas Sriganganagar and Ludhiana populations exhibited low level of resistance towards spiromesifen. Sublethal doses of the insecticides exhibited feeding cessation and reduction in egg hatch, although fecundity was unaffected with few exceptions. Investigations on the detoxifying enzymes cytochrome P450 monooxygenases, glutathione S-transferase and esterase levels on both nymphal and adult stages indicated significant variations among the different populations of B. *tabaci*. Positive correlation was observed between cytochrome P450 and GST activity with the susceptibility of B. *tabaci* populations towards all the test insecticides. Elevated levels of cytochrome 450 was observed among Ludhiana (8.985, 3.426 nmol/min/mg of protein), Amravati (8.557, 3.112 nmol/min/mg of protein) and Sriganganagar (2.214, 3.117 nmol/min/mg of protein) populations at both adult and nymphal stages whereas New Delhi (5.566, 2.077 nmol/min/mg of protein) and Indore (5.610, 2.009 nmol/min/mg of protein) populations recorded lower activity of cytochrome P450. Similarly elevated levels of glutathione S-transferase was observed among Ludhiana (1.680, 0.648µmol/min/mg of protein), Sriganganagar (1.602, 0.579 µmol/min/mg of protein) and Amravati (1.525, 0.548 µmol/min/mg of protein) whereas New Delhi (1.428, 0.376 µmol/min/mg of protein) and Indore (1.400, 0.343 µmol/min/mg of protein) populations recorded lower activity of GST. Further sublethal doses of test insecticides significantly reduced honeydew production and egg hatch in most and least susceptible populations of *B. tabaci* for each insecticide; flonicamid was found most effective in causing reduction in honeydew with LC_{40} causing 98.63 and 95.28% reduction, followed by fipronil which caused 86.30 and 89.18% reduction in most and least susceptible populations; other insecticides caused significant reduction in honeydew only at field recommended dose.

Studies on the efficacy of phosphine and contact insecticides against saw toothed grain beetle, *Oryzaephilus surinamensis* (L.) and almond moth, *Cadra cautella* (Walker)

Studies undertaken on fumigant toxicity of phosphine and contact toxicity of insecticides viz., malathion, deltamethrin, spinosad, spinetoram, lambda-cyhalothrin, and chlorfenapyr was evaluated against different life stages of *Oryzaephilus surinamensis* (L.) and *Cadra cautella* (Walker) indicated differential susceptibility of various stages of both insects to phosphine and contact insecticides. The lethal concentrations in phosphine bioassay for adults of *O. surinamensis* (LC50= 111.55, 57.90, 36.84 ppm for 24, 48, and 72h) and larvae of both ages 5-10 day (LC50= 22.38, 14.27, 13.12 ppm for 24, 48, and 72h) and 15-20 day (LC50= 71.03, 77.41, 18.68 ppm for 24, 48, and 72h) revealed adult stage as comparative tolerant stage. In the case of *C. cautella*, egg stage (LC50=172.80, 151.80 ppm for 24 and 72h) was found to be more tolerant than pupae (LC50= 119.50, 107.85, 86.53 ppm for 24, 48, and 72h), larvae (LC50= 43.98, 14.43, 12.03 ppm for 24, 48, and 72h) and adults (LC50= 29.85, 12.79, 8.61 ppm for 24, 48, and 72h). Further contact toxicity experiments revealed chlorfenapyr 10SC to be most toxic to the adult stage of *O. surinamensis* (LC50= 3.67, 0.42 and 0.13 ppm respectively for 24, 48, and 72 h exposure) whereas lambda-cyhalothrin 5EC was effective against larval stages (LC50=7.23, 4.07 and 1.24ppm respectively for 24, 48 and 72 h exposure). Adults of *C. cautella* were found to be most susceptible to deltamethrin 2.5WP (LC50=0.90, 0.53, and 0.11 ppm respectively for 24, 48, and 72 h exposure) whereas larvae were susceptible to lambda-cyhalothrin 5EC (LC50=130.35, 124.24, and 120.06ppm for 24, 48 and 72 h exposure). Conclusions of the present study is that an extended exposure period in case of phosphine fumigation was most effective while insecticides like chlorfenapyr and lambda-cyhalothrin are promising alternative insecticides.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Roshani Ghimire	21199	M.Sc.	Studies on biological and biochemical interaction between *Lipaphis erysimi* (Kaltenbach) and *Brassica juncea* (L.)	Dr. M. K. Dhillon
2.	M. N Rudra Gouda	21268	M.Sc.	Characterization of gut bacteria of Italian honey bee *Apis mellifera* (Apidae: Hymenoptera)	Dr. S. Subramanian
3.	Komal J.	21269	M.Sc.	Taxonomic studies on microlepidoptera of Pusa campus, New Delhi	Dr. P. R. Shashank
4.	Mr. Deepak Kumar Mahanta	21270	M.Sc.	Identification of *Thrips palmi* genes responsive to tospovirus infection	Dr. Amalendu Ghosh
5.	Isaiyamudhini T.	21271	M.Sc.	Investigations on impact of thermal stress on reproductive physiology of *Spodoptera frugiperda*	Dr. Sagar D.
6.	Aarthi Nekkanti	21272	M.Sc.	Changes in transcriptome of whitefly (*Bemisia tabaci* Gennadius) associated with Begomovirus infection	Dr. Amalendu Ghosh
7.	Sangita Basabaraj Kattimani	21273	M.Sc.	Studies on the efficacy of phosphine and contact insecticides against saw toothed grain beetle, *Oryzaephilus surinamensis* (L.) and almond moth, *Cadra cautella* (Walker)	Dr. Mahadev Suresh Nebapure
8.	Sujatha G.S.	21274	M.Sc.	Studies on physiological responses of *Spodoptera litura* exposed to short and long term thermal stress.	Dr. Sagar D.
9.	Asish Kumar Rout	10275	Ph.D.	Impact of climate change on Brown plant hopper (BPH) population with off season survival and host plant resistance perspective	Dr. Subhash Chander
10	Yogesh M. Yele	10436	Ph. D.	Climate change impact assessment and ecological engineering studies on brown plant hopper, *Nilaparvata lugens*	Dr. Subhash Chander
11.	Varun Saini	10796	Ph.D.	Taxonomic studies on tribe Crabronini (Hymenoptera: Crabronidae: Crabroninae)	Dr. Debjani Dey
12.	Sudhakar S. Kelageri	10604	Ph.D.	Toxicity variations of insecticides against cotton whitefly *Bemisia tabaci* (Gennadius)	Dr. G.K. Mahapatro
13.	Ramesh K.B.	10798	Ph.D.	Dynamics of endosymbiont interaction in *Bemisia tabaci*	Dr. S. Subramanian
14.	Chaitra H.S.	10799	Ph.D.	Investigations on the role of gut microbes in *Bacillus thuriengensis* toxicity against pink bollworm, *Pectiniphora gossypiella* (Saunders)	Dr. Vinay Kumari Kalia

15.	Ipsita Samal	11017	Ph.D.	Identification and characterization of *Brassica juncea* L. (Czern & Coss) genotypes for different mechanisms of resistance to aphid, *Lipaphis erysimi* (Kaltenbach)	Dr. M.K. Dhillon
16.	Ms.Sunitha Pola	11021	Ph.D.	Colonization of entomopathogenic bacteria in brinjal plant and interaction with brinjal shoot and fruit borer, *Leucinodes orbonalis* (Lepidoptera : Crambidae)	Dr. Vinay Kumari Kalia
17.	Prabhulinga T.	11242	Ph.D.	Studies on host plant resistance against rice brown plant hopper *Nilaparvata lugens* (Stål) with climate change perspective	Dr. Subhash Chander

Nematology

6

Prof. M. R. Khan

The Division of Nematology is mandated to work on plant parasitic nematodes which are the most numerous multi-cellular organisms inhabiting different habitats. Plant parasitic nematodes inflict indirect damage to crops by pre-disposing plants to other co-inhabiting pathogenic bacteria, fungi, pathogens etc. They are an important biotic stress for the successful cultivation of field and horticultural crops. However, beneficial and useful nematodes, which are potential biocontrol agents, have been successfully utilized as entomopathogenic nematodes (EPNs) for the management of insect pests of crops. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Nematode detection and diversity

Determination of genetic diversity of potato cyst nematodes, *Globodera rostochiensis* and *G. pallida* in India

The potato cyst nematodes (PCNs), *Globodera rostochiensis* and *G. pallida* are obligate and endoparasitic pests that cause major losses in potato crop. In recent years, Loop-mediated isothermal amplification (LAMP) has gained popularity for its uses in the rapid detection of plant parasitic nematodes. Here we developed a rapid and sensitive PCN-LAMP assay to diagnose *Globodera* within one and half hour. The PCN-LAMP assay is specific to genus *Globodera*, could detect up to femtogram quantity of nematode DNA and would be useful for point of care detection of PCNs in future. In addition, for the first time in India, we investigated the genetic diversity of PCN populations using microsatellite markers. It was revealed that all the Indian populations are genetically identical. In addition, the data suggested that the Indian populations of PCNs exhibited high similarity to Bolivian populations of PCN. A recent and single introduction of PCNs in India is predicted from Bolivia, followed by local spread mainly due to the transportation of infested seed tubers.

Detection of entomopathogenic nematodes by loop-mediated isothermal amplification

Heterorhabditis and *Steinernema* are the most famous group of beneficial entomopathogenic nematodes (EPNs) that are used as biocontrol agent to manage insect pests of several crops around the world. Two LAMP assays were developed to detect and identify *Heterorhabditis* and *Steinernema* from soil samples. The Het-LAMP (*Heterorhabditis*-LAMP) and Ste-LAMP (*Steinernema*-LAMP) assays are developed using ITS and 18S regions of rDNA, respectively. The assays can produce detectable results within an hour which is quicker than any morphological such as baiting technique or molecular techniques such as PCR, qRT-PCR, High throughput sequencing (HTS), etc. Also, the Het-LAMP and Ste-LAMP assays are very specific to their target i.e., *Heterorhabditis* spp. and *Steinernema* spp., respectively. In addition, the assays require fewer establishment charges as they can be performed on basic molecular laboratory equipment as compared to PCR methods where sophisticated instruments are used. The designed LAMP assays can detect even minute concentrations of DNA (0.2 to 9.6 picograms), hence can detect even a single nematode from the soil samples.

Theme 2. Nematode biosystematics

Characterization of *Xiphinema, Longidorus* and *Paratrichodorus* populations

Populations of *Xiphinema*, *Longidorus,* and *Paratrichodorus* recovered from around the roots of hedge plant (*Euphorbia* sp.) and citrus grown at the Indian Agricultural Research Institute (IARI) farm, New Delhi were characterized morphologically and molecularly for identification of the species. We observed the morphological characters and measured the required number of specimens for each population and compared those with the morphology and morphometrics of known species. New gene sequence information for all three Indian populations was generated and used for phylogenetic analysis. *Xiphinema basiri* Siddiqi, 1959 was identified based on morphology and gene sequences of ITS rRNA (accession number MZ566842), D2-D3 expansion segment of 28S rRNA (MZ568465), and *COI* of mtDNA (MZ562890) from the roots of hedge plant. Similarly, *Longidorus pisi* was identified from the rhizosphere of citrus grown in the horticultural farm. We recorded a male from India, however, the male is different in respect of morphometrics, size of the spicule, and number and arrangement of supplemental papillae from the male reported from Malawi. A population of *Paratrichodorus* recovered from the rhizosphere of citrus plants was characterized based on morphology, morphometrics, and molecular analyses of 18S rRNA (MZ567177). This population appears to be a new species of the genus, *Paratrichodorus*; however, additional marker gene sequence information is required to confirm this species.

Theme 3. Plant-nematode interaction

Molecular dissection of Rice-*Meloidogyne graminicola* interactions: effectors and their targets

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

Evaluation of wild brinjal germplasm against root-knot nematode, *Meloidogyne incognita*

Wild *Solanum* species related to brinjal including cultivated *Solanum melongena* were screened for resistance against root-knot nematode (*Meloidogyne incognita*) under pot experiment. Among wild species, resistant sources were identified in *S. torvum* (IC545507), *S. aculeatissimum* (IC256193), *S. gilo* (IC419464), and *S. incanum* (IC324556). In two species, *S. khasianum* and *S. sisymbriifolium,* no resistant accession was found, however, moderately resistant accessions showed no or less egg mass production with low multiplication factor (≤1). In all, seventeen accessions were found moderately resistant with less than 30 galls per plant, with the maximum number of accessions found in *S. incanum* (nine) followed by *S. torvum* (four). Multiplication factor was found less than one in all those accessions except one accession of *S. incanum*. All these resistant accessions showed a reduction in the number of galls, number of egg masses, and nematode multiplication. All accessions of *S. melongena* were found to be susceptible to highly susceptible. Nematode penetration was not affected in resistant *S. torvum* accessions, though nematode development was delayed when compared with *S. melongena* in pluronic gel assay. The identified resistant accessions could be useful in crop improvement programs by identification of genes and transfer of resistance to cultivated species.

Theme 4. Silencing nematode genes

Study the RNAi effect of the sex and larval development genes on root-knot nematode development and multiplication

RNAi is a promising gene silencing approach that inhibits the growth and development of nematodes by inhibition of gene expression. Many genes are responsible for the parasitism and development of nematodes. Reproduction is essential for the existence of any species. In this study, we targeted two sex and larval development genes i.e. *Tra-1* and *Bcat-1* using dsRNA construct in *the Arabidopsis* plant. Using gateway cloning protocol, we transformed dsRNA in *Arabidopsis* using agrobacterium. The data show a significant reduction at different stages of nematodes. There was a 50% and 52% reduction in number of galls; 42.22% and 53.33% reduction in number of females; 44.44% and 57% reduction in number of egg masses; 46.12% and 54.26% reduction in number of eggs per egg mass, in *Tra-1* and *Bcat-1* treatments, respectively when compared to non-transformed *Arabidopsis* plants. Furthermore, based on results RNAi will be an important option in the future for the management of nematodes and other crop pests by developing nanoparticles for field application.

Theme 5. Entomopathogenic nematodes for insect pest management

Molecular characterization and expression profiling analysis of *Photorhabdus* toxin receptor genes from greater wax-moth, *Galleria mellonella*

The successful deployment of *Photorhabdus* toxins for insect pest management warrants a detailed analysis of their receptors in the host insect as the intricacies regarding binding/delivery of the toxin protein and their subsequent catalytic action in the target host cell is yet unresolved. The present study was performed to understand the molecular interaction between a *Photorhabdus* toxin (TcaB) and its putative receptors in a model insect, *Galleria mellonella* using RNAi analysis. Firstly, several candidate receptor proteins such as cadherin (CAD), alanyl aminopeptidase N (APN), alkaline phosphatase (ALP), an ATP-binding cassette transporter subfamily C (ABCC) that putatively interact with *P. akhurstii* TcaB, were molecularly characterized from the midgut tissue of *G. mellonella*. GmCAD (1840 aa long) is a membrane-bound protein that contains 14 cadherin repeats in its extracellular domain, a transmembrane domain, and a C-terminal cytosolic tail. GmALP (515 aa) and GmAPN (1000 aa) are extracellular in nature and contain a C-terminal GPI anchor site that putatively functions as receptors for different proteins. Lepidopteran CAD sequences were highly conserved as they formed a distinct clade that diverge from hymenopteran, isopteran, coleopteran, and hemipteran clades. By contrast, GmALP and GmAPN had no homologues in insect orders other than Lepidoptera. GmCAD was highly expressed in the fourth-instar larval stage compared to other life stages. In addition, GmCAD was highly expressed in midgut tissues compared to other body parts such as the Malpighian tubule, foregut, hindgut, head, and fat body. A similar trend was observed with GmALP and GmAPN transcripts. Oral feeding of GmCAD dsRNA was highly effective to suppress *GmCad* mRNA levels in the midgut tissue. Subsequently, the susceptibility of dsRNA-treated insects to *P. akhurstii* TcaB toxin (in lethal and sublethal doses) was significantly reduced as revealed by the mortality data. The present research suggests GmCAD as one of the functional receptors in *P. akhurstii* TcaB-induced toxicity in *G. mellonella* and forms a basis of future research related to the insect gut receptor interactions with *Photorhabdus* toxins.

Development of application technology of *Heterorhabditis indica* and its post-application adaptation under open field and protected cultivation

The delivery system for infective juveniles (IJs) of entomopathogenic nematode, *Heterorhabditis indica* was developed under open-field and protected cultivation for the management of soil-borne insect pests. Compatibility of four types of nozzles, operated at four pressure ranges, using knapsack sprayer revealed that the survival of the IJs lowered with an increase in the operating pressure. With an increase in the operating pressure, there was a corresponding decline in the infectivity of IJs to the larvae of *Galleria mellonella*. Compatibility studies with adjuvants, namely, Tween 20, Tween 80 and Sticker 99, showed minimum mortality of IJs and maximum infectivity of *G. mellonella* larvae with Sticker 99 at all test doses. There was a positive correlation between mortality and negative correlation between infectivity of IJs with incubation time and concentration of adjuvant solutions, respectively. The compatibility of different concentrations (25-200 ppm) of four soluble fertilizers, on the mortality and infectivity, at different days of exposure revealed a lethal effect on IJs at all the tested concentrations and incubation times, except at 25 ppm after one-day of incubation, having a positive correlation between mortality of IJs and incubation time. Maximum infectivity of IJs was recorded in case of Sulphate of potash and urea at all the concentration and incubation times. Foliar spray of *H. indica* @ 5×10^9 IJs/ha was efficacious in inducing significant mortality of 46.79% in *Spodoptera litura* larvae under field conditions, compared to 62.62% mortality achieved using chlorantranilipole @ 10g *a.i.*/ha. No differences in the viability and infectivity of the IJs were recorded when applied through low-pressure drip irrigation system placed 2 m above ground-level. In case of fully automated high-pressure micro-sprinkler irrigation system, no differences were recorded on the viability of the IJs applied at 400 kPa, but *H. indica* infectivity reduced with an increase in the pressure. However, when IJs were applied through fully automated high-pressure drip-irrigation system at 400 kPa, there was 3.71% reduction in viability as compared to 200 kPa pressure. The infectivity of *H. indica* to *G. mellonella* larvae reduced with an increase in pressure as compared to control. Tracking the vertical and horizontal migration of *H. indica* IJs in soil, following their release via drip irrigation system, revealed that after 96 h there was maximum concentration of IJs at 3 inch distance horizontally as compared to 2 and 4 inch distance; while maximum concentration was recorded at 4 inch distance compared to 2 and 3 inch distance vertically, as also evidenced by corresponding increase in mortality of *G. mellonella* larvae at these distances. The migration of IJs was positively correlated with time. The rate of vertical migration was faster compared to horizontal, suggesting positive geotropism. The survival of IJs post-foliar application on soybean and tomato in open field and protected cultivation, respectively was studied. On soybean, the survival was 46.61%, 3.89% and 1.13% after 30, 60 and 90 minutes of spray, respectively, in the morning hours; and 42.89, 13.20 and 4.48% after 30, 60 and 90 min of spray, respectively, in the evening hours. Addition of adjuvant resulted in better survival of IJs. On tomato in protected cultivation, the survival of IJs of *H. indica* was 37.38%, 15.13% and 3.26% at 30, 60, and 90 min post-spray. The overall survival rate of IJs decreased fast and viability remained up to 90 minutes. The results provide critical parameters for scheduling the release of *H. indica* for insect-pest management.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Gagandeep Singh	21316	M.Sc.	Detection of entomopathogenic nematodes by Loop-Mediated Isothermal Amplification	Dr. Vishal S. Somvanshi
2.	Virendra Kumar	21318	M.Sc.	Study the RNAi effect of the sex and larval development genes on root-knot nematode development and multiplication	Dr. Anil Sirohi
3.	Apsara N.	21319	M.Sc.	Evaluation of wild brinjal germplasm against root-knot nematode, *Meloidogyne incognita*	Dr. Bharat Gawade
4.	Basant Deshwal	21320	M.Sc.	Characterization of *Xiphinema*, *Longidorus* and *Paratrichodorus* populations	Dr. M.R. Khan
5.	Veeresh A. M.	21374	M.Sc.	Molecular characterization and expression profiling analysis of Photorhabdus toxin receptor genes from greater wax-moth, *Galleria mellonella*	Dr. T.K. Dutta
6.	Manoranjan Dash	10845	Ph.D.	Molecular dissection of rice-*Meloidogyne graminicola* interactions: effectors and their targets	Dr. Uma Rao
7.	Vikas	10849	Ph.D.	Development of application technology of *Heterorhabditis indica* and its post-application adaptation under open field and protected cultivation	Dr. Sharad Mohan
8.	Amit Ahuja	11297	Ph.D.	Determination of genetic diversity of potato cyst nematodes, *Globodera rostochiensis* and *G. pallida* in India	Dr. Vishal S. Somvanshi

Plant Pathology

7

Prof. V. K. Baranwal

The Division of Plant Pathology focuses research on mycology, fungal pathology, bacteriology and virology. The Division has mandate to conduct basic and applied research leading to detection, identification and management of plant pathogens; serve as a Centre for academic excellence in the area of Post-Graduate education and training in Plant Pathology; to provide national leadership in plant pathological research through the development of new concepts and technologies. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Disease diagnosis and pathogen characterization

Multilocus gene specific characterisation of phytoplasma associated with bamboo species and its natural reservoirs

Phytoplasma-like symptoms of witches' broom, shoot proliferation, little leaf, yellowing, drying and decline of the clumps of eleven bamboo species were recorded from eight bamboo growing states (Bihar, Karnataka, Sikkim, Tamil Nadu, Tripura, Uttar Pradesh, Uttarakhand and Delhi) of India. Utilisation of group-specific primers of multilocus genes like *rp* and *tuf,* enabled further wet-lab validation and identification of *Ca.* P. australasia (16SrII) group of phytoplasmas associated with *D. strictus* samples from Karnataka, New Delhi and Tripura. Association of *Ca.* P. australasia related strains (16SrII-C and 16SrII-D) was also confirmed in seven symptomatic weed species (*Ageratum conyzoides*, *Cannabis sativa*, *Cleome viscosa, Datura stramonium, Parthenium hysterophorus*, *Phyllanthus niruri* and *Tephrosia purpurea*) collected from the vicinity of the bamboo plantations in Karnataka, Delhi, Uttar Pradesh, Uttarakhand and Tripura.

Morpho-molecular characterization of *Ganoderma* spp. collected from Arecanut (*Areca catechu*)

A survey was carried in potential arecanut growing regions of West Bengal and Assam during 2019 and 2020 to characterize and identify the *Ganoderma* species associated with arecanut plant. Twelve isolates in the form of basidiocarp sample were collected and the fungus of interest was isolated from basidiocarp on *Ganoderma* selective medium. ITS sequence based molecular identification was also done for all 12 isolates using ITS 5/1 and ITS 4-primer pairs. Phylogenetic analysis using ITS sequence nucleotide data of different *Ganoderma* species were made and the study revealed that 7 isolates were found to be closer to *G. orbiforme* and 5 isolates were found to be closer to *G. boninense*.

Morphological, pathogenic and genetic variation among *Alternaria brasssicae* isolates infecting Indian mustard and evaluation of its toxins on *Brassica juncea*

Alternaria blight diseased leaf samples were collected from diverse geographical regions (11 different states) of India. Further identification was done by microscopic observation for mycelial and conidial characters and using

DNA markers based on ITS regions. Phenotyping screening of host indicates that out of 36 genotypes screened against Alternaria blight disease, none of them showed resistant or moderately resistant reaction to *Alternaria brassicae*. The genotype Pusa Jai Kisan found less susceptible with minimum average percent disease intensity (PDI) to the five highly virulent isolates of *A. brassicae.*

Identification and molecular characterization of viruses and phytoplasmas associated with carrot

A survey was conducted in carrot fields at Delhi, Hapur and Gorakhpur during 2019-21 and 52 samples of carrot were collected showing different kind of symptoms. Electron microscopic observation showed flexuous filamentous particles (750 x12 nm) and geminate particles (18-20 nm x 35 nm) in samples showing mild mottling and leaf curl symptoms, respectively, collected from IARI field. Samples showing flexuous particles were subjected to DAC- ELISA using polyclonal antibodies of PVY, PVX and carlavirus. Out of 52 samples, only 5 samples reacted serologically positive with polyclonal antibodies to PVY but not with PVX and carlavirus. To further confirm the presence of PVY, total RNA was extracted and RT-PCR assay was performed using potyvirus coat protein (CP) region group specific degenerate primer resulted an amplicon of 750 bp. RT-PCR product was cloned in pGEMT Easy vector and the CP sequence analysis revealed 100% identity with carrot thin leaf virus (CTLV). This is a first report of CTLV, CtoLCV and Ca. P. australasia infecting carrot crops in India.

Characterization, diversity and PCR based diagnostic of bacterial stalk rot of maize caused by *Dickeyazeae* (*Erwinia chrysanthemi* pv. *zeae*)

Bacterial stalk rot (BSR) of maize caused by *Dickeyazeae* is an emerging disease in different agro-climatic regions of India and damaging the crop at a significant level. The results of phenotypic, physiological and biochemical characterization revealed that all the isolates belong to genus Dickeya and it was confirmed by using ADE1 & ADE2 primers based on pel gene. For molecular characterization of four representative isolates (UKMDZ-3, PBMDZ-7, TSMDZ-11 and HPMDZ-16) of the bacterium, 16SrRNA sequence analysis and multilocus sequence assay (MLSA) using five housekeeping genes (recA, gyrB, recN, dnaX and dnaJ) were used for species level identification. The phylogenetic analysis of 16S rRNA gene by using maximum likelihood method also revealed that the selected isolates of pathogenic bacterium found to be closely clustered with showed maximum homology with Mexican strain DZ-E4-2 (99.78–99.93%; accession no. KJ438951) of D. zeae in BLAST analysis. For further determination of species level identity of four Indian BSR isolates, multilocus sequence analysis was performed using five housekeeping genes (recN, gyrB, dnaX, recA, and dnaJ). The concatenated sequences of housekeeping genes from all four pathogenic maize bacterial stalk rot isolates revealed 99.41-99.52 % nucleotide identity with strain *D. zeae* EC1 from China in BLAST analysis, all were clustered with this in phylogenetic analyses and confirmed their identity as D. zeae. Based on the percent disease index data, all 17 isolates of *D. zeae* were grouped into three groups (highly virulent, moderately virulent, and least virulent). The six maize cultivars (Pusa HQPMs improved, Pusa HM4 improved, Vivek-QPM-9, PC4, Syngenta Hybrid 30, and Pioneer Hybrid 3502) were screened using highly virulent group isolates (UKMDZ3, PBMDZ7, TSMDZ10 and HPMDZ16), and Only two cultivars, Pusa HQPMs and Pusa Hm 4, were found to be moderately resistant to D. zeae isolates. The genetic diversity of 17 *D. zeae* isolates as well as three outgroup bacteria (*Erwinia carotovora* subsp. *carotovora, Xanthomonas oryzae* pv. *oryzae*, and *Bacillus subtilis*) was determined using repetitive based PCR (rep-PCR) with the ERIC, BOX, and REP PCR and their fingerprinting data showed diversity among *D. zeae* isolates and it was not affected by agro-climatic conditions based on their clustering to form a group. For detection of *D. zeae* from symptomatic and asymptomatic maize plants, three sets of primers based on recN gene (DRN1F& DRN1R, DRN2F& DRN2R) and DRF1F& DRF1R (fliC) of D. zeae were designed. These primers were standardised and tested for sensitivity and specificity in a PCR assay. Both the primers DRN2F & DRN2R, DRF1F& DRF1R (fliC) were more sensitive to amplify at 198 bp and 230 bp upto 10-7 and 10-8 dilution of 100ng of DNA respectively and they were highly specific to D. zeae.

Theme 2. Pathogenomics

Evaluation of resistance behaviour of Ty-gene containing donor lines of tomato and indexing of naturally occurring begomoviruses infecting them

Seventeen tomato genotypes with different Ty-gene combinations, those are used as parental donor lines for incorporating resistance in tomato breeding programme, along with a susceptible check cv. Pusa Ruby were evaluated for understanding their response against tomato leaf curl disease under field condition. PCR based indexing of begomoviruses in those genotypes were also carried out to understand the status of occurrence of different begomoviruses. Highly resistance response was observed in five genotypes (EC814916, EC2901, EC904111, EC751804, EC904117) containing both Ty-2 and Ty-3 genes. Complete genome of the begomovirus, from this sample and from another sample where only CYVMV infection was detected, was isolated, cloned and sequenced. A detail sequence analysis of the CYVMV infected sample showed that the virus is actually a new species of Begomovirus. The name Tomato leaf curl Ty Pusa virus (ToLCTyPV) was proposed for the new species.

Identification of robust approaches for virome analysis for understanding the seasonal dynamics in virome of grapevines exhibiting leafroll (LR) syndrome

RNA datasets of grapevine and least-virome explored plant species available in public domain were utilized for identification of robust bioinformatic approaches for known/novel viral/viroidal identification and genome reconstruction. Twenty-three viruses and viroids (including two variants of grapevine leafroll associated virus 4) were identified from two tissues (fruit peels and young leaves) of three grapevine cultivars grown in India by *de novo* assembly of reads using RNA assemblers and BLASTn analysis against reference viral genomes (RefSeq), among which nine unique grapevine viruses and viroids were identified for the first time in India. Through *de novo* assembly of transcriptomes followed by mapping against reference/closely related genome, 19 complete/coding-complete genomes of identified viruses and viroids were reconstructed. Next Generation Sequencing (NGS) of ribo-depleted total RNA pool was emplyed to study the seasonal fluctuations in the entire viral population of two grapevine cultivars grown in Pune, India depicting leafroll syndrome using samples collected during September 2019, December 2019 and March 2020. Grape vine leafroll associated virus 3 (GLRaV3) was found to be the predominant in both the cultivars. Besides, eleven grapevine viruses/viroids and two mycoviruses were identified among which grapevine polerovirus 1 (GPV1) was reported for the first time in India. In total, 33 viral/viroidal genomes were recovered across seasons and cultivars. Relative titres of grapevine fleck virus and grapevine virus L were validated in cvs. Fantasy Seedless and ManjariMedika, respectively, through real time PCR assays while GLRaV3 titre was determined in both the cultivars. In general, viral titres including GLRaV3 were lower in December and higher in September and March and this corresponded to the observed symptoms. However, the viroidal titres during December were similar to that of September/March.

Population biology and genetic analysis of blast pathogen, *Magnaporthe grisea* infecting pearl millet

Seventeen pearl millet blast isolates and three non-pearl millet blast isolates (one isolate each from rice, Eleusine indica and finger millet) were used. Pathogenicity tests showed that Delhi region blast isolates were highly virulent in nature. Particularly the isolate PMg_LB2 showed maximum per cent disease severity of 77.8%. Few virulent isolates from other regions also identified. In a host range experiment, the pearl millet and finger millet blast isolates were able to infect both pearl millet and finger millet crop. Cross infectivity exists between pearl millet and finger millet isolates. But they were fail to infect rice crop. In case of matting type distribution, it was observed that except three pearl millet blast isolates viz. PMg_IARI, PMg_LB1 and PMg_LB2 all the rest of the pearl millet blast isolates belong to mating type MAT 1-1, while these three isolates belong to mating type MAT 1-2. Comparative annotation of whole genome of *Magnaporthe grisea* strain PMg_Dl and *Magnaporthe oryzae* strain RMg_Dl led to the identification of five shortlisted Pearl millet blast specific hypothetical virulence loci. Among the five virulence loci identified in pearl millet infecting *Magnaporthe*, four loci such as i. 20007-Mg.00g031250-v1.0.a, ii. 20007-Mg.00g034390-v1.0.a, iii. 20007-Mg.00g080210- v1.0.a, iv. 20007-Mg.00g080580-v1.0.a were found specific to pearl millet *Magnaporthe* by PCR validation.

Theme 3. Disease management

Structural and functional analysis of rice endophytic microbiome for antimicrobial compounds against rice blast caused by *Magnaporthe oryzae*

Leaf endophytic microbiome of rice genotypes namely Pusa Basmati-1 & Pusa Basmati-6 (Both are Aromatic rice); BPT-5204 & HPR-2143 (Both are Non-aromatic rice) planted in three geographical locations were explored, characterized and evaluated against rice blast disease. The geographical locations represented two contrasting agro climatic zones of India such as Palampur, Himachal Pradesh; Almora, Uttarakhand (Both are Mountain zone); and Hazaribagh, Jharkhand (Plateau zone). Polyphasic microbiome analytical tools such as conventional microbiological methods and metagenomic Next Generation Sequencing (mNGS) were used. Microbiological investigation resulted in a total of 283 endophytic bacterial isolates. All bacterial isolates were phenotypically characterized, DNA fingerprinted, species identified and preserved. Most of the bacterial isolates displayed volatile mediated antifungal antagonism against *Magnaporthe oryzae*. The investigation culminated in isolation and identification of rice leaf endophytic microbial communities belonging to fourteen distinct bacterial genera such as *Acidovorax, Acinetobacter, Bacillus, Caballeronia, Chryseobacterium, Curtobacterium, Luteibacter, Massilia, Microbacterium, Pantoea, Pseudacidovorax, Pseudomonas, Xanthomonas, Staphylococcus* for microbiome assisted rice blast disease management.In addition to direct antagonism by secreted or volatile metabolites, the endophytic bacterial communities were found to activate rice innate immunity or Microbe Associated Molecular Pattern triggered immunity (MTI). Transcriptional profiles of key innate immunity marker genes such as OsCEBiP, OsCERK, OsPAD4, OsNPR1.3, OsPDF2.2, and OsFMO1of rice were found altered or up-regulated in bacterized rice seedlings.

Structural and functional analysis of rice phyllospheric bacteria for their antimicrobial properties and defense elicitation against blast disease

The phyllosphere microbiome of rice genotypes namely PRR78 (Susceptible to blast disease) and Pusa1602 (resistant to blast disease) grown at two contrasting geographical locations were further characterized and evaluated against rice blast. The geographical locations represented two contrasting agro-climatic zones of India such as Palampur, Himachal Pradesh (Temperate ‘Mountain zone’) and Port Blair, Andaman Islands (Tropical ‘Island zone’). Phyllomicrobiome analysis was conducted using polyphasic tools such as metagenomic Next Generation Sequencing (mNGS) as well as conventional culture-based microbiological analysis. The classical microbiological analysis resulted in the isolation of 59 distinct bacterial isolates falling into 13 genera and 29 species based on 16S rRNA gene sequence-based identification. Pantoea was identified as the most dominant genus on the rice phyllosphere based on both mNGS and microbiological analysis. Further, blast disease suppression assay under artificial epiphytotic conditions culminated in the identification of 17 bacterial isolates representing genera such as *Pantoea*, *Enterobacter*, *Microbacterium*, *Aureimonas*, *Rhizobium*, *Stenotrophomonas*, *Pseudomonas*, and *Sphingomonas*, which gave more than 50 % disease suppression on blast susceptible variety Pusa Basmati 1. Transcriptional profiles of key innate immunity marker genes such as OsCEBiP, OsCERK1, OsPAD4, OsNPR1, OsEDS1, OsPDF2.2, OsFMO1, and OsPR1.1 in rice were found altered or up regulated in bacterized rice seedlings. OsCEBiP was up-regulated by all tested 17 bacterial isolates.

Genotyping of *Fusarium graminearum* isolates for trichothecene toxins and identification of head scab resistant sources in wheat

Head scab of wheat caused by *Fusarium graminearum* being emerging disease posing major threat to the grain production throughout the world including India. Twenty-seven pure cultures of pathogen were established from the 120 diseased wheat spikes collected from the Wellington (Tamilnadu). Morphological, cultural characterization coupled with molecular characterization with species specific markers were carried out to identify the *Fusarium* species associated with the disease. Twenty-four isolates were tested positive for the genes responsible for the production of DON toxin whereas all 27 isolates showed positive result for genes responsible for 15-ADON toxin. Pathogenic variation among the *F. graminearum* isolates was studied on a set of durum genotypes viz., HI 8591, HI 8708, HI 8713, HI 8737, HI 8765, HI 8774, HI 8777 and HI 8802. The isolates Fg-W20-8 and Fg-W20-18 were found more aggressive as compared to other isolates. Three hundred forty-four wheat genotypes including released cultivars, advance lines and indigenous germplasm were evaluated for resistance against head scab. Out of all the genotypes under evaluation, one genotype DBW 302 and nine indigenous germplasm lines IC 335992, IC079040, IC 266978, IC 585643, IC 585659, IC 35611, IC 145983, IC 138554 and IC 0111868 were found moderately resistant based on percent spikelet infection recorded at 21DAI.

Genotyping, virulence analysis of *Tilletia indica* and identification of Karnal bunt resistant sources

Thirty nine *Tilletia indica* cultures were established from infected wheat grains collected from 33 location of India. Double digest restriction-site associated -DNA genotyping by sequencing was carried out and the generated libraries upon sequencing were with 3,346,759 raw reads in average, and 151x2 nucleotides read length. The obtained bases per read ranged from 87 Mb in Ti 25 to 1708 Mb in Ti 39. Trait association mapping was performed using 41,473 SNPs, infection phenotyping data, population structure and Kinship matrix, to find single nucleotide polymorphisms (SNPs) linked to virulence genes. Whole proteome analysis of *Tilletia* species revealed variable number of extra localized proteins. Carbohydrate active enzymes were prevalent in the secretome of *T. indica*, cutinases and pectinases were highly prevalent, which required for plant cell wall degradation. SCRSPs were present in the secretome which suspected to be effectors. Some conserved pathogenic motifs were assessed and some motif required for appressorium formation, effectors translocation and the one which targets MAPK were highly prevalent. Screening of wheat germplasm for Karnal bunt resistance, showed presence of 31 resistant genotypes, 18 moderate resistant, 22 susceptible genotypes, and 25 highly susceptible genotypes. Using 13 SSR markers linked to resistance ingermplasm screening, none of the used markers was able to distinguish between susceptible and resistant genotypes.

Identification of putative “mild cross protecting strains of Citrus Tristeza Virus (CTV)” for management of severe decline diseases in citrus.

Several citrus samples were collected from seven citrus cultivars belonging to four citrus species viz., *Citrus reticulata* cvs Khasi, Kinnow and Nagpur mandarin; *C. sinensis* cvs Sweet and Valencia orange; *C. limon* cv. Assam lemon; *C. jambhiri* cv. Rough lemon, of three citrus farms of Assam, HRS farm, AAU farm, Guwahati;

CEC farm, Kamrup Rural, and URF, AAU, Jorhat. Based on DAC-ELISA and PCR the overall incidence of CTV was estimated upto 65.7% ranging from 40.9- 85.54% in different farms. In the present study, effort has been made to identify mild cross protecting strain (MCPS) of CTV with the help of *in silico* molecular-based techniques based on codon usage bias (CUB) analysis. The CP gene of 12 CTV isolates from Northeast India and some globally recognized CTV genotypes were taken for the study. The N_C vs GC3 plot analysis indicated that codon choice of CTV is influenced by translational selection, gene length, and gene function along with mutational bias. GC1/ GC2 vs GC3 plot analysis showed unique pattern of higher GC1 and lower GC2 value similar to *Citrus* sp. which indicate that codon biasness of CTV is more dependent on host tRNA pool.

Microbial antagonists in biocontrol of wheat powdery mildew pathogen

A experiment was conducted to evaluate the potential of five different microbial antagonists including two fungal antagonists, viz., *T. harzianum* strain Pusa- 5SD and *A. niger* strain An-27, and three bacterial antagonists, viz., *P. fluorescens* strainDTPF-3, *B. amyloliquefaciens* strain DTBA-11 and *B. subtilis* strain DTBS-5, along with their combinations in bio-protecting wheat against powdery mildew pathogen, and also to determine the induced resistance and plant growth promotion attributes in wheat after Bgt infection under greenhouse conditions. Maximum increase of defence related enzymes (POD, PPO, CAT & Chitinase) and biochemicals (phenolic & soluble protein) activity changes were noticed in plant treated with B. subtilis strain DTBS-5 @ 10 gm/kg seeds and Bgt at 120 hpi followed by *B. amyloliquefaciens* strain DTBA-11 and P. fluorescens strain DTPF-3. Antagonistic combinations of P. fluorescens DTPF-3 + B. subtilis DTBS-5 and P. fluorescens DTPF-3 + *B. amyloliquefaciens* DTBA-11 @ 10 gm/kg seeds were also showed a comparatively moderate increase in induced resistance activity at 120 hpi.

Mechanism of disease resistance in maize during maydis leaf blight infection

The response of certain attributes was studied at biochemical, histopathological and molecular levels that are associated with disease resistance and susceptibility in maize against MLB in two maize genotypes at different time intervals. To identify transcriptional mechanisms conferring non CMS maize resistance, a RNA-seq comparative transcriptome profiling was conducted on a highly resistant maize genotype SC-7-2-1-2-6-1 with unknown molecular basis of resistance was studied against variety CM 119 a standard susceptible check at 48 hr post inoculation (PI, disease period) and their corresponding non infected control. Transcriptional changes were studied 48 hr PI. mRNA sequencing generated total 38.4 Gb data where 9349602 reads were mapped uniquely in SC-7, wherease 2714725 reads were mapped uniquely in CM-119. In resistant inoculated genotype SC-7, total number of differentially expressed genes (DEGs) against control was 1413, in which 1011 genes were up regulated and 402 genes down regulated. In susceptible inoculated genotype CM 119, number of DEGs against control was 2902, where 1703 genes were up regulated and 1199 genes down regulated.

Theme 4. Host pathogen interaction

Deciphering the *Chaetomium globosum* induced defense signaling networks in tomato against early blight (*Alternaria solani*)

The potential induced defense of *Chaetomium globosum* (Cg-2) was evaluated against early blight disease of tomato caused by *Alternaria solani*. The result showed that *C. globosum* induces systemic resistance in tomato plants through enhancement of defense responses of plants thereby reducing the early blight disease severity by 30-38 %. *C. globosum* is also reported to have promising effects on plant growth and development. Temporal transcriptomics was performed for Cg-2 treated plants to gain deep insight into the molecular mechanism of induced defense in tomato plants against early blight. The temporal expression analysis of hormone signaling pathways in tomato plants after Cg-2 treatment revealed the maximum expression of genes at 12 hrs post Cg-2 inoculation. A total of 22473 DEGs were expressed in tomato at 12 hpCi as compared to control plants and among these 922 DEGS had a fold change of -2 to +2 with $p<0.05$. Overall, it is concluded that Cg-2 induces systemic defense in plants which involves both SAR and ISR due to active participation of SA and JA signaling. The plant defense signaling progresses in sequential manner with time course after Cg treatment. The Cg-2 treatment induces systemic defense in plants which get boosted up on counter inoculation with pathogen (*A. solani*).

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Manish R.	21326	M.Sc.	Multilocus gene specific characterisation of phytoplasma associated with bamboo species and its natural reservoirs	Dr. G.P. Rao
2.	Venkata Dinesh Kumar Pasumarthi	21327	M.Sc.	Identification and molecular characterization of viruses and phytoplasmas associated with carrot	Dr. R. P. Pant
3.	Md. Firoz Mondal	21328	M.Sc.	Evaluation of resistance behaviour of Ty-gene containing donor lines of tomato and indexing of naturally occurring begomoviruses infecting them	Dr. Anirban Roy
4.	Bhoopathi N.	21329	M.Sc.	Morpho- molecular characterization of *Ganoderma* spp. collected from Arecanut (*Areca catechu*)	Dr. T.K. Bag
5.	Shaivya Singh	21330	M.Sc.	Identification of putative “mild cross protecting strains of Citrus Tristeza Virus (CTV)” for management of severe decline diseases in Citrus.	Dr. K.K. Biswas
6.	Basavaraj Andaneppa Dodamani	21331	M.Sc.	Morphological, pathogenic and genetic variation among *Alternaria brasssicae* isolates infecting Indian mustard and evaluation of its toxins on *Brassica juncea*	Dr. Lakshman Prasad
7.	Babu B.	21332	M.Sc.	Genotyping of *Fusarium graminearum* isolates for trichothecene toxins and identification of head scab resistant sources in wheat	Dr. M.S. Saharan
8.	Ish Prakash	21333	M.Sc.	Population biology and genetic analysis of blast pathogen, *Magnaporthe grisea* infecting pearl millet	Dr. G. Prakash
9.	Kariyappa Choudaker	21334	M.Sc.	Microbial antagonists in biocontrol of wheat powdery mildew pathogen	Dr. V. K. Singh
10.	Mohamad Ayham Shakouka	21369	M.Sc.	Genotyping, virulence analysis of *Tilletia indica* and identification of Karnal bunt resistant Sources	Dr. Malkhan Singh Gurjar

11.	Mukesh Kumar	10515	Ph.D.	Structural and functional analysis of rice endophytic microbiome for antimicrobial compounds against rice blast caused by *Magnaporthe oryzae*	Dr. A. Kumar
12.	Kuleshwar Prasad Sahu	10651	Ph.D.	Structural and functional analysis of rice phyllospheric bacteria for their antimicrobial properties and defense elicitation against blast disease	Dr. A. Kumar
13.	Shweta Meshram	10866	Ph.D.	Mechanism of disease resistance in maize during maydis leaf blight infection	Dr. Robin Gogoi
14.	Kavi Sidharthan V.	11085	Ph.D.	Identification of robust approaches for virome analysis for understanding the seasonal dynamics in virome of grapevines exhibiting leafroll (LR) syndrome	Dr. V.K. Baranwal
15.	Jagmohan Singh	11307	Ph.D.	Deciphering the *Chaetomium globosum* induced defense signaling networks in tomato against early blight (*Alternaria solani*)	Dr. Rashmi Aggarwal
16.	Rajender Jatoh	11317	Ph.D.	Characterization, diversity and PCR based diagnostic of bacterial stalk rot of maize caused by *Dickeyazeae* (*Erwinia chrysanthemi* pv. *zeae*)	Dr. Dinesh Singh

School of
Natural Resource Management

Discipline	Number of Thesis Submitted	
	M. Sc./M. Tech	Ph.D.
Agricultural Engineering	11	11
Agricultural Physics	05	02
Agronomy	11	04
Environmental Sciences	08	--
Microbiology	07	--
Soil Science and Agricultural Chemistry	12	03
Water Science and Technology	02	-
Total	**56**	**20**

Agricultural Engineering

8

Prof. D. K. Singh

The Division of Agricultural Engineering develops appropriate machinery, implements and soil water conservation systems in Indian agriculture. The Division has the mandate for conducting strategic research on development of technologies / precision equipment in the area of farm machinery and power, precision farming, post-harvest engineering, protected cultivation and renewable energy; post graduate studies in the disciplines of Farm Power and Equipment, Agricultural Structures and Process Engineering and Soil and Water Conservation Engineering; testing of farm machinery; production and supply of prototype for improved agricultural equipment under revolving fund; training of farmers, rural artisans extension workers, technical officers and subject matter specialists on agricultural engineering and technologies. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Resource conservation technologies

Development and performance evaluation of battery-operated groundnut decorticator

A battery-operated groundnut decorticator was developed and its performance was evaluated. An experimental setup was developed to determine mechanical and ergonomic design parameters. The design values obtained from the experiment were incorporated to develop the decorticator. The values were optimized mechanically and ergonomically. Decorticating efficiency was highest at 70 strokes/min and lowest at 50 strokes/min at all clearances and sieve sizes. This indicated that as the speed increases, the decorticating efficiency also increases. At 50 strokes/min, the kernel's breakage percentage was lowest and highest at 70 strokes/min for all clearances and sieve sizes, indicating that the breakage percentage increased with increase in speed. The power consumption was lowest at 50 strokes /min at all clearances and sieve sizes, but the time consumed in decorticating was more. The worker's heart rate was lowest for developed battery-operated groundnut decorticator, whereas it was highest with manual standing type decorticator, which indicates less drudgery with the developed machine. The lowest The cost of operation per kg groundnut pods was lowest with developed battery-operated groundnut decorticator compared to other methods.

Theme 2. Precision farm equipment

Design of smart device for on-field crop cutting energy measurement

A study was undertaken to design and develop a smart device for on-field crop cutting energy measurement. The selection of design values involved study of physical (Internode length, stem diameter and stem wall thickness), engineering properties (shear force, shear energy and shear strength), anatomical properties (cellular components) and chemical composition (cellulose, hemicellulose and lignin) of prominent Indian rice cultivars (PB-1509, PB-

44, Jaya, PB-1121, Swarna and BPT-5204). Variations in cutting force and cutting energy with bevel angle (15^0, 20^0 and 25^0), cutting angle(25^0, 30^0 and 35^0), cutting speed (2.9, 3.44 and 4.1ms-1), stem position (Internode and Node) and stalk size (1, 2 and 3) of rice cultivar PB-1509 was studied by developing a customized sensor based experimental set up. Based on optimum design values, a protype device was developed for crop cutting energy measurement at field level. The results revealed that selected rice cultivars (PB-1509, PB-44, Jaya, PB-1121, Swarna and BPT-5204) varied significantly in their physical, engineering and anatomical characteristics. Shear strength was maximum at upper internodes when compared to lower internode region. The shear cutting force and cutting energy of rice cultivar was closely related with its anatomy. The maximum percentage of stem hollowness (88.21%) was observed rice cultivar BPT-5204 for which cutting energy was minimum. Similarly, the minimum percentage of stem hollowness (70.96%) was observed in rice cultivar PB-44 for which cutting energy was .maximum. Cutting force for single, double and triple stalk rice cultivar were in the range of 0.79-1.10 N, 1.86-2.03 N and 2.74-2.84 N and similarly cutting energy was in the range of 1.96-2.92 N.mm, 9.23-10.95 N.mm and 20.45-22.72 N.mm, respectively. Linear regression model showed best fit correlation between crop cutting force, the blade bevel angle, cutting angle and stalk size (R2=92.78). Similarly, the crop cutting energy showed good correlation with same operational factors (R2= 93.39). Effect of cutting angle on the cutting force and cutting energy was non-significant. The minimum cutting force of 0.48 N was observed at a bevel angle of 15^0, cutting angle of 25^0 and cutting speed of 4.1ms-1, at internode position of single stalk. Hence, for mechanical harvesting of rice, the energy efficient can be attained at a bevel angle of 15^0, cutting angle of 25^0 and cutting speed of 4.1m s^{-1}. The developed smart device consisted of different functional units like compression system, crop holding system, crop cutting system and sensor system for measurement of force, speed and height of cut. Speed measurement and force measurement with less error was achieved with an incremental rotary encoder and 5 kg force sensor. Ultrasonic and Gyroscope sensor MPU 6050 for distance and angle measurement performed better with low drift in output values. The developed device could measure the cutting force, cutting speed, cutting stem height and cutting angle under field conditions with accuracy of 98.88, 97.6, 97.5 and 94.29 %, respectively.

Design of sensor-based control volume sprayer for grape clusters

A cluster specific pesticide and growth regulator application system with improved penetration and minimum off-target losses was developed for saving chemicals and overall cost. Preliminary information was collected through survey in grape growing Marathwada region of Maharashtra. For determination of design values of control volume unit, physical properties (cluster length, width and level of compactness) of grape clusters from seventeen major genotypes selected from vineyard research farm ICAR-IARI, New Delhi, were studied. For design of grape cluster detection unit, two different types of sensors i.e., ultrasonic sensor (HC SR-04) and infrared proximity sensor (B0115NCT4U) were evaluated for their performance using a customized experimental set-up. The performance of selected sensors was evaluated in terms of ability to detect target (grape cluster) and the response time. The design of spraying unit for control volume sprayer involved selection of suitable nozzle and operational parameters. Two hydraulic nozzles (Flat fan and hollow cone type) were evaluated for their performance at three different distances form target (2.5cm, 5cm, 7.5cm) and at five operating pressures (2.5, 3, 3.5, 4, 4.5 kg/cm2) . The parameters evaluated for selected nozzles were spray width, discharge rate, spray cone angle and coefficient of uniformity (CU). The different components of sensor-based control volume sprayer were fabricated based on optimum design values obtained through laboratory experimentation. Control volume unit was fabricated using 3D printing system. The other components like spray tank of 16 litre capacity, battery (12V DC) commonly used in knapsack sprayer were directly procured from the local market, New Delhi.The developed sprayer was evaluated for application of plant growth hormone (Gibberelic acid) and the performance was monitored in terms of droplet size, chemical application per cluster, cluster and berry growth characteristics (size, volume, number of berries per cluster), sprayer application rate, uniformity coefficient and field capacity. The survey data revealed that adoption level of farm machinery for pesticide and plant growth regulator application in grapes is greatly influenced by land holdings. Among marginal landholding (< 1 ha) grape growers majority (75 %) were using back-pack type sprayer while in case of small (1-2 ha) and medium (2-4 ha) land holdings 51.85% and 76% had adopted HTP sprayer and tractor operated sprayer, respectively. It was observed that as the land holding increased, adoption of tractor operated sprayer increased. The data on physical properties of grape clusters revealed maximum cluster length of cluster of 24.00±0.91 cm and maximum cluster width of was 18.80±0.15 cm. The maximum beam angle of ultrasonic sensor was 30º and maximum sensing range was 1000 mm. The ultrasonic sensor had comparatively higher sensing range, beam angle and lower price compared to infrared sensor. The spray uniformity for the hollow cone and flat fan nozzle was in the range of 46.34-73.90 % and 55.40-83.72 %, respectively for the operating pressure range of 2.5-4.5 kg.cm^{-2}. With the use developed sensor-based control volume sprayer there can be 30% saving in chemical use and 35.48% saving in operation time compared to conventional dipping method. The estimated cost of developed prototype was INR 3275, making it a feasible technology option for small and marginal land holding farmers.

Design and development of combine harvester mounted sensor based microbial inoculum spraying system

A speed sensor based microbial inoculum spraying system for combine harvester was designed and developed for simultaneous application of microbial inoculum over rice residue during combine harvesting. Study comprised of determination of the physic chemical properties of microbial inoculum, selection of spray nozzle and development of speed sensor based spraying system. The physico-chemical properties like pH, electrical conductivity (EC) and specific gravity were measured at two dilution ratios (1:0 and 1:10). Settling rate of fungus particles of microbial inoculum in terms of percent settlement of fungus particles was determined at 1:10 dilution ratio. The average value of pH for selected concentrations of microbial inoculum was 3.51 which showed that the microbial inoculum with or without water were acidic in nature. The specific gravity of selected concentrations of microbial inoculum was found within close range as that of water. The electrical conductivity of microbial inoculum increased with increase in concentration and the average value of 0.6 for dilution ratio of 1:10 with water and 4.22 µS/cm for concentration microbial inoculum. Three nozzles (flood, twin orifice flat fan and hallow cone) were evaluated for their microbial inoculum spray distribution performance at three different pressures (1.5, 2.5 and 3.5 kg/cm^2) and three operating heights (40, 50 and 60 cm). A flood nozzle was selected for spraying of microbial inoculum due to its greater spray uniformity, spray width, spray angle and discharge rate. The effect of operating speed and microbial inoculum operating pressure on spray deposition and its effect on rice residue decomposition were analysed. The spray deposition of microbial inoculum spraying in terms of VMD, NMD and droplet density varied between 347 to 243 µm, 87.08 to 75.41 µm and 250.2 to 403.9 droplets/cm^2,respectively. The decomposition of rice residues were quantified by measuring the physical, chemical and biological changes like carbon, total nitrogen, potassium, and phosphorus and microbial growth in terms N-acetyle glucosamine content of rice residue after microbial inoculum application of 10 and 20 days. The variation in different rice residue parameters after 20 days of microbial inoculum was significant as compared without microbial inoculum. Inductive a proximity speed sensor was used to control the microbial inoculum spraying as per the forward speed of combine harvester. For uniform and effective application of microbial inoculum, two flood nozzles were used on spray boom with spray overlapping of 50%. A sensor based microbial inoculum spraying system consisted of storage tank, microcontroller, DC motor driven pump, nozzle buck converter and battery. The accuracy in change of application rate with respect to change in combine harvester speed was observed in the range of 87.9 to 99.5%.

Design and development of semi-automatic pineapple harvester

The pineapple (*Ananas comosus*) is one of the world's most valuable commercial fruits. Among major operations in pineapple cultivation, harvesting of pineapple is laborious and energy-intensive which involves approximately 306 man-hours per acre. Manual harvesting by sickle is always injury prone which reduce the harvesting efficiency due to the fact that the pineapple consists of long-pointed leaves usually needle tipped and generally bearing sharp, up-curved spines on the margins. To facilitate easy and drudgery free harvesting, a portable semi-automatic pineapple harvester was designed and evaluated in NEH regions of India. Study on the variation in physical dimensions and engineering properties of selected cultivars of pineapple i.e., Kew and Queen, was carried out to select design values. Physical dimensions like transverse diameter, vertical diameter, diameter of stalk and weight were determined. Engineering properties of fruit like coefficient of static friction, outer skin displacement due compression force and shear cutting force for stock were determined. The mean vertical, transverse diameter and stalk diameter were found to be 132.89 ±31.14 mm, 102.110 ±11.73 mm and 20.87 ± 4.13 mm respectively. The mean weight was 1.11 ± 0.37 kg. The coefficient of static friction ranged between 0.49-0.58. The maximum displacement of the outer skin of the pineapple due to compression force (70N) was observed as 10.63 mm on Kew cultivar and was 9.19 mm for Queen Cultivar. The peak stock cutting force was in the range of 155.36 – 210.35 N. The maximum cutting energy and force of pineapple stem was obtained as 1243.313 mJ and 168.15375 N, respectively for Queen cultivar and 2037.511 mJ and 190.91 N, respectively for Kew cultivar. A prototype of semi-automatic pineapple harvester consists of grabbing unit with linear actuator, cutting unit (cutting blade and DC motor), handle and battery. The semi-automatic pineapple harvester was powered by a 12V 7Ah lead acid battery and has capacity to harvest 200 number of fruits per hour. The harvesting time of semi-automatic pineapple harvester was 30% higher than the manual harvesting. The harvesting efficiency of the developed harvester was observed to be 25.3% higher compared to manual harvesting. The breakeven point was 11.46 hours/yr with payback period of 0.2 years for the developed harvester.

Modelling of tractor-trailer system vibration for safe haulage

Tractor-trailers are major means of transport in rural India. A study was undertaken to quantify tractor-trailer vibration under selected operating conditions, develop a model for tractor-trailer system vibration, and assess vibration-induced damage during haulage of selected agricultural produce. Vibration magnitude of two types of trailers (single-axle and double-axle), with a 39 hp tractor, were determined under three loading conditions (no-load, full load, and half load), on three terrains (asphalt, farm and village) at three-speeds (on asphalt and village terrain:10, 12, and 14 km/h; and on-farm terrain:4, 5 and 7km/h). The vibration measurements were observed at three positions of the trailer (rear, middle and front) in all three directions, i.e., longitudinal (X-axis), transverse (Y-axis) and vertical (Z-axis). Vibration magnitude was measured using a tri-axial accelerometer, vibration meter and analyzer. Vibration magnitude for asphalt terrain, farm terrain, and village terrain, in longitudinal direction varied from 0.51 m/s^2 to 6.02 m/s^2, 0.34 to 6.31 m/s^2, and 0.92 to 8.95 m/s^2 in the case of single axle trailer, whereas it varied from 0.50 m/s2 to 5.13 m/s2, 0.34 to 3.86 $m/s^2$and 0.70 to 7.62 m/s^2in the case of double-axle tractor-trailers respectively for different loading conditions. In the vertical direction, on asphalt terrain, farm terrain and village terrain vibration magnitude varied from 0.16 m/s2 to 1.76 m/s^2, 0.16 to 4.88 m/s^2 and 0.26 to 4.47 m/s^2 in the case of single axle and 0.10 to 3.01 m/s^2, 0.11 to 4.12 m/s^2, 0.16 to 8.38 m/s^2 in the case of double-axle tractor-trailer, respectively. In the transverse direction, vibration magnitudes were very low compared to the longitudinal and vertical directions. Trailers, terrains, speed, loading, position significantly affected the magnitude of vibration in longitudinal and vertical directions. An eleven degree of freedom model of the tractor-trailer was developed, considering it as a spring-damper mass system. The track elevations in the form of smooth and rough surfaces as defined in ISO-5008 (1979) were used as input, and trailers vibration acceleration was obtained as output. The MATLAB (R2020b) software was used for the simulation. The developed model could predict vibration magnitude in single and double-axle tractor-trailers for smooth and rough surfaces. Finally, a vibration tester was used for the simulated vibration study on tomato, brinjal and cucumber to assess the damage and effect on quality during storage. Two types of packaging materials, namely; plastic crates and corrugated fiberboard boxes at three layers, top, middle and bottom, were used in the study. Maximum damage (%) of 79, 23 and 15% was observed in tomato, brinjal, cucumber in PC(Top), respectively. Maximum Bruised Area (mm^2)/vegetable was observed as 28.75 and 14 mm^2, for tomato and brinjal respectively in PC (Top) and negligible for cucumber. Firmness decreased with time and the lowest firmness of 2.94, 15.69, and 11.28 N was observed in tomato, brinjal and cucumber in plastic crate located at the top. In the case of tomatoes, Total Soluble Solids (TSS) increased with time. Lightness and yellowness decreased with time, whereas redness increased with time. The bottom layers for both packaging materials showed better results compared to the top layers. Overall corrugated fiberboard boxes performed better than plastic crates for all three vegetables.

Modelling of manual chaff cutter for ergonomic design

A study was undertaken to assess the workload in operating manual chaff cutters and develop a suitable mathematical model for assessing the work. The existing chaff cutter operation was carried out in terms of operational, physiological and mechanical parameters. The performance evaluation and physiological study of existing chaff cutter operation revealed that the manually-operated fodder cutter needs to be modified to reduce human power and energy requirement for cutting fodders. The existing fodder cutter was modified by having four different number of blades of the same size i.e., flywheel with a single blade, double blades, three blades and four blades, along with a reduction in throat area by the full throat, 50%, 66% and 75%respectivelyfrom the existing chaff cutter. The mathematical model was developed to predict the work done during the cutting operation. The developed model has a high co-relation (co-efficient of 0.98) between measured and predicted power consumption values for cutting. The average cutting force required in chopping fodder is 111.85N, 58.26N, 64.60 N and 50.53N for single, two, three and four blades, respectively. The average power available in cutting the fodder is maximum for four blades and minimum for three blades, i.e., 184.39 W and 92.03 W. The average power required for single and two blades are 128.20W and 122.96W, respectively. During work performance, the average heart rate of operation was 133bpm,131bpm,127 bpm, and 137 bpm for single, two, three, and four-blade chaff cutters. The heart rate was maximum for four-blade flywheels, i.e., 137 bpm under a “heavy” workload. This is because of the continuous chopping operation in four blades flywheel; the operator rarely gets rest-pause during the operation. Therefore, among four combinations, three blades flywheel have the least heart rate. Therefore, according to the least physiological power consumption, less mechanical power consumption, and desired quality of fodder chopped, three-blade chaff cutters with a 66% reduction in throat size is more ergonomically compatible

Studies on spray characteristics of selected nozzles with bio-pesticides

The chemicals are broadly used all over the world to control pests in agricultural production system despite the harmful consequences involved in the use of chemicals. Bio-pesticides are eco-friendly, affect target pest only, require less amount and biodegradable. A study was conducted for an efficient delivery of bio-pesticides for controlled spray application for different orifice diameters of hollow cone nozzles and operating pressures for getting maximum viability of microbes in the bio-pesticides solution. Two different classes of bio-pesticides viz. bacterial-based Bacillus thuringiensis (BBP solution) and fungal-based Beauveriabassiana (FBP solution) were evaluated for spray discharge by three hollow cone nozzles (1.14, 2.31 and 3.56 mm diameters in size) at four operating pressures (145, 245, 345 and 445 kPa). The spray discharge, spray width, cone angle, uniformity of spray in transverse direction, volume median diameter (VMD), droplet volume fractions at 90% (DV0.9) and 10% (DV0.1) and spans of water-only solution and two bio-pesticide solutions were measured. The viability of bio-pesticide solutions containing *Bacillus thuringiensis* and *Beauveria bassiana* microbial agents were also measured at different operating parameters viz. operating pressures and different sizes of hollow cone nozzles at different pumping periods of 10, 20 and 30 min. The results indicated that there was no significant difference in mean discharge, spray width and cone angle among water, bacterial-based bio-pesticide (BBP) and fungal-based bio-pesticide (FBP) solutions. But, these spray parameters for the selected solutions differed significantly ($p<0.001$) with different sizes of nozzles and operating pressures. There was significant difference ($p<0.001$) in uniformity of spray in transverse direction when bio-pesticide was added to water. The type of spray solutions, nozzle orifice diameter and pressures had significant effect ($p<0.001$) on mean VMD, DV0.1, DV0.9 and span of spray. The means of solutions indicated that the values of droplet spectra were the highest for FBP solution, followed for BBP solution and water-only solution. The viability of the bio-pesticide solutions decreased significantly ($p<0.001$) with increase in operating pressure, decrease in nozzle size and increase in length of pumping period due to stresses developed by spraying components such as pump, valve, delivery line and nozzles. The maximum viability of 6.63×10^{6}cfu/ml and 6.0×10^{6}cfu/ml were observed for BBP solution and FBP solution, respectively without compromising the spray quality at optimized operating parameters of 145 kPa and 3.56 mm diameter nozzle orifice size. The VMD was found in the range from 226 to 232 µm at this optimized condition. Therefore, it may be concluded that the bio-pesticide solutions could be sprayed as foliar spray at minimum possible operating pressure with a large size orifice nozzle to avoid microbial loss of bio-pesticide without losing the spray quality. The findings of the study can provide guidance for spraying bio-pesticides in foliar application through existing spraying system.

Operators' workplace layout of self-propelled combine harvester

A study of the dimensions and locations of controls, as well as the operator seat design on self-propelled combine harvesters was undertaken in order to make the workplace more comfortable and efficient while increasing operators output. The operational frequencies of the various controls, their actuating forces, and locations in the operators' workplace on selected self-propelled combine harvesters were measured. The designs of seats on the selected combines were studied for their match with anthropometric data of Indian users. The hand and leg reach envelopes in the side and plan views were developed considering the anthropometric data of male agricultural workers. The measured control locations on the harvesters were superimposed on the reach envelopes to know whether the controls were within or beyond the reach of the operators. Recommendations for the control dimensions, locations, and their actuating forces were made, considering the Indian operators' capabilities for easy, comfort and safe operation. Optimum seat design was proposed, considering the physical characteristics of the Indian operators for comfortable and safe accommodation. The operational frequencies of the various controls on selected combine harvesters were measured during harvesting of the wheat crop. Based on the frequencies, the controls were categorised into frequently and infrequently operated controls. The frequently operated controls included the steering wheel, header assembly control lever, clutch pedal, brake pedal, gear shift lever, and ground speed control lever with operational frequencies ranging from 89 to 1169 actions/h. The rest of the controls were categorised as infrequently operated and their operational frequencies ranged from 4 to 7 actions/h. The maximum actuating force on the frequently operated hand controls in push and pull modes was observed to be 24 N and 27 N, respectively. The results of the match-mismatch analysis indicated that seats on selected combines are not appropriate for Indian operators and need ergonomic interventions in the seat design to improve the comfort and safety of the operators. Based on pertinent anthropometric measures for seat design of Indian agricultural workers, the recommended dimensions for seat height, seat length, seat pan width, seat backrest height, upper backrest breadth, lower backrest breadth, and steering wheel clearance are 400, 362, 456, 400, 243, 386, and 190 mm, respectively. Based on the reach envelopes, it was recommended that the frequently operated hand controls should be placed at 318–485 mm forward of the SIP and 186-410 mm vertically above the SIP. The controls should not be placed farther than 469 mm laterally to the left and right of the centre line of the SIP. The brake and clutch pedals should be placed at 410–493 mm forward of the SIP, 261-396 mm vertically below the SIP and 90–215 mm lateral to the SIP. The recommended design of workplace based on Indian anthropometric dimensions may provide better accessibility, easy reach and comfortable operation of controls by Indian operators.

Design and development of tractor drawn automatic vegetable transplanter for pot seedlings

An automatic tractor drawn automatic vegetable transplanter for pot seedlings using auger conveyor type metering mechanism was designed and developed. A wooden tool was developed to make cylindrical shape paper-pots using newspaper material. Experiment was conducted to identify the best combination of pot mix and pot size for raising good quality seedlings of tomato, brinjal and chilli. The 75 cm^3 pot volume with farmyard manure blended with soil and sand in the proportion of 65:17.5:17.5 by volume was found to be the best combination. Considering the properties of pot seedlings, an auger conveyor type metering mechanism was developed and evaluated in the soil bin to optimize its operational parameters. The performance of auger conveyor type metering mechanism was found optimal at a forward speed ranging from 1.6 to 2.0 km/h. The overall efficiency, deviation of seedling spacing and tilted planting were found as 93.28%, ±3.7 cm and 5% at operating speed of 2.0 km/h. Shovel type furrow opener with disc type furrow closure mounted at 15° closure angle, operated at 2.0 km/h speed and 60 mm depth was found as the best combination of furrow opener and furrow closure. This combination was used for the development of tractor-drawn 3-row automatic vegetable transplanter using auger conveyor type metering mechanism and evaluated under actual field conditions. The actual field capacity, field efficiency, deviation of seedlings spacing and planting rate of the developed transplanter were 0.125 ha/h, 46.4%, ±3.6 cm and 56 seedlings/min/row, respectively at 2 km/h forward speed. Missed planting and tilted planting were observed as 4.8±1% and 5.3±1%, respectively. The overall planting efficiency was found 90.1%. The use of auger conveyor type automatic vegetable transplanter saves 95%, 80% and 60% of labour; 93%, 80% and 20% of operating time over transplanting by manual method, hand-held transplanter and semi-automatic transplanter, respectively. The cost of the transplanter was ₹36,000/- and operating cost was ₹1250/h. The benefit-cost ratio, payback period, break-even point and net present worth were 2.18, 0.61 year (*i.e.* 183 hours), 90.1 h/year and ₹1,89,220/-, respectively.

Theme 3. Climate change impacts and integrated water resource management

Climate change impacts on crop water footprint of Trans Indo-Gangetic Plain

The crop water footprint (CWF) concept is relatively new indicator to analyze water resource usage throughout agricultural production processes. A study was undertaken for assessing CWF and analyzing the impacts of climate change on the CWF for suggesting suitable adaptation and mitigation measures for reducing CWF in the Haryana state which lies in the North-West region of Indo-Gangetic plain. It is an agriculturally dominant state. Water scarcity and decreasing fresh water availability is a major concern in the state. The study included the estimation of crop water use (ETc), estimation of green crop water use (CWUgreen) and blue crop water use (CWUblue), estimation of virtual water content (VWC), assessment of CWF of 11 major crops cultivated in Haryana and assessment of impact of climate change on CWF. The FAO CROPWAT 8.0 model was used to estimate CWU at district level. The impact of climate change was assessed for generated climate change scenarios of temperature and rainfall for the period 2030s (2020-2049), 2050s (2040-2069) and 2080s (2070-2099) for RCP 2.6, RCP 4.5, RCP 6.0 and RCP 8.5. The findings revealed that crop water use (ETc) varied significantly within the AESRs and all over the state. Hence district boundary was considered for estimating ETc, CWUgreen, CWUblue, and CWF. Among all the crops, VWC of cotton crop was highest (21766 m3/t) followed by sorghum (10059 m3/t), black gram (6534 m3/t) and sugarcane (3285 m3/t). The VWC for Potato, barley and wheat were VWC of 264 m3/t, 1298 m3/t and 1420 m3/t, respectively. Potato being short duration rabi crop had lowest blue VWC of 129 m3/t followed by wheat of 524 m3/t. Wheat had highest CWF of 14373 Mm3 in the state followed by rice (10916 Mm3) and cotton (5656 Mm3). The blue CWF accounted for 51.7 % of the total CWF of the state with 29.2 % share of grey CWF and 19 % of green CWF. The total crop water footprint of Haryana state for the cropping year 2014-15 was 38023.6 million m3. Sirsa district had highest CWF of ~4539 Mm3 which was followed by Hisar (~3599 Mm3), Jind (~3500 Mm3), Bhiwani (~3055 Mm3), Fatehabad (~2623 Mm3), Kaithal (~2520 Mm3) and Karnal (~2508 Mm3). Panchkula district had the lowest CWF of ~265 Mm^3. The crop water footprint for the districts Mewat, Rewari, Palwal, Panipat, Mahendergarh, Ambala, Jhajjar, Rohtak, Kaithal, Kurukshetra and Sonipat ranged between ~744 to ~1808 Mm3. The CWF was lower for Faridabad and Gurgaon of 307 Mm3 and 503 Mm3. The VWC of barley, black gram, cotton, maize, mustard, potato, rice, sorghum, sugarcane and wheat would increase by (20 to 42 %), (18 to 39 %), (8 to 37 %), (47 to 76 %), (24 to 66 %), (18 to 36 %), (20 to 40 %), (9 to 31 %), (23 to 19 %) and (39 to 70 %), respectively during 2030s to 2080s under various RCPs. The CWF of barley, black gram, cotton, maize, mustard, potato, rice, sorghum, sugarcane and wheat would increase by (15 to 26 %), (12 to 18 %), (7 to 12 %), (21 to 28 %), (17 to 28 %), (22 to 30 %), (4 to 8.5 %), (6 to 11 %), (4 to 10.5 %) and (17 to 25 %); respectively during 2030s to 2080s under the four RCPs. The VWC and CWF for pearl millet would decrease by -1.4 to -11.5 % and -10 to -35 %; respectively during 2030s to 2080s under all RCPs. Advancing sowing date by 10 to 15 days from the present sowing date can reduce the VWC and CWF of Wheat under all RCPs. Improved variety of rice and wheat with enhanced use of fertilizer would also reduce the VWC and CWF under all RCPs.

Modelling impact of water management technologies on groundwater for sustainable utilization

A study was carried out to evaluate impacts of water management technologies on water saving and irrigation efficiencies, to model impacts of water management technologies on groundwater fluctuation and to develop strategies for sustainable utilization of groundwater resources in Muzaffarnagar district of Uttar Pradesh. Evaluation of impacts of different water management technologies on water saving and irrigation efficiency included determination of water requirement, seepage loss, water conveyance and application efficiencies. Crop water requirement was estimated using CROPWAT model. The average irrigation efficiencies of open channel and pipe network system were 65 % and 79 %; respectively. Impact of drip irrigation system and laser land levelling on groundwater behaviour was evaluated using groundwater model. Groundwater model MODFLOW was calibrated and validated to predict the water table fluctuations in terms of rise/fall in water table under various scenarios. Total 8 scenarios consisting open channel with application efficiency of 60 %, 6 % water saving due to seepage in open channel, water saving due to 65 % efficiency, water saving due to laser land leveller (17 % of water saving), water saving due to pipe network system with 79 % efficiency, water saving due to drip irrigation system with 90% application efficiency and water saving due change the cropping pattern (reducing the sugarcane area by 50 % and increase in the kharif maize by 50 %; reducing the sugarcane area by 50 % and increasing in the kharif maize by 25 % and pulses by 25%) were considered for simulation. In order to compare the predicted water table elevations within the various scenarios, the water table elevations of pre monsoon season of 2015 were considered as reference. Water savings were estimated with reference to the irrigation efficiency of 60 %. The rise/fall in water table at the end of simulation varied from -9.47 to 9.44 m under scenarios 1-8 in comparison to pre monsoon water level of 2015. Simulation results revealed that the groundwater levels for the year 2030 under scenarios 1-8 will be forecasted as 213.84, 215.96, 217.20, 221.67, 225.39, 229.37, 232.05 and 232.75 m respectively. The simulated groundwater decline during 2016-2030 would be 0.57 m/yr under irrigation by earthen channel with irrigation efficiency of 60 %. When water saving of 6% in open channel was considered the rate of decline reduced to 0.46 m/yr. For water saving with the average efficiency 65 %, the rate of decline reduced further to 0.39 m/yr. Average water table fall was 0.15 m/yr, when water saving of 17 % due to laser leveling was considered for simulation. For pipe network with 79 % efficiency, the rate of rise would be 0.05 m/yr. If drip irrigation is adopted in sugarcane with efficiency of 90 %, water table during the simulation period (2016-2030) would rise at the rate of 0.27 m/yr. Water table would rise by 0.41 m/yr if 50 % area under sugarcane is replaced with maize or maize and pulse. Pre monsoon water table would increase by 7.83 m under scenario 4 compared to the baseline scenario. Under scenario 5 groundwater elevations in the pre-monsoon period would increase by 11.55 m compared to the baseline scenario if open channel is replaced by pipe network system with 79 % efficiency. Groundwater elevations in the pre-monsoon period (hydraulic heads) under scenario 6 would be higher than the reference scenario by 15.53 m if entire area of sugarcane is brought under drip irrigation system. Pre-monsoon water table would increase by 18.21 and 18.91 m in scenario 7 and 8; respectively if 50 % area under the sugarcane area is replaced with the kharif maize or 50 % area under sugarcane is replaced with 25 % kharif maize and 25 % pulses. Sugarcane based farming system under prevailing water management practices in the study area is not sustainable. Though there was a positive effect of different water management technologies on groundwater level under all scenarios, the first four scenarios (Open channel with application efficiency of 60 %, water saving due to seepage in open channel (6 % water saving), water saving due to 65 % efficiency, water saving due to laser land leveller (17 % of water saving) would not be able to arrest the declining trend of water table whereas the pipe network system is partially suitable to arrest the water table decline. Drip irrigation system and change in cropping pattern has net positive effect on groundwater behaviour.

Performance evaluation of surface and groundwater irrigation for enhancing water productivity

Poor performance of irrigation projects in terms of irrigation efficiency and water productivity is a major concern. Increasing gap between potential created and utilized reflects the poor management and utilization of created infrastructure. This study was conducted at farmers' fields in Jakhania Gobind, Alipur Madra, Mustfabad and Khetabpur villages of Jakhnian block in Ghazipur district of the Uttar Pradesh to determine on-farm irrigation efficiencies at farmers' fields, to assess the performance of surface and groundwater irrigation in terms of water productivity, and to suggest measures to improve crop water productivity. The field conveyance efficiency, field application efficiency, crop water and irrigation water use efficiencies were determined for the selected farmers' fields for paddy and wheat crops. The CROPWAT 8.0 model was used to estimate evapotranspiration, effective rainfall and crop water requirement. The field capacity of the soils in the study area varied from 17.0 to 22.5 per cent. Pre-irrigation moisture content varied from 10.3 to 19.5 per cent whereas the post irrigation moisture content varied from 22.8 per cent to 29.5 per cent. The total volume of water applied to the field was 4309.6, 3218.1, 3361.2 and 3165.5 m3/ha in canal, diesel, electric and hired tubewell; respectively and the yield in selected villages varied from 3781.3 to 4383.3 kg/ha for the paddy and 3218.8 to 4375.0 kg/ha for the wheat. The conveyance loss in channels varied from 1.92-3.37, 1.62-2.86, and 0.63-1.07 l/s/100 m in earthen, lined, and pipe channels; respectively. The average application efficiency of the canal, diesel- tubewell (TD), electric-tubewell (TE), and hired-tubewell (TH) were be 53.4%, 72.7%, 65.92%, and 76.68%; respectively for paddy. The average application efficiency of the canal, diesel-tubewell (TD), electric-tubewell (TE), and hired-tubewell (TH) were 55.5%, 72.7%, 67.8%, and 78.0%; respectively for wheat. The average value of CWUE, IWUE and WP were 0.58, 0.83 and 0.43 kg/m3; respectively for canal irrigation. For diesel operated pumps CWUE, IWUE and WP were 0.58, 0.97, 0.49; respectively and for electric tubewell, these were 0.6, 1.0, 0.5 kg/m3; respectively for paddy. The average value of CWUE, IWUE and WP were 1.41, 0.90 and 0.83 kg/m3 in canal irrigation. The average value of CWUE, IWUE and WP for diesel operated pumps were 1.5, 1.2 and 1.1 kg/m3 and for electric tubewell, 1.6, 1.2 and 1.2 kg/m3; respectively for wheat. There was significant difference in application efficiency between canal and groundwater irrigation at 1% level of significance for both crop paddy and wheat. The water productivity was significantly different for canal and groundwater irrigation at 1% level of significance for both crops. The water productivity was insignificant within diesel operated and electric operated pumps. Various strategies for efficient use of canal and groundwater were suggested for enhancing the overall performance.

Study on groundwater problems in coastal Visakhapatnam

A study was undertaken in the coastal part of Visakhapatnam district to evaluate the groundwater level trend, predict the future trend in the coastal area of Visakhapatnam, and delineate the areas facing the problems of water quantity and quality for suggesting ameliorative measures. Time series data on groundwater levels and quality were analysed using Mann-Kendall- Sen's estimator tool and exponential smoothing method (ESM) to detect trend, and predict the future trend. The isobath and iso-salinity maps were prepared using spatial analyses software. The Piper diagram, Gibb's diagram and Stiff plots were developed to represent the major ionic compositions. To ascertain suitability of water for drinking Water Quality Index (WQI) indicators were determined. Similarly, irrigation suitability criteria were ascertained using USSL diagram. The water quality change maps were subject to probability analyses for their probable migration fromone quality class to another class. Mann-Kendall and Sen's slope trend analysis for over 40 wells both in confined and unconfined aquifer could yield significant trend in 23 and 14 observation wells during pre- and post-monsoon seasons; respectively whereas the significant trend holder in piezometric wells were 12 and 09; respectively for pre- and post- monsoon seasons. Water level in observation wells had registered a monotonic change from -0.541 to 0.395 m/yr and -0.385 to 0.239 m/yr in pre- and post-monsoon respectively. Similarly, in the confined aquifer, the piezometric level registered a change from -0.341 to 0.870 m/yr and -0.401 to 1.148 m/yr in pre- and post-monsoon respectively. Short-term future (2030) trend analysis suggests an alarming pre-monsoon water table decline as high as 11 m (Bhimunipatnma) to 8.2 m (NGR Puram) and post-monsoon decline from 7.9 m (Bhimunipatnma) to 8.7 m (Yelamancili). The future trend in piezometric level decline in confined aquifers also was alarming with maximum is expected to be about 22.15 m (Atchutapuram). The source of salinity has been observed to be from either inland source that might have geogenic origin whereas coastal salinity has been found to be from sea water ingression. Site-specific analysis using Terrset revealed that Nakkapalli, Namavaram, S. Rayavaram, Visakhapatnam and Bhimunipatnam in the unconfined aquifer, and Nakkapalli, Yelamanchili, Atchutapuram, and Chukkavanipalem in the confined aquifer have high salinity due to the intrusion of sea water or mixing of connate water into the fresh-water aquifer. Inoda, Saripalli, Rambilli, Dibbidi, Narsipatnam in the unconfined aquifer and Munagapaka, Kasimkota, Aripaka, and Kothakota in the confined aquifer have inland salinity that may be due to secondary salinity from the higher water table conditions, irrigated and anthropogenic activities.Groundwater salinity, which was moderate to unsafe in 2008, had increasedby 76.92% in 2018. The WQI indicators from the perspectives of drinking suggested that, about 39% and 51.2% of the samples were under poor and very poor water quality; respectively in unconfined aquifer. In confined aquifer, 35%, 45% of area was under poor and very poor condition; respectively. Unconfined aquifer depicts that 72.5 % and 80% of samples fall under C3S1 to C3S2 category in both seasons which indicates high salinity and low to medium alkalinity, 15% wells fall under C4S2 category which indicates the occurrence of very high salinity and medium alkalinity in groundwater of the region. Whereas, in confined aquifer most of the samples (51%) fall under C3S1 to C3S2 category in both pre- and post- monsoon which indicates high salinity and low to medium alkalinity, 2 wells fall under C4S2 category in both monsoons indicating very high salinity and medium alkalinity. Water sample belonging to Nakkapalli falls under C4S3 category which falls under very high salinity and high alkalinity. However, a forecast trend suggests a reduction in salinity from a base line period of 2018 for pre- and post-monsoon season in most of the areas alike. In unconfined aquifer, it is evident that Na^+, Cl^- are the dominant hydrochemical facies in all the monsoons and Na-Cl dominance has been increased about 58.3% from post-2008 to post-2018 in the study area. In confined aquifer the occurrences of Ca^{2+}–Mg^{2+}–$Cl^−$ type suggests that Na^+–$Cl^−$ mix with fresh groundwater (Ca^{2+}–Mg^{2+}−$HCO_3^−$) is causing salinization of the groundwater. Saline water has increased about 50% from 2008 to 2018. Evaporation and rock weathering are the major geochemical processes controlling the chemistry of groundwater in the region. Based on the above indicators of water quality and water table variability in a spatial frame work, ameliorative measures that include increased groundwater recharge, relocation of pumping wells, and control of seawater intrusion through an extraction barrier and combination

Assessment and planning for enhancing water productivity in Eastern Marathwada

A study was conducted in Nanded district which one of the most drought prone districts in Marathwada region of Maharashtra for developing strategic water management solutions using Water Resource Planning and Management (WEAP) model-based analysis. Water demands, such as agricultural, livestock and domestic, were calculated using appropriate tools and techniques. The crop water demand was estimated using metrological, edaphic, and standard crop details by employing the FAO CROPWAT 8.0 model. The demographic pattern and growth rate were used to estimate domestic water demand based on the WHO municipal standards. Water demand for growing cattle was estimated using appropriate methodology. Rainfall analysis and stream flow constituted the supply side. Monthly utilizable water resources available for the Nanded district of Maharashtra and the total monthly water demands were considered for water balancing. The monthly time series data of the streamflow of the Godavari River recorded at the Vishnupuri gauging station was considered for water balance analysis. However, after leaving the environmental flows, only the district's legitimate and rightful share of the total streamflow; based on the area ratio of Nanded over the entire Godavari River basin; has been considered as the net utilizable water resources instead of the total stream flow of Godavari at the Vishnupuri gauging site because that would be unrealistic, impractical and technically not feasible. A good agreement between observed and predicted stream flow based on RMSE, NSE, NNSE, Kendell's Coefficient of Concordance (W) and Mean Absolute Percentage Error (MAPE) could be achieved while calibration and validation of WEAP model. Therefore, the WEAP model could be applied successfully to the hydrologic water balance of the Nanded district in the Godavari River basin. The average reference evapotranspiration (ETo), effective rainfall (Peff) and net crop irrigation requirements (NIR) ranged from 2.44 to 4.56 mm/day, 5.5 to 152.4mm, and 3.9 to 367.6 mm/year, respectively. The current annual GIR for major field crops in the Nanded district of Maharashtra using a project irrigation efficiency of 35 %, were found to be 27057.3 and 69526 (m^3/ha/year), corresponding to 2705.73 and 6952.6 mm/year, respectively. The total annual irrigation water requirement for the Nanded district of Maharashtra was 689.01 Mm^3. The Monthly net and gross irrigation requirements (MNIR and MGIR) for major crops grown in the Nanded district; varied from 49.3 to 1093 mm/year and 140.9 to 3122.9 mm/year; respectively. The main outputs of the model were unmet demands (UD) for districts. The annual water demand (WD), supply delivered (SD), unmet demand (UD) and stream flow (Qs) in the current account year were 3184809.0 Mm^3, 12065.3 Mm^3, 22755.302 Mm^3, and 265.3 Mm^3, respectively forNanded district, while in the reference scenario these were estimated to be 3311145.54 Mm^3, 14334.7 Mm^3, 12636.06 Mm3 and 14670.31 Mm^3, respectively. The total UD in the reference scenario was found to be 2621850 Mm^3, while the total SD was 562958 Mm^3 for Nanded district of Maharashtra. Available water resources in the Nanded district were not able to satisfy water demands in the current development scenario. The total available streamflow during the reference period was estimated to be 24103.77 Mm^3, while the total WD was estimated to be 3184809 Mm^3. The projected annual WD, SD, UD and Qs for the current year were 1211.57 Mm^3, 265.3 Mm^3, 946.57 Mm^3, and 265.3 Mm^3; respectively, while in the year 2050 these are projected to reach 2673801.6 Mm3, 15745.5 Mm^3, 2658056.1 Mm^3, 15745.43 Mm^3; respectively. The result revealed that demand far exceeds the supply; hence, prudent water management strategies have to be adopted for abridging the supply-demand gap.

Theme 4. Precision irrigation

Conditional controller based fertigation system for water and nutrient management in soil-less cultivation

Soil-less cultivation inside the protected structure is one of the promising technologies to increase the water and nutrient use efficiency. It enables round the year production of high value horticultural crops inside protected structures. Prototype of weight sensing system was developed to continuously monitor weight loss from soilless grow bag based plants due to transpiration. Weight based fertigation scheduling strategies were optimized for higher cucumber and capsicum production in soilless cocopeat grow bag inside greenhouse. Experiments were conducted on cucumber using treatments comprised of T1, where the weight loss of growing media having plants by transpiration was fully replenished by nutrient solution; T2 and T3, which received 10% and 20% less amount of nutrient solution, respectively as compared to T1 treatment; T4, where 20% more amount of nutrient solution applied compared to T1 treatment. Further experiments were conducted during second trial on cucumber and capsicum with developed weight sensing system to establish an appropriate fertigation strategy without drainage. The treatments comprised of T1, where the weight loss of growing media having plants due to transpiration, was fully replenished by nutrient solution; T2, T3 and T4, which received 10, 20 and 30% less amount of nutrient solution, respectively as compared to T1 treatment. Based on above experiments, it was concluded that fertigation strategy corresponding to 100% nutrient solution against the weight loss (T1) gave maximum yield and water use efficiency (WUE) for both cucumber and capsicum plants. The developed conditional controller consisted of a programmable microcontroller-based circuit which was integrated with inputs (i.e. sensors, keypad) and outputs (i.e. pumps, solenoid valve, LCD display) components to ensure automation in soilless fertigation system. Sensors, including load cell, flow sensors, pH sensor and float level sensor were calibrated and provided measurements within accepted values. Developed indigenous automated fertigation controller system was found capable to detect the water loss which was helpful for automatic fertigation scheduling and to prepare the fertigation solution in real time. User interface was designed and developed to provide the modified and calibrated input data to the microcontroller and also modified the mode of irrigation and different user defined condition. The developed system allowed both sensor and timer based control. The designed and developed indigenous conditional controller was successfully tested with cucumber and capsicum crops grown on cocopeat grow bag under greenhouse at Centre for Protected Cultivation Technology, ICAR-IARI, New Delhi, India.

IoT based aeroponics monitoring and alert system

Aeroponics is an emerging technology for protected agriculture. Yield of the crop in aeroponics cultivation is dependent upon nutrient supply to plants and spraying duration. Manual monitoring of the different parameters in aeroponics is difficult, laborious and costly. Therefore, it is essential to develop automated IoT based real time monitoring system for successful and profitable aeroponics cultivation. Continuous monitoring of the system parameters and simultaneously an alert system which give alert to user smartphone needs to be incorporated in the developed IOT based aeroponic system. This included design, development and evaluation of the IoT based monitoring and alert system for aeroponics. Monitoring system was designed and developed for monitoring and alert system. Twenty five lettuce plants were grown on normal and automated IoT controlled aeroponic system. ESP-32 microcontroller based monitoring system equipped with EC sensor, pH sensor, temperature sensor, ultrasonic sensor, DHT sensor was designed and developed taking into account the desired range of values of EC (1.6-2.0 dS/m) and pH (5.5 -6.5) of nutrient solution required for lettuce plant fertigation. System parameters like EC, pH, temperature and level of nutrient solution, humidity and temperature of air inside the greenhouse were monitored. Real time data of the parameters could be monitored on the user smart phone and computer in graphical form using Thingspeak platform via internet. Alert system was integrated with monitoring system using IFTTT software platform which gives alert notification to the user smart phone when any of the parameters was not in the desired range. The performance of the IoT based system was evaluated by measuring growth parameters of lettuce like plant height, no of leaves, plant fresh weight, head diameter, root length, root volume, root shoot ratio and dry matter content. Paired sample t-test statistics revealed that there was significant effect of IoT based monitoring and control on plant fresh weight, head diameter, root-shoot ratio and dry matter content with the recorded values of 351.34 and 288.61gm, 15.66 and 13.40 cm, 0.17 and 0.23, 7.29 and 6.01%, respectively for IoT based aeroponics system and normal indigenous aeroponics system. Crop water use efficiency was 64.42 and 89.65 gm/litre in normal indigenous aeroponics system and developed IoT based aeroponics system, respectively. In addition 12.5% water and nutrients were saved for lettuce in the developed IoT based aeroponics system.

Theme 5. Solar powered farm equipment and storage structures

Design of control system for improving cooling efficiency of solar refrigerated evaporatively cooled (SREC) structure for safe storage of vegetables

A control system was designed to improve the cooling efficiency of refrigerated evaporatively cooled (SREC) structure for safe storage of vegetables. The SREC structure operated on off-grid and hybrid types of inverters with oil thermistor resistance of 45 and 39.4 kΩ and air thermistor resistance of 21, 18.91, and 16.94 kΩ. The control system helped lower temperature of SREC structure from 16 °C to 4°C improving cooling efficiency of the refrigeration system by 1.61 times. The highest cooling efficiency improvement of 2.29 times was found in the off-grid/hybrid inverter with coil and air thermistor resistances of 39.4 kΩ and 21 kΩ, respectively. The leafy vegetables were stored when the SREC structure was operated at the highest cooling efficiency. The Physiological weight loss in spinach varied from 0 to 22.80% and for lettuce, it varied from 0 to 20.52% during 14 days of storage. The leafy vegetables can be stored for up to 14 days and the control system with an off-grid inverter refrigeration system is very helpful for establishing cold storage at remote locations. The control system has proven to be very useful in enhancing the cooling performance of the SREC structure and increasing the storage life of agricultural produce.

Study of solar refrigerated and evaporative cooled (SREC) structure for storage of perishable agricultural commodities

Solar refrigerated and evaporative cooled (SREC) structure was evaluated for storage of perishable agricultural commodities. The SREC maintained considerably lower temperature and higher RH. The leafy vegetables stored in the SREC and REF remained marketable for an additional 3–5 days in comparison to the leafy vegetables stored at ambient room conditions. The quality parameters of tomatoes were well preserved in SREC structure up to 32nd day as compared to 20th and 10th day in EC and UL (ambient) storage condition respectively. The apparent energy of activation (Ea) for rCO2 was found to be 55.8 kJ mol^{-1}. This is the first report of an apparent Ea for amaranth respiration. The values frequency factor A for amaranth from the fitted line was 2.16x10^6 g kg^{-1} h^{-1}. The coefficient of determination (r^2) value was 0.9. The cumulative respiration for amaranth rose most rapidly in UL, followed by EC, then SREC and was lowest in REF.

Design and development of hempcrete and hempfabric evaporatively cooled storage structure for perishables

Hempcrete and hempfabric evaporatively cooled storage structure was designed and developed for storing perishables. Tomato and spinach were stored in Hemp evaporatively cooled storage (HECS) and Aramid evaporatively cooled storage (AECS) for 6 days. The inside temperature varied from 15 - 26 °C in HECS and 17 - 28 °C in AECS structure. The maximum ambient temperature was 38 – 40 °C.The temperature difference obtained in ambient and EC structures was 15 to 18 ^{o}C when ambient temperature was at its peak (40^{o}C).The EC structures are beneficial for short term storage of 5-6 days of agriculture produce and its eco-friendly and easy design makes it possible to be constructed on farms. It doesn't require any energy to operate. Only utility required is continuous water flow to keep the fabric wet.

Theme 6. Post harvest technologies for preservation and storage

Development of LED based photodynamic inactivation system for surface decontamination of carrot

Root vegetable carrot (*Daucuscarota L.*) is one of the significant salad items for any cuisine across the globe. It is claimed to be the perfect health food due to presence of α and β carotene, fibre, potassium, and antioxidants, but being a root crop it is more prone to contamination. The present study was undertaken to see the effect of wavelength, irradiance, flickering frequency and treatment time on carrot surface and develop a photodynamic inactivation system. The carrots were treated at wavelength of 390 (16, 25 and 42 W/m^2) and 420 nm (7, 12 and 22 W/m^2) for 10, 20 and 30 min. It was observed that wavelength of 390 nm was more effective for microbial inactivation compared to 420 nm. The effect of irradiance and time at both wavelengths was found significant for bacterial and fungal reduction, moisture loss and decrease in firmness, while for colour and TSS change it was non-significant. At 390 nm, optimized irradiance and treatment time of 25 W/m^2 and 30 min, respectively, resulted in approximately 1.49 and 1.28 log reductions of bacteria and fungi, respectively with a desirability of 0.83. At optimised parameters, the values of firmness and moisture loss, colour change and TSS increase were 18.39 N, 0.78 % w.b., 2.72 and 0.34 °Brix, respectively. The selected parameters were 25 W/m^2 at 390 nm and the frequency varied from 500 Hz to 10 kHz and continuous. The treatment time varied from 20 to 30 min. Maximum bacteria and fungus inactivation with minimal change in quality parameters and moisture content was achieved with a frequency and treatment time of 500 Hz and 30 min, respectively, and a desirability of 0.74. Bacterial and fungal reduction at this frequency and 2treatment time was 1.67 and 1.39 $\log_{10}$ CFU/g. The values for firmness and moisture loss, colour change, and TSS increase were 12.44 N, 1.07 % (w.b.), 3.95, and 0.37 °Brix, respectively. The LED based PDI system was developed using selected wavelength (390 nm), irradiance (25 W/m^2) and frequency (500 Hz). In this system 10 carrots can be surface-decontaminated at a time and have a capacity of 3 kg/h (approx.). The carrots were decontaminated for 30 min and kept for 15 days storage period at refrigeration condition. This system decontaminated carrots from both sides and reduced aerobic plate count, gram-negative bacteria, coliforms, and fungus by 2.49, 1.53, 1.2 and 1.91 $\log_{10}$ CFU/g, respectively. The change in quality parameters with treatment and storage was insignificant, while the bioactive compounds increased dramatically with storage. The LED-treated carrots had a non-significant rise in microbial load after 5 days of storage, while quality was preserved. There was a significant increase in microbial load after 5 days, but it was less than in untreated samples. The developed LED based PDI system can be used in restaurants before serving salad and for final decontamination before packaging in any minimal processing unit. It can be also be used for surface decontamination of other products with minor modification in tray design according to product.

Digital image processing based system for real-time monitoring of potato slices in hot air dryer

A laboratory scale sensor enabled dryer was developed with controls and air distribution systems to ensure uniform distribution of temperature and air flow throughout the chamber. Experiments were conducted on drying of potato slices. Drying was monitored on real-time basis during at 4 levels of the drying air temperature (T) *i.e.,* 45, 50, 55 and 60 °C, 3 levels of potato slice thickness (L) *i.e.,*1, 2 and 3 mm and 1.5 m/s of air velocity. The sample weight data was recorded till constant weight was achieved. To visualize the colour, texture and morphological changes during drying progression, the dryer was equipped with an image acquiring system. The images were processed using the algorithms written in MATLAB® platform. Image features were extracted to obtain the various quality related parameters (colour, image texture and product morphology) about the object of interest. For studying the time series data of the image properties at different temperatures and slice thicknesses; recurrent neural network (RNN) was used that predicts the future while using the past data. Since three categories of image properties, viz., morphological, chromatic and textural properties, were studied; initially the attributes from each property were used as an input to the network to observe the predictability of the output (moisture content) and later the combinations of two and all three properties were used. Additionally, different number of nodes, number of hidden layers, transformation function and training algorithm used were determined, on hit and trial basis, since it depended on the complexity of the problem to be investigated. Algorithm was developed with the intent of creating a graphical user interface (GUI). The developed GUI helped in simplifying communication of information between the system and operator, being user friendly. To check the efficiency of the developed algorithm, the moisture content of the product displayed during drying was compared with the moisture content obtained from the sample weight (manually recorded). RNN trained with any one of chromatic, morphological or textural features, have R^2 value less than 0.93 (RNN 1). When trained with any two of the three properties, the R^2 value slightly increased up to 0.95 (RNN 2). However, when the network was trained with all the three properties together (RNN 3), it performed excellently (R^2>0.97). In RNN 3, the network consisting of three hidden layers with 15-5-10 number of nodes in first, second and third hidden layers, respectively was selected as optimal topology to predict the moisture content of the potato slices during drying. In order to evaluate the performance of the developed algorithm on real time basis, the drying data were taken manually and compared with the moisture content predicted by the developed algorithm at 47, 54 and 58 °C for slices of thickness 2, 1 and 3 mm, respectively. The statistical parameters R^2 (0.9981, 0.9991 & 0.9957), MSE (2.77×10^{-4}, 1.62×10^{-4} &8.88×10^{-4}) and MAPE (0.0708, 0.3668 & 0.2242) indicated that the developed network as well as the algorithm perform efficiently.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the Student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Anand Mallikarjun Shivashimpar	21212	M.Tech	Design of smart device for on-field crop cutting energy measurement	Dr. Roaf Ahmad Parray
2.	Dattatray Ganesh Bhalekar	21213	M.Tech	Design of sensor based control volume sprayer for grape clusters	Dr. Roaf Ahmad Parray
3.	Rekha	21214	M.Tech	Design and development of combine harvester mounted sensor based microbial inoculum spraying system	Dr. Satish Devram Lande
4.	Megha Sadanand Ugargol	21215	M.Tech	Development and performance evaluation of battery-operated groundnut decorticator	Dr. S. P. Singh
5.	Mayanglambam Aarbindro Singh	21216	M.Tech	Design and development of semi-automatic pineapple harvester	Dr. Satish Devram Lande
6.	Monpara Milan Chandulal	21217	M.Tech	Design of control system for improving cooling efficiency of solar refrigerated evaporatively cooled (SREC) structure for safe storage of vegetables	Dr. Sangeeta Chopra
7.	Omkar Satish Nagawade	21218	M.Tech	Design and development of hempcrete and hempfabric evaporatively cooled storage structure for perishables.	Dr. Sangeeta Chopra
8.	Shivam Chaubey	21220	M.Tech	Performance evaluation of surface and groundwater irrigation for enhancing water productivity	Dr. D. K. Singh
9.	Chavda Dhavalkumar Ranchhodbhai	21221	M.Tech	IoT based aeroponics monitoring and alert System	Dr. Murtza Hasan
10.	Rongali Mahesh	21222	M.Tech	Study on groundwater problems in coastal Visakhapatnam	Dr. D. K. Singh
11.	Kadam Arti Maroti	21371	M.Tech	Assessment and planning for enhancing water productivity in eastern marathwada	Dr. A. K. Mishra
12.	Man Mohan Deo	10236	Ph.D.	Modelling of tractor-trailer system vibration for safe haulage	Dr. Adarsh Kumar
13.	Ravindra Dhondibhau Randhe	10239	Ph.D.	Conditional controller based fertigation system for water and nutrient management in soilless cultivation	Dr. Murtza Hasan
14.	Jaya Sinha	10394	Ph.D.	Modelling of manual chaff cutter for ergonomic design	Dr. Adarsh Kumar
15.	Laulina Kumari	10398	Ph.D.	Climate change impacts on crop water footprint of Trans indo-Gangetic plain	Dr. D. K. Singh

16.	Manoj Kumar	10680	Ph.D.	Modelling impact of water management technologies on groundwater for sustainable utilization	Dr. D. K. Singh
17.	Rudragouda chilur	10710	Ph.D.	Design and development of tractor drawn automatic vegetable transplanter for pot seedlings	Dr. P. S. Tiwari
18.	Alka Mishra	10739	Ph.D.	Development of LED based photodynamic inactivation system for surface decontamination of carrot	Dr. Nachiket Kotwaliwale
19.	Manish Kumar	10747	Ph.D.	Studies on spray characteristics of selected nozzles with bio-pesticides	Dr. C. R. Mehta
20.	Priyanka Sharad Mahangade	10942	Ph.D.	Study of solar refrigerated and evaporative cooled (SREC) structure for storage of perishable agricultural commodities	Dr. Indra Mani
21.	Mousumi Sabat	10945	Ph.D.	Digital image processing based system for real-time monitoring of potato slices in hot air dryer	Dr. Nachiket Kotwaliwale
22.	Prabhakar Shukla	10952	Ph.D.	Operators' workplace layout of self-propelled combine harvester	Dr. C.R. Mehta

Agricultural Physics

9

Prof. P. Krishnan

The Division of Agricultural Physics is endowed with a mission to study soil-water-plant-environment energetic for eco-friendly and sustainable exploitation of agricultural resources. The Division has made significant progress on research, teaching and training in the subject areas (Soil Physics, Agricultural Meteorology, Remote sensing and GIS and Plant-Biophysics). The research findings of post graduate students have been grouped under the following themes:

Theme 1. Image processing

Thermal imaging for characterization of abiotic stresses in wheat under field condition

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

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

Artificial intelligence-based image classification for identification of seeds of wheat cultivars

Agriculture is the world's oldest and the most significant, of all the human occupations and has a substantial impact on the national economy. According to market projections for the next decade, the next change will be a "digital agricultural revolution," which will help and assure agriculture can fulfil the demands of the global population in the future. Artificial intelligence (AI) is founded on the concept that human intelligence can be represented in such a way that a computer can easily reproduce it and do tasks ranging from simple to complex. At present, Artificial Intelligence could be used in the agricultural sector to produce healthy crops, control pests, keep an eye on the soil and growth circumstances, systematise data for farmers, reduce effort, and enhance a widespread range of farm-related jobs along the food supply chain. Image processing, machine learning, and deep learning were utilized in agriculture in the recent years, to identify varieties and cultivars of different crops. Convolutional Neural Networks (CNN) were used in deep learning for image classification. In this thesis, experiments were conducted to compare the performance of 5 state of art CNN architectures namely VGG16, VGG19, ResNet50, ResNet101 and InceptionResNetV2. The goal of the study was to apply the principles of convolution neural network to classify the seed images of wheat cultivars. Total of nine thousand images were captured from 10 wheat cultivars (HS 490, HD 2967, HI 1500, HB 208, C 306, CPAN 3004, DPW 621-50, HS 1097-17, HD 2864, AKAW 3722) in controlled illuminated chamber. Results showed that the InceptionResNetV2 based model trained on seed images of wheat cultivars performed better than other CNN architectures used in this study. This is because InceptionResNetV2 can extract and learn more features from images with help of Inception and ResNet module and use this learning to classify the images. In addition, augmented dataset was generated from original seed image dataset which was used to train InceptionResNetV2 - CNN architecture to improve its performance. To enhance the further application of this technology, an attempt was made to use hyperparameter optimization technique in the best selected CNN architecture - InceptionResNetV2 model that was trained on augmented seed image dataset. Results showed that the overall performance of hyper parameter optimized model, trained on augmented seed image dataset, was enhanced. This was supported by the evaluation of model on test seed image dataset. Hyper parameter optimized model showed an overall accuracy of 86.37 % along with an average F1 score of 0.84. Thus, the present study clearly showed that CNN based InceptionResNetV2 model could be applied as a non-destructive, rapid, objective technique to identify the seed images of different wheat cultivars.

Theme 2. Remote sensing application in agriculture

Remote sensing of rice residue burning and conservation tillage in wheat

For solving the problem of rice residue burning in north western India, the policy makers need real time information on its spatiotemporal patterns to target specific areas for residue management and popularize conservational tillage practices in succeeding wheat crop. There is a major challenge in the monitoring of crop residue burning due to spatio-temporal heterogeneity, scattered and smaller size of burnt area, but could be overcome by employing remote sensing technology. Against this backdrop, this research study was carried out at both field and regional levels. At the field level, efforts were made to discriminate between mature, harvested and burnt rice crops by critically analysing their spectral signatures. Among the various spectral indices computed, CARI and dNBR were identified as the best performing spectral indices to distinguish mature crop from harvested crop and burnt crop from harvested crop, respectively. These identified indices were subsequently used in the regional study for mapping the rice residue burnt fields in the Karnal and Kaithal districts of Haryana using Sentinel-2 MSI images and ground truth sites. Using training sites with maximum likelihood classification, the rice map was prepared at the first step with an overall accuracy of 95.49%. Then using ground truth sites, the threshold of CARI and dNBR were determined to discriminate mature paddy crop from harvested paddy crop and harvested paddy crop from burnt paddy crop, respectively. A decision tree classifier based on CARI and dNBR thresholds was used to map burnt rice fields for images between 1-Oct and 20-Nov-2020 with an overall accuracy of 92.57%. Further, remote sensing data was explored to discriminate between conventional tillage and conservation tillage sown wheat grown after rice crop. Based on ground truth survey, the happy seeder and super-seeder sown wheat in standing rice stubble were considered as conservation tillage fields, while wheat sown on fine seed-bed prepared using harrow and rotavator were taken as conventional tillage. Nine cloud-free Sentinel-2 images obtained between 21-Oct to 20-Dec-2020 were used. Based on temporal profile analysis of various spectral indices (CARI, NDVI, NDTI, NSSI, BI) calculated for ground truth sites, the ratio of CARI and NDTI was found to clearly discriminate between conservation and conventional tillage. A hierarchical decision tree classifier based on identified thresholds of CARI to NDTI ratio was used to map wheat sown under conservation tillage in the two districts with an overall accuracy of 85.0%. The study developed new methodologies to map rice burnt area and conservation tillage in wheat using time-series of Sentinel-2 MSI images. There is a good potential to further scale the methodologies to whole of north-west India to provide critical information for implementing suitable schemes for rice residue management and promotion of conservation tillage.

Mapping of rice crop using microwave and optical remote sensing data

Rice is the main diet of nearly 65 per cent of the Indian population, and Punjab and Haryana have contributed most in total rice production. Due to increasing population and the growing demands of food in India we should have knowledge on the spatial extent of rice crop. Theobjectiveofthisstudyisto classify the rice area from the other non-rice areas and to prepare a map of Punjab and Haryana state. The microwave and optical remote sensing data were derived from Sentinel 1 and Sentinel 2 satellites respectively. Time series (May-Oct 2019), dual polarised (VV+VH) Sentinel 1A data were used to delineate temporal signatures of crops which are generally grown in both the states in kharif season. Time series of VH polarized data have shown more dynamic variation starting from land preparation to harvesting than the VV polarization for rice crop. In this study rice area was also estimated from Sentinel-2, optical data and area were classified using NDVI based threshold technique. But due to the presence of cloud cover during kharif 2019, use of time series data was not possible so images at vegetative stage (September, 2019) and reproductive stage (October, 2019) of rice crop were considered to classify the rice area. For rice detection a threshold a is used -5 dB as this threshold can minimize the incident angle effect and b and c were -19dB and -20 dB, for water threshold -20 dB is used. The minimum and maximum NDVI values obtained from the image processing of Sentinel-2 data sets is 0.07 and 0.89 with a mean value of 0.51.It has been observed that in most of the cases the NDVI based estimated rice area is less than the area estimated by SAR data. The total area estimated for rice crop for Punjab and Haryana by Sentinel-1 (SAR) is 31, 12,700 ha and 14, 25,250 ha respectively and by Sentinel-2 (NDVI) is 30, 01,700 ha and 10, 02,880 ha respectively. When area derived from both the data were compared against the government reported area, the microwave estimated area having less deviation compared to optical data. SAR data overestimated the rice area for Punjab and Haryana by 9,690 ha and 3,250 ha respectively whereas Sentinel-2 data underestimated for both the states by 10, 13,000 ha and 42, 23,700 ha respectively. In this study we found that though the trend of backscatter dynamics for rice crop is similar for both the VH and VV polarization, the VH polarization had a larger dynamic range in the entire rice growth period. It can be concluded that area estimated from SAR data is more accurate as it is very close to rice area reported by the Government and rice area estimated from NDVI derived threshold is unable to estimate the rice area accurately in the kharif season. Recommendations from present study are for future SAR-based crop area estimation studies is use of cloud free optical imagery may be used for crop mask, multi-polarized data is necessary for further improvement of the accuracy.

Theme 3. Soil physics and conservation agriculture

Digital soil mapping using imaging spectroscopy

Accurate and detailed mapping of soil properties is important for effective soil management. A large number of soil samples needs to be explored to address the spatial variability for detailed mapping purpose. As the traditional techniques of soil analysis and mapping are time consuming and labor intensive, reflectance spectroscopic technique can supplement the previous techniques for rapid and cost-effective assessment of soil properties. These spectroscopic data can also be fused with multiple data sources using machine learning techniques for producing accurate digital maps of various soil properties at high resolution scale. Therefore, the present study was conducted in an intensively cultivated region of Katol, Nagpur, Maharashtra, India with the objectives namely: (i) spatial prediction of soil properties from hyper-spectral data using machine learning tools, (ii) to develop digital soil map by integrating imaging spectroscopic data and environmental covariates, and (iii) to evaluate the protocol for digital soil mapping at a high-resolution scale. First, the potential of various spectroscopic techniques including lab-based and airborne VIS-NIR, MIR (absorbance and emissivity) were assessed employing six important multivariate models namely PLSR, SVMR, GPR, MARS, RF and ANN for the prediction of various soil fertility properties. About 132 georeferenced surface soil samples were collected during the campaign of AVIRIS-NG over the study area and these were analyzed chemically to estimate SOC, available N, P, K, S, DTPA extractable Zn, Cu, Fe and Mn, soil particle size fraction (sand, silt and clay), pH and EC following the standard protocols. The descriptive statistical analysis showed considerable amount of spatial variability for almost all soil properties except pH (CV = 7.21%). The analytical results also demonstrated that the study area had neutral to alkaline pH (mean pH = 7.35), negligible salinity (mean EC = 0.17), moderate amount of SOC (SOC = 0.62%), sufficient amount of all the studied macro nutrients and micronutrients. The spectral data were recorded using various instruments and they were resampled at 5 nm interval and preprocessed before spectral model development for soil property prediction. All the models were evaluated and ranked on the basis of their overall performances both in calibration and validation datasets employing statistical indices like R^2, RMSE, RPD and RPIQ and the lowest ranking model was considered as the best model. The spectroscopic data analysis revealed that the SVMR model outperformed the other multivariate models in predicting most of the soil properties in all four types of spectroscopies. Next to SVMR, other models such as RF, ANN and PLSR also performed well in predicting various soil properties. The lower performances were observed for GPR and MARS models in soil property prediction. For SVMR, the R^2 value of validation ranged from 0.65 (for DTPA extractable Fe) to 0.86 (for DTPA extractable Zn), 0.51 (for pH) to 0.78 (for available K), 0.91 (for sand, clay) to 0.95 (DTPA extractable Mn) and 0.68 (available N and % silt) to 0.85 (for available K), for lab-based VIS-NIR, airborne VIS-NIR, MIR (absorbance) and MIR (emissivity) data respectively. MIR (absorbance) spectroscopy was found superior to other techniques. The combined VIS-NIR-MIR spectra were unable to further improve the prediction accuracy over MIR-absorbance spectra. The significant spectral wavebands were identified using PLSR based VIP technique for lab-based VIS-NIR and MIR (absorbance) spectroscopy and factor loading plots for other two spectroscopic techniques. Generation of digital soil maps for various soil fertility properties were developed using the airborne imaging spectroscopic data of AVIRIS-NG sensor, topographic data of SRTM-DEM, vegetation indices of remotely sensed data (Sentinel-2 data) and lab measured soil properties data using random forest technique. Among the DEM derived variables, slope, elevation (DEM), LS factor, aspect, analytical hill shading, total catchment area, MRVBF, TWI, profile curvature etc. were observed to be the major factors controlling the spatial distribution of those soil properties. Inclusion of airborne data (PCs) with other variables significantly improved the prediction performances of the RF model for various soil properties. Some PCs were found to be the most important factor (relative importance 100%) in prediction of so many soil properties like PC6 for SOC, PC2 for available S etc. Therefore, airborne imaging spectroscopic data proved its efficacy in predicting and digital mapping of soil properties. The uncertainty of the RF model was mapped and quantified as standard deviation (SD), standard error (SE), lower and upper prediction limits (LPL and UPL) of the predicted soil properties employing bootstrapping method. The uncertainty analysis revealed that the actual mean value of a particular property was always happened in between the corresponding LPL and UPL of that property. The digital maps performed better than kriged and airborne maps in predicting most of the soil properties. The protocol developed in this study can be further utilised to predict and map other soil properties and has important implications in site specific soil management of the study area.

Evaluation and prediction of structural stability and hydraulic conductivity in saline soils using machine learning

The inability to maintain proper soil structure, soil hydraulic properties and soil organic carbon levels can seriously hamper soil health and crop production. Soil salinity can degrade soil quality, decrease crop yields. To evaluate the effect of soil salinity on structural stability and hydraulic properties, and to predict those properties, total 121 soil samples were collected from 0-15 and 15-30 cm of soil depths from eighteen villages of Nilokheri, Nissang and Assandh block of Karnal district, Haryana. Result showed that in 0-15 cm soil depths, soil pH varied from 8.24 to 10.08 and EC of 0-15 cm soil layer varied from 2.46 to 16.4 dS/m. The range of MWD varied from 0.18 to 1.21 mm and showed high variability. Fractal dimension of the soil particles ranged from 2.59 to 2.97 and it has lowest variability among all the parameters. The results of D showed that D is positively related with the clay and silt % but negatively related with sand %. Hydraulic conductivity (HC) of the study area varied from 1.59 to 19.16 cm/hr with a SD of 3.72 and highly variable in nature. Out of 121 soil samples, 65.3% (79) were under low carbon category, whereas, 14.87 % (18) were under medium and high carbon content classes. Total organic carbon (TOC) in class 2 (pH>9.5) soils were 0.02% more than class 1 (pH= 8-9.5) soil, though the difference was not statistically significant. Average MWD was 0.11 mm more in class 2 soils as compared to class 1 soils. Glomalin content had positive correlation with HC and sand content and negative correlation with BD, clay and silt %, but the correlations were not significant. No significant correlation was obtained with MBC and other soil parameters. The soil pH had significant negative correlation with sand content whereas, it showed significant positive correlation with sand content. Soil EC showed a strong positive correlation with soil pH. Labile pool of 0-15 cm soil was 3.13 g C/kg soil and was 15.49% more than 15-30 cm. Recalcitrant pool of 0-15 cm soil layer was 2.85 g C/kg soil and was 21.79% more than 15-30 cm. Inclusion of D in prediction of HC by MLR model did not show any improvement, rather it performed poor both for training and testing dataset.In case of ANN, for both the input sets, ANN with three hidden layers performed better. Inclusion of D in input set (i.e., ANN-HCD), RMSE value was reduced by 17% in training dataset whereas, 25.12 % in testing dataset. Inclusion of fractal dimension in input dataset (CART-HCD) has no improvement in both training and testing dataset. RF performed better both in RF-HC and RF-HCD models in prediction of HC as compared to CART. The results showed that among all the models, SVMHCD performed best based on the statistical evaluation criteria. The correlation value is found to be higher in case of SVM-MWDD by 11.11% than SVM-MWD in training dataset but, in testing dataset the SVM-MWDD the correlation coefficient is higher by 5.08% than SVMMWD. SVM models predicted the HC and

MWD with more satisfactory performance as compared to the other models owing to their more flexibility and capability to model non-linear relationships. Evaluation of effects of soil salinity on different soil parameters are very much required for improving soil structure and organic carbon content of soil. Identification of critical soil pH and EC in maintenance of soil structure, TOC and hydraulic properties is very much essential. Comparative study can be made in future to find out the prediction efficiency of different geostatistical techniques and machine learning approaches. As plant growth is a direct indicator of soil health, plant parameters can be included in input dataset to check the model efficiency.

Theme 4. Crop simulation modeling

Simulation of soil profile moisture and water productivity of mustard cultivars using AquaCrop model

India has made excellent progress in the total food grain production, still we import edible oil. Low productivity due to biotic and abiotic stress is a major concern. Among the abiotic stresses, heat stress as well as soil moisture deficit are the main issues to be tackled. Terminal heat stress and uncertain rainfall are huge obstacle particularly for the rabi season crops. Indian mustard or oilseed Brassica is a rabi season oilseed crop which suffer from above mentioned abiotic stresses along with biotic stresses due to pest and diseases. These stresses resulted in low productivity. For enhancing the productivity of mustard, systematic study to detect the appropriate sowing time and cultivars, water requirement under different rainfall scenario needs to be assessed through modelling approach.A field study was conducted at the farm of Indian Agricultural Research Institute (IARI) in the rabi season 2020-21 with three cultivars, two sowing dates (normal and late) and two levels of irrigation. The data generated in the first sowing were used to calibrate a water driven model, AquaCrop (V 6.1). The calibrated model was run to simulate biomass, seed yield and total soil profile moisture content using weather data of IARI Agro met observatory. The model underestimated the biomass of Pusa Vijay and Pusa Mustard-21 for the period of 70-110 DAS and overestimated that of Pusa Bold for the same period and overestimated the seed yield in all cases. The difference between simulated and observed final biomass and seed yield was within ± 10 %. The simulated and observed total soil profile moisture were also in close agreement. The R^2 values ranged between 0.86 to 0.93 suggesting 86% to 93% variability in total profile soil moisture content can be accounted by the model. The model was validated for the second sown crop. During validation, it simulated the above-mentioned parameters with good accuracy except water productivity. The model accounted 87%, 85%, 85% variation in profile moisture content for one irrigation and 92%, 91%, 87% variation in profile moisture content for two irrigations for cultivars Pusa Vijay, Pusa Mustard-21 and Pusa Bold, respectively. Water Productivity was validated and the model account 98%variation in water productivity, but nRMSE value was high. The calibrated and validated model was run to select irrigation requirement and the best cultivar for wet and dry rabi seasons under normal and late sowing conditions. From this study, it is recommended that in wet rabi season the biomass, seed yield and water productivity may increase with one irrigation at rosette stage of the crop for both normal and late sowing conditions. In a dry rabi season, with the increase in irrigation level the biomass and seed yield may increase progressively. If sufficient water is available, two irrigations (one at rosette stage and one at seed filling stage) may be given. If water is limited one irrigation at rosette stage may be given for both normal and late sown conditions. The cultivar, Pusa Bold was found to be the best seed yielder for any scenario.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Tarun Kumar	21231	M.Sc.	Artificial intelligence based image classification for identification of seeds of wheat cultivars	Dr. P. Krishnan
2.	Sailja Rastogi	21232	M.Sc.	Remote sensing of rice residue burning and conservation tillage in wheat	Dr. V. K. Sehgal
3.	Bibhuti Bhusan Sethi	21233	M.Sc.	Mapping of rice crop using microwave and optical remote sensing data	Dr. Joydeep Mukherjee
4.	Abhradip Sarkar	21234	M.Sc.	Evaluation and prediction of structural stability and hydraulic conductivity in saline soils using machine learning	Dr. Pragathi Pramanik Maiti
5.	Krishna Kumar Sudhansu	21235	M.Sc.	Simulation of soil profile moisture and water productivity of mustard cultivars using AquaCrop model	Dr. D. K. Das
6.	Koushik Banerjee	10761	Ph.D.	Thermal imaging for characterization of abiotic stresses in wheat under field condition	Dr. P. Krishnan
7.	Bhabani Prasad Mondal	10970	Ph.D.	Digital soil mapping using imaging spectroscopy	Dr. R. N. Sahoo

Agronomy

10

Prof. T.K. Das

The Division of Agronomy has a mandate to provide leadership in crop and cropping system-based agronomic research by developing new concepts and approaches of sustainable crop production suited to farmers; to develop appropriate crop production technologies to enhance the production and productivity of major cropping systems on a sustainable basis; to provide post-graduate teaching and develop human resources. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Nutrient management

Need based nitrogen management in wheat using precision gadget for optimum crop productivity and higher nitrogen use efficiency

An experiment was conducted during winter season in 2020-2021 at the research Farm of ICAR–Indian Agricultural Research Institute (IARI), New Delhi, India. Results showed improvement in all the plant growth parameters under precision nutrient management practices following Nutrient Expert + GreenSeeker protocol/ device recording the highest CGR (13.02 g/m^2/day), NAR (3.74 g/m^2/day), leaf area (3.48 m^2), LAI (3.48) at 90 DAS. All yield parameters namely, spike length (16 cm), grains/spike (45.4 grains), grain weight/spike (3.09 g), spikes/m^2 (345 spikes) and 1000 seed weight (44.0 g) were also improved proportionately with Nutrient Expert + GreenSeeker aided nutrient management. As a result, grain yield (4.72 t/ha), straw yield (6.87 t/ha) and the total biomass yield (11.59 t/ha) of wheat were significantly higher under Nutrient Expert + GreenSeeker based nutrient management than other nutrient management options. Accordingly, maximum net return (INR 57,559.00/ha) and monetary efficiency (INR 384.00/ha/day) as well as the highest amount of N, P and K concentration in grain (1.64, 0.28 and 0.33 %) and straw (0.44, 0.16 and 1.38%) and nutrient uptake (107.9, 24.3 and 110.6 kg of N, P and K/ ha respectively) were also recorded under Nutrient Expert + GreenSeeker based nutrient management practice.

Effect of Zn fertilization and microbial inoculants on productivity of chickpea

This study showed that T7 (RDF + 25 kg ha^{-1}+ Meso + AM + PSB) accumulated ~46-48% greater shoot biomass than the T1 (no Zn or microbial inoculants). Plots under T7 and T8 (RDF + 0.5% ZS foliar spray + Meso + AM) had greater leaf chlorophyll content, nodules dry weight plant^{-1}, and yield traits over other treatments. The T7 produced significantly ($p<0.05$) higher chickpea seed and stover yields, which were 22.8% and 20.4% greater than in T1. but gave statistically similar yield to T3 &T8 (RDF + 25 kg ha^{-1} ZS and RDF + 0.5% ZS foliar spray + Meso + AM). Also, different treatments caused significant ($p<0.05$) impacts on the soil dehydrogenase (DHA) and alkaline phosphatase (AP) activities. On an average,in 0.0-0.15 m and 0.15-0.30 m soil profile, microbial inoculated (T5-T8) plots registered12.5% and 36.4% greater DHA and AP than the T1 and T4, respectively.

Effect of residue and potassium management on productivity and nutrient-use efficiency of wheat

This study revealed that crop residue retention @ 3 t/ha recorded the higher plant height, LAI, dry matter accumulation and tiller/m^2 at 60 and 90 DAS. Crop residue retention recorded highest grain (5.98 t/ha), straw (7.58 t/ha) and biological yield (12.68 t/ha) followed by crop residue incorporation compared to no crop residue. The crop residue incorporation @ 3 t/ha recorded highest concentration of N, P and K (1.68, 0.38 and 0.53%) in grain and straw (0.57, 0.19 and 1.75 %), respectively. The SOC, available N, P and K content in soil after harvest was also recorded higher under crop residue incorporation @ 3 t/ha. The residue retention @ 3 t/ha significantly improve the soil microbial biomass carbon (134.22 µg C /g of soil), dehydrogenase (35.15µg TPF/g soil/day) and alkaline phosphatase (18.85 µgPNP/g soil/hr) activity. Potassium management practices significantly influenced the growth parameters, yield and yield attributes compared to control (no potassium). The value for all the growth parameters were observed maximum with the split application of 100% recommended dose of potassium (½ at basal + ½ top dress at 25 DAS). Overall, it can be concluded that the residue retention treatment with the split application of 100% of recommended dose of potassium (½ at basal + ½ top dress at 25 DAS) was found optimum in terms of yield, economics and use efficiency of applied potassium.

Performance of mustard under differential placement of fertilizers and phosphorus enriched composts

A field experiment that the placement of 40 kg RDN through RC-PE and rest of RDF with fertilizers recorded highest values of yield attributes *viz*. siliqua plant^{-1}(411), seeds siliqua^{-1} (15.2) and 1000-grains weight (4.88 g) and was at par with placement of 40 kg RDN through FYM. This treatment also recorded highest seed yield (1994 kg ha^{-1}), stover yield (6377 kg ha^{-1}) but showed non-significant effect in HI. The placement of 40 kg RDN through RC-PE recorded highest protein (19.06 %) and oil (39.1 %) content as well as protein (380.1 kg ha^{-1}) and oil (778.6 kg ha^{-1}) yield. The highest value of alkaline phosphatase (130.3, 120.3 and 132 µg PNP g^{-1} day^{-1}), dehydrogenase (38.7, 40.9 and 41.1 µg TPF g^{-1} soil day^{-1}) and microbial biomass carbon (181, 179.7 and 184 µg g^{-1}soil) were recorded due to application of balanced nutrient sources through both organics (FYM, RC and RC-PE) and fertilizers as compared to application of RDF through fertilizers alone (96, 33.4, 173, respectively). Highest net returns (Rs. 79,915 ha^{-1}) was found due to placement of RDF but the highest gross returns (Rs. 1,19,640 ha^{-1}) was recorded due to placement of 40 kg RDN through RC-PE and was at par with placement of 40 kg RDN through FYM (Rs. 1,11,900 ha^{-1}).

Response of chickpea varieties to zinc fertilization

This study showed the effect of variety and zinc fertilization on growth and yield parameters, input-cost relationships, soil enzymatic activities in rhizospheric zone, and nutrients concentration in grain and stover and their uptake. It was found that the *desi* variety, 'Pusa 547' showed better growth characters, chlorophyll, leghaemoglobin content, grain yield, Zn concentration and its uptake, protein content, protein yield, net returns and net benefit-cost ratio but had lower nodules growth, zinc harvest index and agronomic as well as physiological use efficiencies of applied Zn than *Kabuli* variety, 'Pusa 3022'. With respect to Zn biofortification, total zinc uptake by 'Pusa 547' was ~58% higher than 'Pusa 3022' with highest Zn concentration in grain (45.7 mg/kg). Combined application of Zn @ 2.5 kg/ha at sowing and 0.5% foliar spray through ZnSHH at flowering stage resulted in ~20–30% greater shoot biomass, ~15% greater leaf chlorophyll content, ~46 and~58% higher super oxide dismutase and carbonic anhydrase enzyme activities, respectively, along with ~9% higher grain yield, ~36% greater Zn concentration in grain, ~14% greater crude protein in grain and

~11% greater net returns than control. This study highlights that Zn fertilization and microbial inoculants can be beneficial options for improving crop yields, nutrient uptake, enhancing farm profits and improving soil properties in chickpea.

Nitrogen management options for different crop establishment methods in wheat under rice-wheat cropping system

This study revealed that the ZT+R recorded significantly higher values of growth parameters, yield attributes, grain yield (4.99 t/ha), straw yield (8.03 t/ha) and economic returns of wheat over rest of the cropestablishment methods. The CT recorded minimum root length density, root volume and root surface area at the flowering stage over rest of the treatments while maximum was recorded under ZT+R. The highest available N, phosphorous, potassium and mineral nitrogen in soil after harvest of the crop and higher nitrogen content and uptake were also recorded with ZT+R. Among the N management options LCC-guided N applicationrecorded maximum and significantly higher growth parameters at almost all growth stages, yield attributes, grain yield (5.39 t/ha), straw yield (8.36 t/ha) and economic returnsover rest of the treatments. Similar growth parameters like root length density, root volume androot surface area at the flowering stage were also recorded maximum in this treatment. LCC-guided nitrogen application significantly increased N content, mineral N and uptake over rest of the treatments. Therefore, a combination of ZT+R and LCC-guided N application may be recommended for better growth, productivity, soil health and higher returns in wheat under rice-wheat system.

Effect of summer green manuring and sulphur fertilization on productivity and nutritional quality of *Basmati* rice–durum wheat sequence

A field experiment was undertaken at New Delhi. The treatments consist of two summer green manure crops (Sesbania, sunhemp) and fallow (no green manuring) in the main plot, and six doses of sulfur. Results showed that *Sesbania* added additional macronutrients of 7.2 kg/ha of nitrogen, 2.4 kg/ha of phosphorus, 2.8 kg/ha of potassium, and 11.6 kg/ha of sulphur than sunhemp (*Crotalaria juncea*). Summer green manuring with Sesbania recorded 18% higher grain yield, 6% higher straw yield, 9% higher biological yield, and 10% higher harvest index than control (fallow) in *Basmati* rice. Highest B:C (1.24 in 2018 and 1.30 in 2019) was recorded in *Sesbania* green manuring in *Basmati* rice. The cumulative effect of 40 kg S/ha to rice and wheat could increase filled grains per panicle by 14%, 7% higher total grains per panicle and 13% fertility percentage, 0.47 t/ha higher grain yield, straw yield by 1.49 t/ha, biological yield by 2.00 t/ha, and harvest index by 4% compared to control (no sulphur).

Theme 2. Weed management

Effect of land configuration and weed management on growth and yield of pigeonpea [*Cajanus cajan* (L.) Millsp.] under semi-arid conditions

A field experiment was carried out at the Research Farm of Indian Agricultural Research Institute, New Delhi during *kharif* seasons of 2020. It revealed that growing of pigeon pea under broad bed and furrow land configuration practice significantly increased growth and yield attributing parameters, nutrient uptake, weed control efficiency and water use efficiency, consequently highest seed (1.8 t ha^{-1}), stalk (5.19 t ha$^{-1)}$ and biological yield (6.96 t ha^{-1}). Similarly, broad bed and furrow method showed its superiority for providing highest gross returns (107.4 ×10^{3} INR ha^{-1}), net returns (65.0 ×10^{3} INR ha^{-1}), B: C ratio (2.53) and economic efficiency (INR 481.81-day $^{-1}$ ha^{-1}). All the weed management treatments resulted in significantly higher growth and yield attributing parameters and seed yield of pigeon pea over weedy check. Among the weed management treatments, two hand weeding given at 30 and 60 days after sowing resulted in highest weed control efficiency (83.07 and 82.80%) at 60 and 90 days after sowing, water use efficiency (3.40 kg ha-mm^{-1}) and economic productivity (INR 203.99 ha-mm^{-1}), growth and yield attributing parameters and seed yield (1.8 t ha^{-1}). However, owing to lesser cost of cultivation,pre-emergence application of metribuzin 0.25 kg ha^{-1} + imazethypr+imazamox 75 g ha^{-1} fetched highest net returns of 68 ×10^3 INR ha^{-1} with B:C ratio of 2.74 and economic efficiency (INR 486.32 day $^{-1}$ ha^{-1}). It was concluded that growing of pigeon pea crop under broad bed and furrow method with the pre-emergence application of metribuzin 0.25 kg ha^{-1} + imazathypr+imazamox 75 g ha^{-1} registered higher net returns, B:C ratio and economic efficiency under semi-arid conditions.

Integrated weed management in Indian mustard

A study was conducted in New Delhi. Results showed that the application of pendimethalin at 0.75 kg/ha (PE)+ 1 hand weeding at 30 DAS was found very effective in controlling all grassy, broad leaved weeds and sedges including, *Cyperus rotundus*. It also produced significantly higher seed yield of mustard over weedy check. Also, oxadiargyl at 75 g/ha (PE) plus 1 hand weeding at 30 DAS was found effective in reducing weed density and dry weight. Pendimethalin at 0.75kg/ha (PE)+ residue mulching and oxadiargyl at 75gm/ha (PE) plus residue mulching proved effective in controlling monocot and dicot weeds in early growth stage of mustard, but failed to reduce weed density and dry weight at later crop growth stage. Integrated weed management treatments provided a yield advantage of 21.58 to 57.55 % over weedy check. Highest net returns (INR 73,285/ha) was obtained under weed free situation, which was closely followed by pendimethalin at 0.75 kg/ha (PE)+ 1 hand weeding at 30 DAS (INR 67,287/ha). But the B:C of weed free treatment (1.72) obtained was relatively lower than pendimethalin at 0.75 kg/ha (PE)+ 1 hand weeding at 30 DAS (1.95) and oxadiargyl at 75 g/ha (PE) plus 1 hand weeding at 30 DAS (1.84). Application of imazethapyr at 50 g/ha proved toxic to mustard crop and caused complete crop failure.

Theme 3. Conservation agriculture

Integrated weed management in wheat under conservation agriculture-based maize-wheat-mungbean system

A study was conducted on various weed management practices under different establishment techniques. Among the establishment methods, the highest grain yield (4.85 t/ha), straw yield (9.03 t/ha), and biological yield (14.32 t/ha) were recorded under ZT-wheat with previous brown manuring and highest grain yield (4.88 t/ha), straw yield (8.59 t/ha), and biological yield (13.92 t/ha) were recorded under weed free check (W2) among various weed management practices, respectively and thereby concluded that the efficiency of weed management by brown manuring and its synergy with herbicide combinations suppress weeds, and contribute to crop and soil productivity.

Nitrogen management and weed dynamics in a conservation agriculture-based maize-wheat-mungbean system

An experiment was conducted in the 9th and 10th year of a long-term CA experiment with ten treatments comprising of different methods of crop establishment, along with 75% and 100% recommended doses of nitrogen were integrated with CA practices. Results showed that, compared to CT practice, the CA-based practices resulted in reduction in weed seed density in soil by 2.5-45.1%, 5.0-53.1%, and 3.4-47.6% at 0-7.5 cm, 7.5-15 cm and 0-15 cm soil layers, respectively. The PBB+R+100N treatment resulted in 22.1%, 27.1% and 56.8% increase in maize, wheat and mungbean yields, respectively compared to CT practice. In both years, the PBB+R+100N gave significantly higher gross returns, net returns and net benefit: cost and also resulted in 36.9%, 56.5% and 99.7% higher total water productivity, respectively in maize, wheat and mungbean crops compared to CT practice. The treatments FB+R+100N and PBB+R+100N had significantly higher soil organic carbon (SOC) stock at 0-5 cm, 5-15 cm and 15-30 cm soil depths. Also reduction in GHGs (CO_2, N_2O) emission was observed in this study under PBB+R and PNB+R, which could improve environmental sustainability.

Precision nutrient management under conservation agriculture (CA) based maize–wheat rotation

A two-year field experiment revealed that CA practices enhanced growth, total dry matter and yield attributes, grain yield of both maize and wheat crops. A CA-based PB (19.85%) and ZT plots (13.05%), thus, had higher MW system productivity compared to CT plots (two-season mean). The improved nutrient management options enhanced growth, total dry matter and yield attributes, grain yield of maize and wheat crops, thus attained MW system's productivity with SSNM treatment having the highest increment (30.85%; two-season mean) compared to FFP (farmers fertilizer practices). CA-based PB and ZT plots recorded higher mass equivalent basis total organic stock, C-sequestration potential, soil available N, P, and K, soil microbial biomass carbon and soil enzymatic activity compared to CT. While a higher mass equivalent basis total organic C stock and C-sequestration potential, soil available N, P and K, soil microbial biomass carbon and soil enzymes activity were observed in SSNM among nutrient management options.

Theme 4. Irrigation management

Deficit irrigation management in mustard using drip under agri-horti system

A field experiment was conducted during *Rabi* season 2020-2021 at ICAR-IARI, New Delhi. Five AHS, viz. moringa-based AHS (M_1), phalsa-based AHS (M_2), karonda-based AHS (M_3), aonla-based AHS (M_4) and guava-based AHS (M_5) were applied with three deficit irrigation scheduling (DIS) viz. S_1 (rainfed), S_2 (IS at 0.4 IW/CPE ratio), S_3 (IS at 0.6 IW/CPE ratio). The moringa based system had 7.7%, 15.9% and 36.9% higher numbers of siliqua/plant over phalsa, karonda and aonla based AHS. The highest numbers of siliqua were in a 0.6 IW/CPE ratio (396) that are statistically superior to those with a 0.4 IW/CPE ratio (354). Significantly higher seed yield (1939 kg ha^{-1}), stover yield (6067 kg ha^{-1}), and biological yield (8143 kg ha^{-1}) were recorded under moringa-based AHS. Among DIS, 0.6 IW/CPE had highest yield, followed by 0.4 IW/CPE and rainfed. There was 10.9 % and 36.1 % higher seed yield and 7.6% and 16.1% rise in stover yield recorded with 0.6 over 0.4 IW/CPE and rainfed treatment. Under moringa based AHS, WUE of Indian mustard was 13.8%, 16.7% 19.7% and 30% higher over phalsa, karonda, aonla and guava based AHS, respectively. Also, highest net returns (Rs 52516 ha^{-1}) and monetary efficiency was achieved with 0.6 IW/CPE treatment.

Theme 5. Crop diversification

Performance of mustard varieties in diversified maize-based system under different production systems

A field experiment revealed that plant height (cm), dry matter accumulation (DMA), LAI of Indian mustard under diversified production scenarios was significantly ($P \leq 0.05$) influenced at 30, 60 90 days after sowing (DAS). LAI at 60 DAS ranged between 4.15 to 4.37 under different production systems and 4.19 to 4.29 under different varieties. Yield attributes of Indian mustard like number of primary branches (PB), secondary branches (SB), siliquae on main shoot, siliquae on PB, siliquae on SB, main shoot length were significantly ($P \leq 0.05$) influenced in different varieties of mustard under diverse production systems. Under ICM production system, higher oil

(40.1%) and protein content (18.93%) were observed. There was almost 14% increase in seed yield under ICM compared to CS. Mustard variety, PM 26 resulted in maximum seed yield (2206 kg/ha), closely followed by PM 28 (2123 kg/ha). Highest net returns was obtained under ICM (Rs 77935/ha) and among the varieties, PM 26 gave maximum NR of Rs 76118/ha. Among mustard varieties, higher N, P and K content and uptake was under ICM production system. Soil organic carbon varied from 0.55-0.68 % at initial stage of field experimentation in different production system. There was higher build-up of SMB in soil under OMS. This may be concluded that PM 26 gave maximum productivity under ICM, followed by PM 28 and also led to better soil health in terms of nutrient build up and soil microbial properties.

Theme 6. Integrated farming system

Livelihood security, resource budgeting and soil health management under integrated farming system (IFS) in North-West India

An experiment was conducted at the IFS model of ICAR-IARI, New Delhi. Treatments were ten IFS models comprising of seven diversified cropping systems, dairy, fishery, poultry, duckery, apiary, boundary plantation, biogas unit and vermicompost) along with conventional rice-wheat system. Results showed that the economic yield of cropping system multi-cut sorghum (54.6 and 54.9 t/ha)–potato (35.5 and 36.8 t/ha)-onion (29.3 and 30.7 t/ha) and straw yield of the cropping system baby corn (25.86, 26.18 and 26.02 t/ha)-berseem–baby corn (28.10, 28.32 and 28.21 t/ha) were significantly higher than other systems in both years. A cropping system brinjal (27.5, 28.7 and 28.1 t/ha)–ratoon brinjal (9.5, 9.4 and 9.4 t/ha)–cowpea (6.4, 6.5 and 6.5 t/ha) had maximum yield, system productivity (43.4, 44.6 and 44.0 t/ha) and net returns during both years. The model M_{10} had considerably higher system productivity (60.2, 62.9, and 61.5 t/ha), system production efficiency (164.8, 172.3 and 168.5 kg/ha/day), cost involved (566.9, 595.2 and 581.0 × 10^3 INR/ha) and gross returns (1019.2, 1000.1 and 979.8 × 10^3 INR/ha). However, the system economic efficiency (1239.9, 1351.9 and 1295.9 INR/ha/day) and net returns were highest in M_9 (392.9, 405.5 and 399.2 × 10^3 INR/ha) while returns over investment was higher in M_2 (316.6, 314.9 and 315.8 × 10^3 INR/ha) than other IFS models tested.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Abhishek Swain	21245	M.Sc.	Integrated weed management in wheat under conservation agriculture-based maize-wheat-mungbean system	Dr. Kapila Shekhawat
2.	Shashank Patel	21246	M.Sc.	Performance of mustard varieties in diversified maize based system under different production systems	Dr. S.S. Rathore
3.	Kajal Arora	21247	M.Sc.	Effect of residue and potassium management on productivity and nutrient-use efficiency of wheat	Dr. R.S. Bana
4.	Prakash Chandra Singha	21248	M.Sc.	Performance of mustard under differential placement of fertilizers and phosphorus enriched composts	Dr. Shiva Dhar
5.	Amlan Nath	21249	M.Sc.	Effect of Zn fertilization and microbial inoculants on productivity of chickpea	Dr. Vijay Pooniya
6.	Ashok Singh	50046	M.Sc.	Integrated weed management in Indian mustard (*Brassica juncea* L.)”	Dr. Rajvir Sharma
7.	Sudarshan S.	50047	M.Sc.	Nitrogen management options for different crop establishment methods in wheat under rice-wheat cropping system	Dr. Kapila Shekhawat
8.	Anamika Barman	50048	M.Sc.	Deficit irrigation management in mustard using drip under agri-horti system	Dr. V.K. Singh
9.	Avaneesh Kumar	60046	M.Sc.	Effect of land configuration and weed management on growth and yield of Pigeon pea under semi-arid condition	Dr. Raj Singh
10.	Santhosh Kumar S.R.	60047	M.Sc.	Need based nitrogen management in wheat using precision gadget for optimum crop productivity and higher nitrogen use efficiency	Dr. Amal Ghosh
11.	Ganesh Patel	60048	M.Sc.	Response of chickpea varieties to zinc fertilization	Dr. Y. S. Shivay
12.	Bharat Raj Meena	10771	Ph.D.	Precision nutrient management under conservation agriculture-based maize–wheat rotation	Dr. C.M. Parihar
13.	Sonaka Ghosh	10980	Ph.D.	Nitrogen management and weed dynamics in a conservation agriculture-based maize-wheat-mungbean system	Dr. T.K. Das
14.	Sunil Mandi	10999	Ph.D.	Effect of summer green manuring and sulphur fertilization on productivity and nutritional quality of basmati rice (*Oryza sativa* L.), durum wheat (*Triticum durum* Desf.) sequence	Dr. Y.S. Shivay
15.	Ayesha Fatima	11218	Ph.D.	Livelihood security, resource budgeting and soil health management under integrated farming system in North-West India	Dr. V.K. Singh

Environmental Sciences

11

Prof. S. Naresh Kumar

The Centre for Environmental Science and Climate Resilient Agriculture (CESCRA), a multi-disciplinary Centre, has the mandate of conducting basic and strategic research for environment and climate resilient sustainable agriculture with a special emphasis on rainfed and small-scale farmers; to impart post-graduate education and training on agriculture-environment inter-relationships; to provide advisory and consultancy services on environment monitoring, assessment and climate change in agriculture**.** The research findings of post graduate students have been grouped under the following themes:

Theme 1. Global climate change and agriculture

Interactive effect of irrigation and temperature on growth and development of *Phaseolus vulgaris* L.: field and simulation study

To understand the physiological response of kidney bean to different moisture and temperature regimes a field study was conducted to i) quantify the interactive effect of elevated temperature and irrigation on the growth and yield parameters of kidney bean and ii) calibrate and validate a kidney bean model and apply it for quantifying the climate change effects on kidney bean in selected locations of India and Kenya. A field experiment, conducted during January-April of 2020 in the IARI, New Delhi Research Farm, with a total of 14 treatments of temperature and irrigation combinations, with i) elevated temperature during entire crop growth period at 4.6 ^{o}C , 3.1 ^{o}C and 2.8 ^{o}C over mean ambient (19.6 ^{o}C); and in the ambient field with iv) ambient temperature (AT, 25.9/13.4 ^{o}C), elevated temperature during pre-flowering (3.7 ^{o}C over 19.6 ^{o}C), flowering (5.3 ^{o}C over 23.1 ^{o}C) and pod filling phase (5.2 ^{o}C over 28.9 ^{o}C) all under two and three irrigation regimes. Results indicated hastening of phenological events in elevated temperature regimes, except when crop was exposed to elevated temperature during pod-filling phase. However, supplemental irrigation during pod-filling phase delayed physiological maturity. Crop exposed to continuous elevated temperature from sowing to physiological maturity had higher LAI and NDVI followed by plants exposed to high temperature during pre-flowering and flowering phase. Plants in treatments with supplemental irrigation maintained higher LAI and NDVI. Under continuous elevated temperature in entire crop period and those exposed to high temperature during pre-flowering showed higher net photosynthetic rate, transpiration rate, stomatal conductance and both instantaneous and intrinsic water use efficiency. Overall, total dry matter and seed yield at physiological maturity was highest in treatments under continuous elevated temperature compared to other treatments. Supplemental irrigation during pod filling phase led to higher total dry matter in plants. Plants exposed to high temperature during pre-flowering and flowering recorded lowest yield. The calibrated and validated kidney bean model could simulate days to 50% flowering (RMSE- 2 days, AI- 0.98), days to 50% physiological maturity (RMSE- 3 days, AI- 0.99), leaf area index (RMSE- 0.55, AI- 0.93), total dry matter (RMSE- 487 kg ha^{-1}, AI- 0.99) and seed yield (RMSE-223 kg ha^{-1}, AI-0.95) within acceptable level of accuracy. Simulation modelling based climate change impact analysis projected a yield change in the range of 5-60% over baseline yield for selected locations representing kidney bean growing areas in India and Kenya. Inter-annual variation in seed yield is projected to increase in all climate change scenarios of representation concentration pathways (RCP) 4.5 and 8.5 for most of the locations due to projected decrease in rainfall coupled with increased variability, in addition to increase in maximum and minimum temperatures despite CO_2 fertilization. It can be concluded that kidney bean cultivation at mean temperature of 24.2 ^{o}C led to higher yields than at lower temperatures. Temperature shocks of (>3^{o}C) during pre-flowering and flowering significantly reduced seed yield. Additionally, water stress with soil available water content 35% is projected to be more detrimental to kidney bean yield in future climates. Management options such as adjusting sowing time and provision of supplementary irrigation in addition to varietal improvement may be explored for minimizing the negative impacts of climate change on kidney bean.

Carbon storage in standing tree vegetation on campus ecosystem of IARI, New Delhi

A study to quantify the arboreal carbon storage of various tree species at Indian Agricultural Research Institute (IARI), New Delhi campus and to draw a comparative analysis for the same was completed through field survey, laboratory analysis and by implication of allometric equations. Two parameters namely tree height and diameter at breast height (DBH) of total 5,368 individual native trees belonging to 63 diverse species and 27 different families were used to calculate their above ground biomass (AGB), below ground biomass (BGB), carbon storage and CO_2 equivalent. The prominent carbon storing trees were identified as *Terminalia arjuna* (14.18 tons) > *Ficus religiosa* (11.62 tons) > *Eucalyptus tereticornis* (9.18 tons) > *Syzygium cumini* (7.14 tons) > *Azadirachta indica* (6.80 tons) > *Ficus virens* (5.72 tons) > *Dalbergia sissoo* (4.04 tons) as the carbon stock. The biomass and carbon storage potential of Combretiaceae family was found to be significantly higher than the other tree families. The girth of the tree was found to be positively correlated with carbon storage value of tree ($R^2 = 0.72$). Total 119.31 tonnes carbon is stored by 64 diverse tree species in IARI campus which is 436.83 tons in terms of CO_2 equivalent. Trees like *Terminalia arjuna, Ficus religiosa, Syzygium cumini, Azadirachta indica, Ficus virens* were found to store more carbon and better CO_2 sequestering trees. Therefore, these species should be preferred during afforestation and plantation programs of the area. Thus, protection and preservation of native trees of the IARI campus is crucial to maintain the carbon stock.

Optimizing growth and yield of greenhouse grown tomato: field and simulation study

To understand the impact of temperature shocks at various stages of open field grown tomato as well as to optimize climatic conditions for greenhouse grown tomato plants a study was conducted with objectives to i) quantify the growth, development, physiological response and yield of tomato to different temperature regimes under protected cultivation and in open field and ii) dynamically simulate the tomato growth and yield under open field and protected cultivation for optimization of micro-climatic conditions. Tomato variety NS-4426 was subjected to seven temperature treatments during November 2020 to June 2021 viz., three temperature regimes in greenhouse viz., i) +1.5, ii) +2.5 and iii) +3^{o}C over ambient, four temperature regimes in open field viz., iv) ambient (seasonal average 20 ^{o}C), v) elevated temperature during vegetative to pre-flowering phase (+2.9 ^{o}C over ambient mean during that period 11.08 ^{o}C), vi) during first flowering to fruit harvest phase I (+3.6 ^{o}C over 17.34 ^{o}C), and vii) elevated temperature during flowering and fruit harvest phases II (+5.25 ^{o}C over 26.52 ^{o}C) in RBD. Results indicated that the plants exposed to high temperature regime for an extended period of time in greenhouse took minimum days to complete the phenological phases and attained flowering stage10 days earlier, first harvest stage 23 days earlier and had extended growth for final harvest up to 199 days as compared open field grown tomato. Plants inside greenhouse had higher leaf dry weight, NDVI, instantaneous water use efficiency and fruit ascorbic acid and lycopene contents, while net photosynthetic rate and transpiration rate were lower in greenhouse grown tomatoes. Plants in open field conditions had higher LAI, fruit dry weight, cumulative fruit number per plant cumulative fruit weight per plant. Crop grown in greenhouse conditions had significantly lower fruit yield than in plants in ambient condition. Crop exposed to high temperature during vegetative to pre-flowering phase 14 ^{o}C mean gave highest fruit yield among all the temperature treatments owing to higher LAI and high photosynthetic rates. Tomato yield gets affected when the temperature range goes beyond 34 ^{o}C/13 ^{o}C for a prolonged period of time. Also high temperature stress coinciding flowering to fruit harvest phase I will cause significant yield loss. Following the experimentation, tomato model was calibrated to simulate the tomato plant's response to temperature regimes at various growth stages in terms of phenology, LAI (root mean squared error 0.78, agreement index 0.78), total dry matter (31.9 g plant^{-1}, 0.87) and fruit yield (267.7 g plant^{-1}, 0.96) with acceptable levels of accuracy. The calibrated model was used to run simulations to optimize the micro-climatic conditions. The analysis indicated that micro-climatic conditions of greenhouse should be set to 24 ^{o}C /10 ^{o}C with CO_2 concentration of 500 µmol mol^{-1} and PAR levels of 500 µ mol m^{-2} s^{-1} for obtaining higher productivity of tomato.

Impact of plant extracts and plant growth promoting microorganism on tomato crop yield and fruit quality

The impact of plant growth-promoting microorganisms (PGPM) and plant-derived extracts (PDE) was studied on tomato seed (var. Pusa Rohini) germination under low temperature and optimum temperature, as well as their effect on plant development, yield, and quality of tomato fruits under polyhouse and open field condition. Results revealed that moringa leaf extract (MLE) treated seeds showed higher seed germination percentage (+9%) and seedling vigour index (+149%) over untreated seeds under low temperature and higher seedling vigour index (+91%) over control under optimum temperature. The PDE such as MLE and aloe vera leaf extract (ALE) and PGPM such as *Bacillus subtilis*, *Trichoderma harzianum* and their co inoculation showed higher seedling vigour index under low temperature and optimum temperature. When they were applied to tomato plants in pots under ambient and poly house conditions with varying temperature, the PGPM and PDE significantly improved the growth attributes of tomato plants, while mitigating the deleterious effects of temperature variation on tomato crops. These inoculated plants showed increase in antioxidant enzyme (superoxide dismutase, peroxidase), proline, relative water content, leaf area, NDVI and on the other hand decreased electrolyte leakage and malondialdehyde. The fruit quality parameters such as ascorbic acid, lycopene, titratable acidity and total soluble solid (TSS) were also positively influenced by PGPM and PDE. In comparison to control, the MLE treatment showed better fruit quality parameters such as ascorbic acid content (+ 136%), lycopene content (+ 80%) and titratable acidity (+25%) under ambient conditions. ALE treatment under poly-house condition recorded 45% higher total soluble solid over control. The overall fruit yield was increased in *B. subtilis* (+ 1.1 times) treated plants under ambient condition and ALE (+ 0.56 times) treated plants under poly-house condition. Therefore, PGPMs and PDEs offer a promising mode that can be used to improve yield and quality of tomato fruit under changing climatic conditions.

Theme 2. Environmental pollution

Reducing ammonia volatilization using organic and inorganic amendments in wheat (*Triticum aestivum L.*)

In agricultural systems, applied N fertilizer to the crop is mainly prone to losses through ammonia (NH_3) volatilization, nitrate (NO_3^-) leaching, and denitrification causing negative effects on biodiversity, eutrophication, and nitrate accumulation in waters, acidification of soil and water bodies. To test the use of organic and inorganic amendments to reduce these losses, a study was conducted with an objective to unveil the effect of organic and inorganic amendments on NH_3 volatilization on the nitrogen use efficiency and productivity of wheat. Under this study, 10 treatments were applied in experimental RBD design, viz., T1 (Control with no recommended dose of nitrogen), T2 (RDN), T3 (RDN+ N-(n-butyl) thiophosphoric triamide (NBPT)), T4 (RDN + Hydroquinone (HQ)), T5 (RDN+ Calcium carbide (CaC_2)) T6 (RDN+ Vesicular Arbuscular Mycorrhiza (VAM)), T7 (RDN +*Azotobacter*), T8 (RDN +Garlic powder), T9 (RDN +Linseed oil), T10 (RDN + Pongamia oil). The highest volatilization losses were observed in T2 (RDN) of about 20.4 kg ha^{-1} $season^{-1}$. Significant reduction in NH_3 volatilization losses were observed in T3 (RDN+NBPT) by 40%, T4 (RDN + HQ) by 27%, and T8 (RDN +Garlic powder) by 17%. In all amendment added plots, it was observed that there was an increase in nutrient availability (N, P, K) and soil organic carbon. An upsurge in soil microbial activity was found in T7 (RDN +*Azotobacter*) and T6 (RDN+VAM). Soil urease activity was found decreased in plot receiving amendments i.e. NBPT (T3), HQ (T4), and CaC_2 (T5). The available N forms, mainly ammonical N (NH_4^+-N) and nitrate N (NO_3^--N), decreased from the plant tillering stage to the physiological maturity due to uptake and losses. The highest grain yield was observed in the T7 (RDN +*Azotobacter*) treated plot with 5.09 t ha^{-1}, and straw yield was increased in T4 (RDN + HQ). Thus, economically affordable inorganic and organic amendments to reduce N losses to minimize environmental pollution need to be explored. `

Effect of industrial gypsum from Linz–Donawitz (LD) slag on soil health and tomato yield

Linz–Donawitz (LD) slag is a by-product of the steel industry and rich in calcium-containing silicates and sulphates. It could be a good source of industrial gypsum with some modification to reduce the waste disposal problem in the steel industry. This can be a substitution of environmentally and economically problematic mined gypsum. A field experiment was conducted to evaluate the efficacy of LD slag-based gypsum as a substitute for mined gypsum. The effect of industrial gypsum assessed on soil health and fruit quality of tomato. Various combinations of both mined and industrial gypsum along with recommended dose N, P and K fertilizers were evaluated under field condition using tomato as test crop. Results show that the physico-chemical characteristics of soil such as electric conductivity, soil nutrients availability, dehydrogenase activity, microbial biomass carbon and organic carbon slightly improved with application of mined as well as industrial gypsum. Application of mined gypsum and industrial gypsum significantly increased the tomato fruit yield as compared to without gypsum treatment. In addition, industrial and mined gypsum application significantly improved the quality parameters of produce (vitamin C content, lycopene content, pectin content). Among the treatments combinations of recommended fertilizer along with 40 kg S as gypsum performs better for most of the analyzed parameters. However, results show that the difference in the effects for both industrial and mined gypsum are not significant, hence industrial gypsum from LD slag can be used as a substitute for mined gypsum in the agricultural field.

Effect of chelating agent treated LD-slag on growth and heavy metal accumulation in spinach (*Spinacia oleracea*)

LD-slag, a multi-nutrient by-product of steel industries, is used in agriculture as soil fertilizer and soil stabilizer, as it's a good source of various nutrients such as Ca, Fe, Cu and Zn. But the trace amount of heavy metal content present in the slag may likely to cause environmental issues. A study was conducted using different chelating agents for the reduction of heavy metal content in LD-slag and to study the effect of transfer of heavy metal from the treated and untreated slag into spinach. In this study, optimization was done using response surface methodology and the highest extraction efficiency for Cd and Pb removal was observed using concentration of 10 mM, liquid to solid ratio of 5:1 and shaking time of 60 minutes. Total of 12 treatments where applied using complete randomized design (CRD). The treatments were T1 (control), T-2 (RDF), T-3 (RDF+ untreated steel slag), T-4 (50% RDF + untreated steel slag), T-5 (RDF+ EDTA treated steel slag), T-6 (RDF + DTPA treated steel slag), T-7 (RDF+ EDDS treated steel slag), T-8 (RDF + CA treated steel slag), T-9 (50% RDF+ EDTA treated steel slag), T-10 (50% RDF+DTPA treated steel slag), T-11 (50% RDF+ EDDS treated steel slag), T-12 (50% RDF + CA treated steel slag). The highest reduction was observed while using the chelating agent EDDS followed by EDTA then DTPA and least extraction was observed using the citric acid. Among the 100% RDF + treated steel slag with different chelating agent there were no significant difference was seen. But there was a significant difference showed in between 100% RDF treated steel slag and 50% RDF treated steel slag with different chelating agents. The highest in case of number of leaves, fresh leaf weight per pot, leaf biomass was showed by T-7 (100% RDF + EDDS treated steel slag) followed by the T-5 (100% RDF + EDTA treated steel slag) then T-6 (RDF + DTPA treated steel slag) the least was observed in T-9 (50% RDF+ EDTA treated steel slag) among the 100% RDF amended with treated steel slag. The study showed no significant difference between the different treatments of treated steel slag and untreated steel slag with T-2(RDF) in case of different soil parameters. The heavy metal analysis showed the almost 98% of the heavy metal content in the treated and untreated steel slag along with 100% RDF and 50% RDF was present in the soil itself, while the shoot and root samples showed below the detectable limit of atomic absorption spectrophotometer (AAS) for Cd and Pb.

Study of microplastics (MPs) contamination in sludge amended agricultural soil

There are no standardized methods for extraction of microplastics (MP) from, that are soil commonly accepted within the scientific community. Different extraction methodologies lead to wide variation in estimations. To address this, a study was formulated to develop an efficient method for MPs analysis suitable for wide range of soil matrix and in parallel to assess the abundance and properties of MPs in sludge amended farm soils. Vis-NIR spectroscopy based method is developed with four different soil matrices belonging to Alfisol, Inceptisol, Mollisol and Vertisol and two different organic matter matrices; FYM and sludge. The developed method was found to be rapid, robust, accurate method for estimation of all three-density group of MPs (low, medium and high) with a prediction accuracy ranging from 1.9g MPs/kg soil (Vertisol) to 3.7 g MPs/kg soil (Alfisol). Two different multiple linear regression models were assessed and PLSR was found with better performance in terms of prediction accuracy and minimum quantification limit. The method avoids any complicated sample preparation steps except drying and sieving and acquisition of reflectance spectrum can be obtained within 18 econds with three replications. To have minimum quantification limit ranging from 1.9-3.7g/kg soil, this vis-NIR method is perfectly suitable for soil samples of plastic pollution hotspots like landfill sites. A second method is developed based on amalgamation of salt-based density-based floatation technique and oleophilic properties of plastics. Extraction through saturated NaCl allows extraction of low density microplastics and the second step with castor oil based separation allows recovery of any medium and high density plastic pieces present in soil and the overall efficiency of this method is 98.5%, most suitable for being applicable for all above six matrices and is being prescribed for low level of MPs polluted soil. Based on the second method, sludge was extracted and characterised for abundance of MPs in sludge sample with further identification through Raman spectroscopy which identified few selected pieces as polyethylene, polypropylene, polyurethane, polystyrene. Further, soils from six years old sludge experimentation field of IARI farm (Inceptisol order) was extracted and quantified. Amongst different doses of application the treatments comprising 22.4 and 33.6 t/ha sludge application rate/year was found to have 3 and 5 pieces of MPs/100 g soil. As of now, the sludge amendment in agricultural soils is found not alarming but continued used causes build-up of MPs in soil with possible transfer to food chain through plants.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Pauline Kimani	21059	M.Sc.	Interactive effect of irrigation and temperature on growth and development of Phaseolus vulgaris L.: Field and simulation study	Dr. S. Naresh Kumar
2.	Mayank Tiwari	21275	M.Sc.	Carbon storage in standing tree vegetation on campus ecosystem of IARI, New Delhi	Dr. Shakeel A. Khan
3.	Laltharmawll	21281	M.Sc.	Optimizing growth and yield of greenhouse grown tomato: Field and simulation study	Dr.S.Naresh Kumar
4.	Kokila M.	21276	M.Sc.	Impact of Plant Extracts and Plant Growth Promoting Microorganisms on Tamato Crop Yield and Fruit Quality	Dr. Anita Chaudhary
5.	Pooja L. R.	21277	M.Sc.	Reducing ammonia volatilization using organic and inorganic amendments in wheat (*Triticum aestivum L.)*	Dr. Renu Singh
6.	Shemeem Shah P.	21279	M.Sc.	Effect of Industrial Gypsum from Linz–Donawitz (LD) slag on soil health and tomato yield	Dr. Manoj Shrivastava
7.	Ajay M. V.	21280	M.Sc.	Effect of chelating agent treated LD-slag on growth and heavy metal accumulation in Spinach (*Spinacia oleracea*)	Dr. Renu Singh
8.	Priyanka Kumari	21278	M.Sc.	Study of Microplastics (MPs) contamination in sludge amended agricultural soil	Dr. Namita Das Saha

Microbiology

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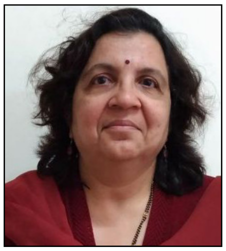

Prof. Radha Prasanna

The Division of Microbiology focuses on basic, applied and strategic research on microorganisms of agricultural importance. The Division is the national lead centre for advancing knowledge and understanding of the microbial domains for agricultural applications which includes utilization of microbial resources gene- and metabolite pool for plant growth promotion as well as protection, natural resource management and value addition of biomass. The mandates of the Division are to undertake research, teaching, and extension in the field of microorganisms useful in agriculture, environment and industry; to serve as the lead centre in the country and to decide national priorities for Agricultural Microbiology. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Microbe-mediated stress alleviation to sustain crop productivity

Pearl millet-*Azospirillum* interactions under moisture deficit conditions

Drought is the foremost and frequent abiotic pressure affecting plant growth and development and retarding agricultural productivity worldwide. Pearl millet, a 'Nutri-cereal' is the staple crop for a majority of people in the semi-arid and arid regions. Mainly grown under rainfed conditions, the crop faces various abiotic stresses including drought that impact plant growth and productivity. Microbial strategies have been advocated in alleviating the effect of abiotic stresses in several crop plants. In the scenario of water deficit stress, the use of PGPR adapted/ tolerant to osmotic stress can be of great importance in in designing bioinoculants for crops grown in stressed agricultural ecosystems. *Azospirillum formosense* strains AIM3, AIM 38, AIM57 and AIM82 previously isolated from rhizosphere of rainfed pearl millet were investigated for their PGP potential under moisture deficit conditions. The strains were first assessed for their growth and physiological responses under osmotic stress conditions (5, 10, 20 and 30% PEG6000). The growth of the cultures was not much affected at 10% PEG6000, however higher concentrations showed a significant negative effect on growth with drastic reduction at 30% PEG6000. Cells were elongated and highly motile under 0% and 10% PEG6000 and non-motile, round with thick exopolysaccharide layer under 20% and 30% PEG6000 conditions. The bacterial accumulation of proline and biofilm formation ability increased with increasing stress levels indicating osmoadaptation. All the five strains could express PGP traits (IAA production, biological nitrogen fixation and siderophore production) under all levels of PEG6000. However, expression of the PGP traits reduced with increasing stress levels with 30% PEG6000 being most detrimental. Seed germination bioassays indicated the positive effect of inoculation on seed germination, root hair density and lateral branching, shoot length and seedling vigour index under different levels of PEG6000. A pot experiment conducted to evaluate the effect of AIM3, AIM 38, AIM57 and AIM82 on the growth of pearl millet (*Pusa Composite 443*) under two water regimes (100% FC and 75% FC) showed positive effects of inoculation on plant growth parameters *viz.* root length, shoot length, root dry biomass, shoot dry biomass. Soil MPN studies indicated the establishment of inoculated strains in the pearl millet rhizosphere under both the conditions. Moisture deficit stress showed a negative effect on leaf chlorophyll and RWC. However, inoculation improved chlorophyll and RWC under both 100% FC and 75% FC. Inoculated plants showed higher leaf proline and sugar contents as compared to uninoculated controls. The activities of the antioxidant enzymes - catalase, ascorbate peroxidase, superoxide dismutase increased under stress conditions and inoculation with *Azospirillum* sp. strains further improved the antioxidant status of the plant. However, the inoculation effect was more prominent under stress conditions. Lipid peroxidation activity was substantially increased due to exposure to moisture stress condition. Inoculated plants also showed significant reduction in lipid peroxidation under 75% FC, resulting in better membrane stability index. To conclude, *Azospirillum* sp. strains exhibited responses and survival mechanisms under osmotic stress which could influence plant growth and physiological responses of pearl millet under stress conditions; this illustrates their potential as bioinoculants for semi-arid and arid region crops.

Characterization of PGP potential of actinobacteria for inducing tolerance to salt stress in rice

Among the various beneficial rice-microbial associations studied earlier, here in this present investigation we mainly focused on rice-actinobacteria interactions and characterization of PGP potential of Actinobacteria for imparting tolerance to salt stress. A total of 40-culturally characterized actinobacterial isolates which were earlier purified from exo-and endo-rhizosphere of rice were screened for their salt (NaCl) stress tolerance based on their growth on ISP-2 medium supplemented with 5%,7.5%,10%,12.5% and15% of NaCl concentrations and its corresponding osmotic potential (ΨS) of -2.667, -2.832, -3.449, -3.598 and -4.568. Out of the 40-actinobacterial isolates, 12 of the rhizosphere and 7 of the endophytic isolates were identified as tolerant to 10% NaCl (ΨS = -3.449) concentration. Three actinobacterial isolates each from rhizosphere (Tap14, Met26 and Ha10) and endo-rhizosphere (Tap1, Tap2V0 and Tap3b) were shown their growth with NaCl tolerance up to 12.5% (ΨS = -3.598) concentration. When all the 27-rhizosphere and 13 endophytic actinobacterial isolates were qualitatively screened for their plant growth promoting (PGP) traits under *in vitro*, number of potential isolates showing Ammonia production, Growth on N- free media, mineral P-solubilization, Siderophore production, HCN production, phytohormone (as IAA or indoles) production, Exopolysaccharide production and ACC deaminase activity were identified. Based on the results of screening, there were six potential rice-actinobacterial isolates selected for their salt stress tolerance potential with multiple PGPR traits. All these selected six-actinobacterial isolates were taxonomically identified through 16S rRNA gene sequencing of these isolates and results revealed to their closest type strains *viz*., Met24 as *Kitasatospora* sp., V04a as *Streptomyces tritolerans*, Humic11a as *Streptomyces* sp., Tap3c as *S. mutabilis*, Tap7 as *S. tendae*and Tap2V100 as *S. mediolani*. Using three different *in planta* experiments (Petri-dishes, growth-tubes and in pots) under salt (150 mM NaCl) stress condition, the seed bacterization/ inoculation effect of six-selected actinobacterial isolates were evaluated. The results of these experiments showed that there were significant improvements in the seed germination and seedling growth related parameters including the improved root architectural changes under salt stress (150mM NaCl) induced conditions. Further, the results of pot experiments showed that there was a significant improvements in the physiological stress tolerance related parameters like RWC, MSI and a two-fold or more increased free proline accumulation and at least one-fold or more increased total antioxidants content in the rice-leaves grown under salt stress imposed conditions in the actinobacterial inoculated plants under salt stress as compared to rice plants grown under normal (No-salt stress) conditions. The selected salt stress tolerant actinobacteria inoculated treatments clearly shown significant improvement for the adaptive responsive parameters to stress and imparting stress tolerance ability in the rice seedlings grown only under salt stress (150 mM NaCl) imposed conditions. Hence, it was concluded that the inoculation of salt tolerant actinobacteria having potential PGP traits can improve plant-growth promotion as well as impart stress tolerance through PGPR-Induced Stress Tolerance (IST) mechanisms and also by improved physiological adaptive responses to salt stress in rice.

Characterization and evaluation of bacteria from stressed habitats for enhancing thermo tolerance of mustard

Mustard is an important oilseed crop in India, and it is typically grown during the rabi season. As a result, extreme temperatures have a significant impact on its growth and yield. Thus, thermotolerant endophytic bacteria with plant growth-promoting activities can be used to enable plants to cope with high temperatures. High temperature stress tolerance of ten bacterial strains, initially isolated from soils exposed to high temperature stress and rhizospheric regions of the plants, were investigated. Two bacterial cultures with significant high temperature stress tolerance were chosen, along with one standard bacterial culture showing well-established plant growth promoting activity. Effect of high temperatures on their growth was determined by measuring protein content. The selected thermotolerant bacterial cultures *Bacillus* sp. strain MRD 17, *Bacillus aryabhattai* strain NSRSSS-1 and *Bacillus licheniformis* strain SSA 61 were characterized for PGP activities under high temperature stress conditions *in vitro*. PGPR activities studied were IAA production, GA production, P-solubilization, ACC deaminase activity. There was beneficial effect of high temperature on their IAA and GA production abilities and ACC deaminase activity. The selected cultures were evaluated for their effect on seed germination and seedling vigour under temperature stress conditions. Inoculation with all the three bacterial cultures improved seed germination and seedling vigour under high temperature stress condition. The stress levels of the seedlings under temperature stress condition were determined through ethylene production. Under both temperature regimes, there was a marked decrease in ethylene produced due to bacterial inoculation. For assessing the impact of selected thermotolerant bacterial cultures in alleviating temperature stress in mustard variety PUSA Karishma LES-34, a pot culture experiment was conducted under control (25°C) and high temperature stress conditions (35°C). Inoculation with the selected bacterial cultures significantly improved plant fresh weight under both the temperature regimes as compared to uninoculated control conditions. Inoculation had a beneficial effect on root system architecture and plant physiological parameters like RWC and MSI under both no stress and high temperature stress conditions. Photosynthetic parameters *viz.* chlorophyll content, chlorophyll *a* content, chlorophyll *b* content was significantly enhanced in inoculated plants under high temperature stress condition, whereas Fv/Fm ratio was enhanced only under no stress condition. Activity of antioxidative enzymes *viz.* catalase, peroxidase and superoxide dismutase were significantly enhanced in the inoculated plants under both the temperature regimes. Plant total ROS content and lipid peroxidation were significantly increased due to high temperature stress, however inoculation led to significant reduction in these parameters. Various plant biochemical attributes *viz.* proline, total sugars were significantly reduced and phenolics, amino acids were significantly enhanced in the inoculated plants under high temperature stress conditions. The response of inoculation with *Bacillus* sp. strain MRD 17 was markedly more under both no stress and high temperature stress conditions than that with the other two bacterial strains *B. aryabhattai* strain NSRSSS-1 and *B. licheniformis* strain SSA 61. However, for most of the parameters studied in the present investigation, the inoculated plants gave better response under both the temperature regimes. As a result, thermotolerant bacteria with plant growth-promoting activity can be utilized to alleviate high temperature stress in crops.

Theme 2. Biomass valorization and processing employing microbes

Demonstrating lignocellulolytic potential of actinobacteria for application in biomass processing

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

Optimization of protocol for enhanced production of phycobiliproteins from a selected *Nostoc* strain

From sixty *Nostoc* sp. cultures present in CCUBGA, ICAR-IARI, New Delhi, ten strains with cell doubling time of 40-100 h and excellent potential for the synthesis of phycobiliproteins (phycocyanin, phycoerythrin, allophycocyanin), were chosen for this investigation. A promising strain among these ten strains was chosen for further research based on phycobiliprotein accumulation at 15th as well as 30th day of growth phase. Furthermore, the chosen strain was kept under different light conditions, pH, di potassium hydrogen phosphate, and magnesium sulphate concentrations separately. At the 15th and 30th day of growth, phycobiliproteins concentration was measured in response to various treatments. At the 15th and 30th day of growth, phycocyanin and allophycocyanin content rose considerably under red light, but phycoerythrin content improved significantly under green light. The most acceptable pH value for increasing the synthesis of the three pigments during the 15th and 30th day of development was 8. Optimal phycobiliproteins synthesis was established at the recommended concentration of di potassium hydrogen phosphate as per chemically specified nitrogen free BG-11 medium. Further increase or decrease in this concentration cause the content of phycobiliproteins in the selected strain to decrease. However, magnesium sulphate at a concentration twice that of specified in the BG 11 medium was shown to be acceptable for increasing the output by the 15th day of development, whilst half the needed dose as per the BG 11 medium was found to be suitable by the 30th day of development. The current investigation found a promising *Nostoc* sp. strain in terms of phycobiliprotein synthesis and the capacity of the identified strain to scale up phycobiliprotein production in response to various environmental and nutritional variables. The identified strain can further be used to boost the synthesis of phycobiliproteins for commercial use in agricultural, pharmaceutical and cosmetic industries.

Theme 3. Plant-microbe interactions and C-N transformations

Assessment of the role of microbial glycoproteins for carbon sequestration in agricultural soil

Soil microorganisms are key agents determining the fate of soil C and aid in its sequestration. The assessment of the impact of agri-management on the microbial activities related to C sequestration was undertaken using two contrasting long-term agricultural managements in the rice-wheat rotation. The organic management included input of a combination of nutrient sources farmyard manure (FYM), vermicompost (VC) and biofertilizers (BF) in the rice -wheat rotation. The treatment VC+CR+BF had significantly higher ergosterol, peroxidase, phenol oxidase, FDA hydrolase activity, β-glucosidase activity & Xylanase activity implying higher fungal populations that are active in the mineralization and subsequent loss of the soil C. While FYM+CR+BF had significantly higher, water soluble phenolic content, SMBC, Melanin & Chitin content at 0-30 cm soil depth. a high degree of homology of these microbial metabolites with the SOM indicates superiority of this treatment with its potential to increase the soil labile C fraction. The long-term conservation agriculture (Rice - Wheat rotation) experiments included Zero tilled direct seeded rice (ZTDSR) and zero tilled wheat (ZTW) along with moong bean and input of respective crop residues. These were compared with the farmers practice conventionally tilled rice and wheat (CTR – CTW). (MR + ZTDSR) – (RR + ZTW) – (WR + mungbean) had significantly higher ergosterol content and β-glucosidase activity. ZTDSR – ZTW had significantly higher peroxidase activity, glomalin content and water soluble phenolic content, (WR + ZTDSR + BM) – (RR + ZTW)) had significantly higher phenol oxidase activity, MBC, melanin content & xylanase activity with respect to (CTR – CTW). Microbial community in ZT was fungal dominated as revealed by higher fungal metabolites/components (glomalin, melanin, chitins) that show homology to recalcitrant C pools. The (CTR – CTW) were dominated by aerobic microbial populations that accounted for the higher activities of oxidative enzymes resulting in loss of C as carbon dioxide. Zero tilled soils were found to aid the development of microbial community and their metabolites that are known precursors of recalcitrant C.

Influence of genotype on root nodule morphology and function in chickpea (*Cicer arietinum* L.)

Chickpea (*Cicer arietinum* L.) an important leguminous crop in the Indian subcontinent and is the second most widely grown crop globally. Chickpea is most commonly nodulated by species of *Mesorhizobium i.e. Mesorhizobium ciceri* or *M. mediterraneum,* however, several other *Mesorhizobium* species are also reported to establish symbiosis with root nodules of chickpea. The nodulation and nitrogen-fixing ability of rhizobia are affected by a variety of factors *viz* genotype, soil type and environmental conditions. As the nodule development and activity depends on legume-rhizobia interaction, it is important to understand that is there any difference in the nodule development and function of chickpea root nodules of different genotype with various *Mesorhizobium* strains. In the present investigation, inoculation effect of three mesorhizobial strains namely *Mesorhizobium ciceri*, *Mesorhizobiumm editerraneumm* and *Mesorhizobium* sp. were evaluated in chickpea genotypes (BG 372 and BG 3022). All *Mesorhizobium* strains used in this study produced IAA in the presence and absence of tryptophan. *M. ciceri*and *Mesorhizobium* sp. showed P-solubilization potential in NBRIP media. *Mesorhizobium ciceri* showed resistance against ampicillin at 2 ppm. Mesorhizobial inoculation has significantly improved plant growth in paper towel assay. Nodulation potential of these strains were evaluated in pot experiment. At early growth stages (seedling and vegetative phase), nodules were round and white colour, however, cylindrical and pinkish nodules were observed at flower initiation and 50 % flowering stage. Light microscopic images of chickpea root nodules confirmed that *Mesorhizobium* entry may be through root hair curling. V shaped bacteroids were observed in nodule thin sections. Nodule fresh weight was peak at 50% flowering with *Mesorhizobium* sp. inoculation in BG 372whereas in BG 3022, nodule fresh weight was more at flower initiation stage. *In-planta* acetylene reduction activity of chickpea root nodules showed higher activity with *Mesorhizobium* sp. with BG-372 genotype (1003.33 nmoles of C_2H_4 /mg fresh weight nodule / h) and *M. ciceri* with BG-3022 genotype (958.47 nmoles of C_2H_4 /mg fresh weight nodule / h) at flower initiation stage. N uptake in chickpea genotypes were significantly improved with mesorhizobial inoculation. The same trend was reflected in plant dry weight also. Our study gave the clear evidence that different *Mesorhizobium* strains vary with their performance and mesorhizobial inoculation effect differed with chickpea genotypes.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the Student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Jayasurya Anegundi	21301	M.Sc.	Pearl millet- *Azospirillum* interactions under moisture deficit conditions	Dr. Minakshi Grover
2.	Sonam Priyadarshani	21302	M.Sc.	Demonstrating lignocellulolytic potential of actinobacteria for application in biomass processing	Ms. Anju Arora
3.	Kavya T	21303	M.Sc.	Characterization of PGP potential of Actinobacteria for inducing tolerance to salt stress in rice	Dr. V. Govindasamy
4.	Kiruthika A	21304	M.Sc.	Characterization and evaluation of bacteria from stressed habitats for enhancing thermotolerance of mustard	Dr. Sangeeta Paul
6.	Manoj M	21305	M.Sc.	Assessment of the role of microbial glycoproteins for carbon sequestration in agricultural soil	Dr. Geeta Singh
7.	Ashwani Dhingra	21306	M.Sc.	Influence of Genotype on root nodule morphology and function in chickpea (*Cicer arietinum* L.)	Dr. K. Swarnalakshami
8.	Pulkit Chawla	21373	M.Sc.	Optimization of protocol for enhanced production of phycobiliproteins from a selected *Nostoc* strain	Dr. O.N. Tiwari

Soil Science and Agricultural Chemistry

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Prof. S.P. Datta

The Division of Soil Science and Agricultural Chemistry has the mandate to carry out research on the fundamental and applied aspects of the physical, chemical and biological properties of soil; fertilizers and manures and their interaction with soil and plant; improvement and maintenance of soil fertility for sustained optimum agricultural production; utilization of organic residues (wastes) as a manure and production of biogas as fuel; soil test crop response correlation studies; advice to the farmers on soil test-based fertilizer recommendations. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Carbon sequestration potential and dynamics in Inceptisol

Assessment of carbon sequestration potential and stability of soil carbon in rice-wheat cropping systems of Indo-Gangetic plains

Long term effect of manuring and fertilization on maximum carbon carrying capacity (C_m), C saturation deficit (S_d), physical and biochemical stability of SOC were studied in three Inceptisols with varying texture and mineralogical makeup under rice-wheat cropping systems of the upper, middle and lower Indo-Gangetic Plains. The soil samples were collected in the year 2015 to a depth of 0-15, 15-30, and 30-60 cm from the ongoing field trials of All India Coordinated Research Project (AICRP) on Integrated Farming System (IFS) located at Kanpur (Uttar Pradesh, since the year 1984), Varanasi (Uttar Pradesh, since the year 1985), and Kalyani (West Bengal, since the year 1986). The treatments comprised of control, 100% NPK- fertilizer, 50% NPK + 50 % N-FYM, 75% NPK + 25% N-FYM, 50% NPK + 50% N-straw (wheat straw in Kanpur and paddy straw in Varanasi and Kalyani), 75% NPK + 25% N-straw, 50% NPK + 50% N-Green manure (GM with *Sesbania aculeata* L.) and 75% NPK + 25% N-GM . The C_m and S_d of soils were estimated by using the C saturation model. The conjoint application of 50% NPK + 50% N through straw emerged as the best treatment in terms of increasing SOC contents by 57% and 77% over control at Kanpur and Varanasi, respectively. In Kalyani, 50% NPK + 50%N-FYM emerged as the best treatment in increasing SOC content by 50% over control in the surface layer. The maximum C carrying capacity (C_m) was observed to be highest in Kalyani (48.5 Mg ha^{-1}) followed by Kanpur (43.1 Mg ha^{-1}) and Varanasi (32.4 Mg ha^{-1}). The SOC stock in 0-60 cm soil depth ranged from 20.8-33.2 Mg ha^{-1} in Kanpur, 28.6-39.0 Mg ha^{-1} in Varanasi, and 27.1-47.5 Mg ha^{-1} in Kalyani under various treatments. The activation energy (A_e) was relatively higher in microaggregates than macroaggreates which indicates higher stability of C in microaggregates. In the 50% NPK + 50% N-FYM treatment, prediction of SOC buildup by DNDC and C saturation model was closest with the difference of only 1, 2, and 6% at Kanpur, Varanasi, and Kalyani, respectively. Overall, 50% NPK + 50% N-PS treatment showed maximum C sequestration potential (CSP) at Kalyani, 75% NPK + 25% N-WS treatment at Kanpur and 75% NPK + 25% N-GM treatment at Varanasi.

Soil organic carbon dynamics under varying tillage, residue and nutrient management in an Inceptisol under maize-wheat cropping system

The study aimed at assessing soil organic carbon (SOC) dynamics under a CA-based maize (*Zea mays*)-wheat (*Triticum aestivum*) system in the Indo-Gangetic Plains (IGP). Soil samples from two depths (0-5 and 5-15 cm) were collected from an on-going CA field experiment on tillage, residue and nutrient management under maize-wheat cropping system established in 2016-17 at the research farm of Indian Agricultural Research Institute (IARI), New Delhi. The field experiment was laid in a split-plot design having four tillage and residue options in the main plots (CTNR: conventional tillage; CTCR: conventional tillage with residue retention @ 3 t ha^{-1}; ZTNR: zero tillage; ZTCR: zero tillage with residue retention @ 3 t ha^{-1}), and four nutrient management options in the sub-plots (STB: soil test-based recommendation, NE: nutrient expert based, STB+GS: soil test-based recommendation with green seeker and NE+GS: nutrient expert and green seeker). Results indicated significant improvement in labile C pool, total SOC, total SOC content and total carbon (TC) content due to tillage, residue and nutrient management. Treatment ZTCR had highest labile carbon in both depths, while lowest was in CTNR. Recalcitrant carbon fraction was lowest in CTNR in the 0-5cm depth. In nutrient management options, STB treatment had the lowest labile carbon, while NE+GS had the highest labile carbon (2.13 g kg^{-1}) in the 5-15 cm layer. Total SOC concentration, total SOC content and TC content were highest under ZTCR in both depths, while lowest was under CTNR. Among nutrient management practices, NE+GS had the highest values of aforementioned parameters and STB had the lowest values in both depths. Microbial biomass carbon (MBC) was significantly enhanced with adoption of ZT and residue retention, more prominently in the 0-5 cm depth.Dehydrogenase activity (DHA) was significantly affected in the 0-5 cm depth only with ZTCR being the treatment with highest DHA and CTNR the lowest. Residue retention along with ZT had significant impact on proportion of macro-aggregates. ZTCR had the highest macro-aggregates proportion in both depths, and among nutrient management NE+GS had the highest macro-aggregates proportion in both depths. In case of nutrient management, NE+GS treatment had highest glomalin (90.1 μg C g^{-1}) which was significantly higher than NE and STB in the 0-5 cm layer. ZT along with residue addition led to maximum amount of macro-aggregate and micro-aggregate associated C in ZTCR in both soil depths, while nutrient management had no significant impact. Residue retention and nutrient management had no significant effect on temperature sensitivity of SOC mineralization (Q_{10}) in the 0-5 cm soil depth, but zero tillage treatments had lower Q_{10} than CT.

Effect of engineered biochar on nutrient retention in an Inceptisol

Fourteen engineered biochars were prepared by treating the washed rice straw biochar (RBC_W) separately with different oxidizing agents (O_3 and $KMnO_4$), acid (H_2SO_4 and HNO_3), alkali (NaOH) to enhance the CEC and different reducing agents ($FeCl_3$-HCl and FeOOH) to augment the anion exchange capacity (AEC). After that the combined treatments of the oxidising and reducing agents were given to further reinforce the CEC and AEC of engineered biochar. Then in a screening experiment, depending upon the removal efficiency and adsorption capacity for NH_4^+-N, NO_3^--N, P, and K, three promising engineered biochars namely RBC_W treated with O_3-$FeCl_3$-HCl (RBC_{OCl}), H_2SO_4-HNO_3-$FeCl_3$-HCl (RBC_{ACl}), and NaOH-FeOOH (RBC_{OHFe}) were chosen for further characterization and soil leaching-cum retention study. Results indicated that $RBC_{OCl,}RBC_{ACl}$ and RBC_{OHFe} recorded 66.4, 45.5 and 27.6% increase in CEC over RBC_W, respectively. Moreover $RBC_{OCl}RBC_{ACl}$ and RBC_{OHFe} recorded the AEC of 58.11, 47.1 and 34.7 meq kg^{-1}, respectively which was significantly higher over RBC_W (AEC 26.6 meq kg^{-1}). FTIR spectral analysis revealed the presence of carboxylate, amino, OH, lactone etc. groups on biochar surface (previously absent in RBC_W) which significantly contributed to enhance CEC, AEC of the engineered biochars. From the soil column-based leaching-cum retention experiment, it was observed that all the engineered biochars reduced the leaching of NH_4^+-N, NO_3^--N, P and K and increased their retention from/in an a sandy loam Inceptisol (Typic Haplustept) of Delhi. Based on the above observation, it can be concluded that among the screened engineered biochars, RBC_{OCl} at the rate of 4.46 g kg^{-1} (D2) emerged as the promising soil amendment for increasing the retention of NH_4^+-N, NO_3^--N, P and K by 33.7%, 27.8%, 15% and 5.74% as compared to RBC_W-D2. Overall, the application of biochar at of higher dose (D1-2.23 g kg^{-1}) was superior over lower dose (D2-4.46 g kg^{-1} for retaining nutrients in soil. The study has greater implications on enhancing nutrient use efficiency by the crops, carbon sequestration, reduce the loss of costly chemical fertilizers leading to environmental pollution.

Theme 2. Assessment of soil quality

Long term effect of fertilization and manuring on soil quality under rice-mustad-sesame cropping system

Long-term effect of fertilization and manuring on soil quality under rice-mustard-sesame cropping system was evaluated. For this purpose, soil samples were collected from six treatments (control, NPK- recommended doses of fertilizer (RDF), NPKG – 50% RDF + green manuring, NPKGB - 50% RDF + green manuring + biofertilizer, NPKF - 50% RDF + FYM@ 7.5 t ha^{-1}, FB - FYM@ 11.25 t ha^{-1} + biofertilizer) at 0-15, 15-30 and 30-45 cm soil depth of ongoing 22 years long-term experiment (1998-2020) under All India Co-ordinated Research Project (AICRP) on Soil Test Crop Response Correlation (STCRC) with rice-mustard-sesame cropping system of Gayeshpur Research Farm of Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal. Results revealed that 22 years of continuous balanced application of synthetic fertilizers and organic inputs such as FYM, biofertilizer and green manures significantly improved physical, chemical and biological properties of soil at all the soil depths however, magnitude of such increase was greatest at surface (0-15 cm) under NPKF and FB treatments. A gradual reduction in microbial activity, physical stability and bioavailability nutrients was observed with depth. Equivalent yield of rice (ERY) was found to be maximum under NPKF treatment followed by NPKGB and NPKG treatment. For developing soil quality index (SQI), two approaches were followed, conceptual Framework (CF) and principal component analysis (PCA) under productivity (P) and environmental protection (EP) management goal. The key indicators selected under productivity goal were: available Fe, sulphur, boron, pH and bulk density and under environmental protection goal were total organic carbon, boron, qCO_2, pH and sulphur through PCA analysis for their inclusion in Minimum Data Set (MDS). Both under CF and PCA, the highest value of SQIs was obtained under NPKF as well as FB treatments. CF based SQI was varied between 0.93-0.46 under productivity goal and 0.93 to 0.42 under environmental protection goal. Whereas, PCA based SQIs yielded greater variation than CF based SQIs where PCA-SQI-P and PCA-SQI-EP stretched between 0.98-0.34 and 0.95-0.45, respectively. MDS variables were able to explain 89% variation in yield when validated against ERY through multiple regression analysis. Also, better agreement was found between CF and PCA based indexing method under both productivity ($R^2 = 0.94$) and environmental protection ($R^2 = 0.95$) management goal. Thus, PCA analysis emerged as a powerful tool for creating MDS for selection of key indicators of soil quality and weighted additive indexing method with linear scoring function was able to differentiate management induced changes in soil quality. Therefore, in view of limited availability of organics and yield sustainability, NPKF treatment may be recommended for rice-mustard-sesame cropping system in Inceptisol of lower IGP.

Labile organic carbon and biological soil health indicators under conservation agriculture-based rice-wheat cropping system in an Inceptisol

An attempt has been made to assess labile organic carbon and biological soil health indicators under conservation agriculture-based rice-wheat cropping system in an Inceptisol. Soil samples were collected from six treatments viz. (ZTDSR-ZTW, ZTDSR + WR – ZTW + RR, ZTDSR + WR + SBM – ZTW + RR, ZTDSR-ZTW – ZTMB, ZTDSR + MR – ZTW + RR – ZTMB + WR, TPR – CTW- CTMB) of three soil depth 0-5, 5-15 and 15-

30 cm of 10 years old CA based experiment with rice-wheat located at IARI Research Farm. The result revealed that residue retention had 19%, 19% and 33% more Walkley-Black carbon (WBC) in the surface layer of soil in rice residue (RR) + wheat residue (WR), rice residue (RR) + wheat residue (WR) + sesbania brown manuring (SBM) and rice residue (RR) + wheat residue (WR) + mungbean residue (MR), respectively. The biological parameters like enzymatic activities of dehydrogenase (DHA), fluorescein di-acetate hydrolase (FDA), acid and alkaline phosphatase (ACP and ALKP), β-glucosidase (GLSD), amidase and urease were generally higher in the plots under residue retention, mostly in the triple residue retention (RR+WR+MR). Microbial population like bacteria, phosphate solubilizing bacteria (PSB), Non symbiotic N_2- fixing bacteria (NFB), cellulolytic bacteria (CLB) were higher in the plot under RR+WR+MR residue retention, whereas fungi and actinomycetes were higher in the triple ZT without residue retention plot. PCA analysis was done to screen out key indicators of biological soil health and β-glucosidase (PC1), *Bacterial amoA* (PC2), *Archaeal* 16S (PC3), *Bacteroidetes* 16S (PC4), *Bacterial* 16S (PC5), Mineralizable C (PC6) were selected. β-glucosidase had the highest contribution in the biological soil health index (BSHI). The highest BSHI was found in triple ZT with residues treatment. The decreasing trend of BSHI was T5 (0.80)>T2 (0.76)>T4 (0.72)>T1 (0.62) >T3 (0.55)>T6 (0.28). The correlation matrix revealed that there was very well correlation among the labile fractions of SOC as well as with the biological health indicators. Regression analysis between the WBC and biological health indicators also supported the well agreement between them. ZTDSR + MR– ZTW + RR – ZTMB + WR treatment maintain higher labile pool of SOC as well as better biological health under CA based rice-wheat cropping system.

Theme 3. Synthesis and evaluation of novel fertilizer products

Synthesis and evaluation of novel nitrogenous fertilizer products for enhancing nitrogen use efficiency

Novel N fertilizer products, viz. nano clay bio polymer composites and coated urea were synthesized and evaluated for enhancing the nitrogen use efficiency. In both the water and soil the newly synthesized products had significantly lower N release than that of normal urea. Also, the novel N fertilizer products had significantly lower nitrate leaching than that of urea. These products were also tested in the field to assess the effect of applied nitrogen through newly synthesized products on yield and nitrogen uptake by maize along with NCPC and urea. The application of 75% N through the newly synthesized N products resulted in statistically similar grain yield, stover yield and biological yield as well as similar root morphology as that of 100% N through urea. Seventy-five per cent N supply through maize NCBPC product recorded statistically at par grain N content and total N uptake with that of 100% N through urea. The N supply through the newly synthesized products also improved the NUE in maize.

Synthesis and evaluation of urea loaded nanoclay biopolymer composites for enhancing nitrogen use efficiency in rice

A greenhouse pot culture experiment was carried out in plant phenomics with five rice genotypes (Swarna, Pusa-44, PB-1, MTU 1010 and N-22) to study the effects of nanoclay biopolymer composites (NCBPC) fertilizers on crop yield, nutrient uptake, nitrogen availability in soil and phenotypic traits of different rice genotypes. The NCBPCs were synthesized based on three different types of polymers (wheat flour, maida) and acrylic acid plus acrylamide via free radical polymerization. Results revealed that NCBPCs were participated in the graft polymerization reaction with acrylic acid and the bentonite layers were exfoliated and dispersed in the polymer network on a nanoscale after the polymerization. Nano clay polymer composites (NCPCs) as well as composites

(NCBPCs) possess slow release properties for nitrogen. Among NCBPC products, NCBPC prepared with maida releases N slowly than NCBPC prepared with wheat flour as a biopolymer. The result of greenhouse experiment indicated that the application of 75 % N through NCBPC products recorded significantly higher grain and straw yield than that of 100 % N through urea. Among the three polymer composites, the NCPC treatment showed higher apparent recovery efficiency (ARE) (51%), followed by NCBPC (maida) (45%) and NCBPC (wheat) (38%). Among varieties, the best variety in terms of N use efficiency was Swarna whereas; Nagina 22 was least N responsive variety irrespective of N fertilizer sources. The effect of NCBPCs treatments on phenotypic traits of the rice plant was confirmed after the image processing under phenomics facility. Plant leaf area, convex hull area and plant height was also increased significantly under different N treatments over control, which was recorded through visual light imaging. The hyper spectral data obtained using spectroradiometer was used to calculate two different spectral indices as NDRE and NPCI. The maximum variation for both the indices NDRE and NPCI was recorded at 70 DAT stage. The maximum R^2 value for NDRE was 0.69 and for NCPI the R^2 value was 0.63 with grain yield obtained from power regression model and exponential regression model respectively. Thus, NCPC and NCBPC products loaded with urea were more effective over conventional N fertilizers in terms of increasing yield, nitrogen uptake, agronomic use efficiency and apparent nitrogen recovery, as well as retaining more mineral nitrogen in soil which was also supported by different parameters obtained from phenomics facility.

Theme 4. Enhancing phosphorus and potassiunm supply capacity of soil

Soil phosphorus fractions and their contribution in phosphorus nutrition of wheat under long-term fertilization and manuring

A long-term field experiment continuing since 1971 on a (*Typic Haplustept*) at the research farm Indian Agriculture Research Institute, New Delhi was chosen to study the soil P fractions and their contribution in P nutrition of wheat under long-term fertilization and manuring. The treatment details were; Control (unfertilized), N (recommended N), NP (recommended NP), NPK (recommended NPK), 150% NPK (150% recommended NPK), NPK+FYM (recommended NPK+5 t FYM ha^{-1}), and NPK+Zn (recommended NPK+ 5 kg Zn ha^{-1}). Results revealed that highest wheat grain yield of 5.74 t ha^{-1} was obtained under 150% NPK which was statistically on par with NPK+ FYM, NPK +Zn and NPK treatments. Similarly, highest P uptake was recorded under 150% NPK followed by NPK + FYM. Lowest grain yield (1.93 t ha^{-1}) and total P uptake (14.7 kg ha^{-1}) was recorded under unfertilized (control). At 0-15 cm soil depth the labile form of P, $NaHCO_3$-Pi and $NaHCO_3$-Po, were significantly greater under treatment receiving 150% NPK. Water extractable P and NaOH-Po were in the range from 6.67 to 15.1 mg kg^{-1} and 44.4 to 82.1 mg kg^{-1}. Highest water extractable P and NaOH-Po were observed under NPK+FYM followed by 150% NPK. The non-labile P forms, HCl-P and residual P, showed highest values under 150% NPK and lowest under control at 0-15 cm soil depth. Similarly at 15-30 cm depth, $NaHCO_3$-Pi (6.04 mg kg^{-1}), $NaHCO_3$-Po (38.1 mg kg^{-1}), NaOH-Po (50.3 mg kg^{-1}), HCl-P (119 mg kg^{-1}) and residual P (179 mg kg^{-1}) were highest under P fertilizer application at super-optimal rate (150% NPK). Water extractable P (14.0 mg kg^{-1}) and NaOH-Po (69.0 mg kg^{-1}) were highest under NPK+FYM treatment. Available P content in soil at initial stage (sowing) ranged from 13.5 to 39.8 and 15.4 to 37.9 kg ha^{-1} at 0-15 cm and 15-30 cm depth, respectively. At the tillering stage, available P was 20.7 to 43.7 and 16.5 to 38.1 kg ha^{-1}, and at panicle emergence, it was 24.1 to 48.4 kg ha^{-1} and 18.6 to 42.3 kg ha^{-1} at 0-15 cm and 15-30 cm depth, respectively. At harvest of wheat, available P ranged from 20.5 to 41.8 and 16.5 to 39.1 kg ha^{-1} at 0-15 cm and 15-30 cm depth, respectively. Availability of P in soil at different stages of wheat was highest under NPK+FYM treatment compared with control and N alone.The effect of fertilizer and manures application on fixation and release measured as change in Olsen-P content, revealed that in control there was no change in available P at in 0 to 30 days and 30 to 60 days after incubation. P fixation and release was significantly increased during 0 to 30 days and the highest values of Olsen-P were observed in the soil from 150% NPK, with application of P+FYM during. With the increasing the time of incubation from 30 to 60 days, P fixation and release in soil decreased under all treatments.The $NaHCO_3$-Pi, water extractable-P and $NaHCO_3$-Po at 0-15 cm soil depth were positively and significantly correlated with wheat grain yield (r-values 0.76**, 0.70**, and 0.51**), respectively and total P uptake (r-values 0.82**, 0.79** and 0.62**) respectively. Similarly at 15-30 cm depth, $NaHCO_3$-Pi and water extractable-P were positively and significantly correlated with wheat grain yield (r-values 0.67** and 0.52**) and total P uptake (0.72**, and 0.64**). Multiple regression equations between yield, P uptake and various organic and inorganic P fractions of soil also indicated that $NaHCO_3$-Pi and water extractable-P were the important fractions of inorganic P, which contributed substantially towards wheat yield and total P uptake.

Effect of silicon rich crop residues on available phosphorus in soils

Effect of silicon rich crop residues on available phosphorus in soils was assessed in two different soils namely, alkaline IARI soil (pH 8.30 and available P content 12.4 kg ha^{-1}) and calcareous Bihar soil (pH 8.6 and Olsen-P content 13.6 kg ha^{-1}). Two Si rich crop residues i.e., rice straw (6.76% Si) and sugarcane leaf (2.65% Si) and one water soluble salt i.e., sodium silicate were used as source of Si. A greenhouse experiment was conducted to assess the impacts of applied Si on available P to wheat crop (variety HD 2967) in IARI soil. Results of P release study revealed that application of Si through various sources significantly enhanced 0.01 M $CaCl_2$ extractable P in both soils. Sodium silicate performed superior as compared to rice straw and sugarcane leaf in both release study and greenhouse experiment. In greenhouse experiment, average Olsen-P content was significantly enhanced from 6.88 mg kg^{-1} in control to 7.46 and 7.78 mg kg^{-1} under 50 and 100 mg kg^{-1} of applied Si. All the three Si sources significantly and positively affected growth parameters of wheat like straw yield, grain yield, straw P uptake and grain P uptake.

Phosphorus dynamics under conservation agriculture based maize-mustard system in an Inceptisol

Phosphorus dynamics under conservation agriculture-based maize-mustard system in an Inceptisol was studied. For this purpose, soil samples were collected after maize harvest from the on-going conservation field experiment started from 2010-11 at ICAR-IARI, Pusa, New Delhi with randomized block design, comprising of four double cropping zero-till and two triple cropping zero-till systems with or without crops residue retention along with two conventional till systems [T1: ZTMZ-ZTM; T2: ZTMZ+BM-ZTM; T3: ZTMZ(+R)-ZTM(+R); T4: ZTMZ(+R)+BM-ZTM(+R); T5: ZTMZ-ZTM-ZTSMB; T6: ZTMZ(+R)-ZTM(+R)-ZTSMB(+R); T7: CTMZ-ZTM; T8: CTMZ-CTM] with three replications. Results showed the significant improvement in organic carbon in triple zero tillage with residue retention. Highest and lowest value of mineralizable N, available K in both the soil layers as well as available P in the surface soil layer were observed in T6 treatment [ZTMZ(+R)-ZTM(+R)-ZTSMB(+R)] and T8 treatment (CTMZ-CTM) respectively. Fractionation study revealed that Ca-bound was the highest fraction, followed by residual fraction. The zero tillage with residue retention significantly increased the WSP and $NaHCO_3$ extractable fraction (labile P) in both 0-5 cm and 5-15 cm soil layers. Total P as well as MBP was observed to be maximum in T6 treatment, whereas lowest values were recorded in T8 treatment. Adsorption-desorption study revealed that that there was a reduction in adsorption capacity in triple zero tillage with residue retention plot when compared to conventional tillage plot. Desorption index values denoting the hysteresis property of soil under different tillage and residue management options ranged between 0.829 and 0.922. Thus, it can be concluded that adoption of CA significantly increased labile P fraction and greater advantage was noticed with retention of legume residue.

Isolation of potential potassium solubilizers and their impact in enhancing the availability of potassium from waste mica treated soil

An attempt was made to utilize waste mica mineral as source of K nutrition modified suitably by K solubilizing bacteria (KSB). Areas near mica mines of Jharkhand was ventured to isolate, characterize and identify potential KSB and an incubation experiment was conducted in laboratory to assess its impact on release of different K fractions in presence of mica and crop residue. Eight bacterial strains were isolated from mica mining areas of Koderma, Jharkhand exhibiting K-solubilizing abilities. Out of eight, two isolates (JHKSB1 and JHKSB4) were selected as potential K-solubilizers based on their high K-solubilizing ability and used for incubation and pot culture experiments. Results emanated from incubation experiments showed that waste mica (<2 mm size) treated with KSB and rice residue (@ 2 g kg^{-1}), maintained higher levels of water-soluble K, exchangeable K and non-exchangeable K. The release was minimal up to 30 days after incubation but increased considerably from 60 to 120 days after incubation and the change was predominantly observed in case of water soluble and exchangeable K as compared to non-exchangeable K. Both JHKSB1 and JHKSB4 were at par with each other in their effect on K solubilization. Pot culture experiment with wheat as test crop also testified that application of waste mica along with KSB and/or crop residue significantly improves yield parameters. The biomass yield in wheat crop under the influence of all the three factors was 26.6 per cent higher as compared to absolute control. Comparable yield and K uptake by wheat was obtained in both the doses of mica application *i.e.* @ 50 mg kg^{-1} soil and @ 100 mg kg^{-1} soil. Application of crop residues alone increased biomass yield by 17.8 per cent over no residue treatment. Significant and positive impact of application of waste mica, continued to be observed in rice in terms of K availability. Relative agronomic efficiency and per cent K recovery by wheat and rice crop in treated soils were higher as compared to absolute control but was on an average half as effective as that of standard K-fertilizer (muriate of potash). Evidence of dissolution of some portion of mica at the edges through images of scanning electron microphotographs, indicated morphological changes of mica due to microbial solubilization. It can be thus be concluded that application of mica treated with rice residue and/or K-solubilizers has the potential to improve available K status of soil with time and may therefore be considered for use in K deficient soils and help in reducing the demand of costly K-fertilizer.

Theme 5. Assessment and remediation of metal and metalloid polluted soils

Assessment of heavy metals in contaminated soils using visible and near infrared reflectance spectroscopy

This study aimed at characterization of metal and metalloid contaminated soil in sewage irrigated agricultural lands using hyperspectral reflectance spectroscopy. The soil sampling was done from five different places *viz.*, Keshopur and Madanpur khadar, New Delhi; Burnawa and Surana, Uttar Prdesh; Debari, Rahjasthan; Nadia, West Bengal and Sonepat,Haryana with a total of 136 samples from surface (0-15 cm). Soil hyperspectral data were collected using ASD spectroradiometer in the spectral range of 350-2500 nm at 1 nm interval. The prediction models like linear multivariate regression (PLSR) and non- linear machine learning (ANN and SVM) were applied in the two study sites for quantitative assessment of soil heavy metals from ASD spectral data and analysed soil parameters. The performances of these models were evaluated on the basis of statistical parameters R^2, RMSE and RPD. The analytical results of pearson's Correlation Coefficient, principal component analysis and hierarchical clustering analysis in comparison with the correlation between the ASD reflectance and metal parameters suggest that Walkey-Black carbon and clay content had a significant impact on the heavy metals to generate the reflectance spectra. Besides, soil heavy metals of Keshopur and Madanpur khadar soil samples were not individually independent to be detected in predictive models. The sites were found to significantly high as environmental risk for the metal Cd, pollution level index suggested the sites crossed the threshold limit to be contaminated, whereas the contamination factor suggested considerable risk for the Cd and As. The analytical outcome of the predictive models suggests that Support Vector Machine (SVM) was more effective at 10 nm resampled wavelength reflectance data over the Partial Least Square Regression (PLSR) Model for prediction of heavy metals As, Pb, Cd and Mn with R square values of 0.55, 0.47, 0.64 and 0.90, respectively; with moderate to poor prediction for Zn, Cu, Cr and Ni. The overall performance can be justified by the fact that SVM is less affected by data transformation and spectralNoise. The reason for poor prediction by ANN and PLSR lies on the intricate relationships between the soil heavy metal content and other soil properties. It can be concluded that SVM model can be used as a promising tool for non- destructive, cost effective and rapid analysing of soil heavy metal content with the Vis- NIR spectral reflectance data of soils. Further research in this field is required for enhancing the efficiency of the prediction models using different algorithms.

Immobilization of arsenic in soil using functionalized clays

Arsenic sorption capacity of inorganic (iron modified kaolinite, iron modified bentonite and iron modified redmud) and organic (dimethyl sulfoxide intercalated kaolinite and dimethyl sulfoxide intercalated bentonite) modified clays and redmud, as well as effectiveness of modified clays for arresting the transfer of As from soil to plant were studied. The adsorption-desorption of arsenic onto screened unmodified and modified clays and redmud products was investigated at various equilibrium times, temperature levels and pH levels. Results indicated that incorporation of functional groups and increasing surface area of modified products increased arsenic sorption. Modification of kaolinites, bentonites and redmud resulted in changes in interlayer space. Fe-bentonite and DMSO-bentonite and Fe-redmud were the most effective among the all-modified clays and redmud. The adsorption of arsenic on modified clays and redmud was higher at low pH. The modified clays and redmud had less adsorption at high temperatures (35 °C) and pH (8.0). Whereas, the amount of arsenic adsorption (µg g^{-1} of absorbent) was high at 25 °C temperature. Due to application of modified clay and redmud products @ 2.50 and 5.00 g kg^{-1} to mustard crop, yield parameters such as leaf biomass, grain yield, stem weight, biological yield and root volume were improved. The hazard quotient (HQ) for leaves of Mustard was significantly reduced in the amended soils, indicating that arsenic was effectively immobilized in soils by using modified clay and redmud products.

Sorption-desorption behaviour of arsenic on clay-organic complex in an Alfisol and Inceptisol of Jharkhand

A laboratory batch experiments was carried out to study the sorption-desorption behaviour of As on soil and clay sized fractions of two different soil orders namely – Alfisol and Inceptisol at varying pH (5.5 and 7.0) and temperature (298 and 308 K). The Alfisol and Inceptisol was dominated with smectite and illite minerals respectively. The content of organic C was lower and free and amorphous aluminium (Al) and iron (Fe) oxides were higher in Alfisol compared to the Inceptisol. The results showed that the adsorption capacity was higher for soil and clay sized fractions in Alfisol compared to the Inceptisol. The adsorption of As on clay-organic complex was higher at lower pH (5.5) compared to the higher pH in both the soil orders. The adsorption isotherms for both soil orders fitted well to Langmuir and Freundlich models. Among clay sized fractions, high adsorption capacity was found for clay-oxides and clay-organic-complex of Alfisol and Inceptisol, respectively. The thermodynamic study indicated that the sorption reactions were exothermic and favourable at lower temperature (298 K) compared to the higher one (308 K). The desorption data showed that the cumulative desorption was higher in Alfisol but the percentage of As desorbed was higher in Inceptisol. The desorption Index (DI) was higher in Alfisol compared to

Inceptisol. Removal of organic matter and Al and Fe oxides decreased the DI in clay for both the soil order. The contents of organic matter, Al-Fe-oxides and type of clay minerals were the major factor to determine the sorption-desorption behavior of As in soil.

Aluminium dynamics and microbial functions in an acidic Inceptisol under organic rice cultivation

A study on aluminium dynamics and microbial functions in an acidic Inceptisol under organic rice cultivation was carried out. For this purpose, soil (0-15 cm and 15-30 cm) and plant samples were collected at physiological maturity stage of rice (November, 2020) from nine-years old ongoing experiment at Assam Agricultural University, Jorhat, Assam. Treatment consisted of control (without fertilization), BC: biofertilizer consortia 3.5 kg ha^{-1}, compost: compost 5.0 t ha^{-1}, compost + BC: compost 5.0 t ha^{-1} + biofertilizer consortia 3.5 kg ha^{-1}, EC-1: enriched compost 2.5 t ha^{-1}, EC-2: enriched compost 5 t ha^{-1} and, Azolla + BC: Azolla 0.5 t ha^{-1} + biofertilizer consortia 3.5 kg ha^{-1}. Results indicated among different Al fractions, exchangeable Al (13.2, 8.0 mg kg^{-1} in 0-15 and 15-30 cm soil depth, respectively) and strongly organically bound and interlayer Al (270and 245 mg kg^{-1} at 0-15 and 15-30 cm soil depth, respectively) were significantly lower over control, whereas weakly organically bound Al fraction, and amorphous Al fraction (844 and 796 mg kg^{-1} at 0-15 and 15-30 cm soil depth, respectively) were significantly increased with EC-2. Free Al had highest concentration in soil and not significantly affected by application of inorganic inputs. The exchangeable acidity was decreased from 0.88 to 0.67 cmol (p+) kg^{-1} and 0.78 to 0.66 cmol (p+) kg^{-1} in the surface and subsurface soil, respectively by application of 5 t ha^{-1} enriched compost. Highest grain yield was recorded with Azolla + BC application (3.23 t ha^{-1}), it was statistically similar with EC-2 (3.21 t ha^{-1}) and 1.29 times higher than BC alone application. The organic farming practices enhanced the grain quality by improving N, P and K and reduce ding Al content of rice, most pronounced effect was observed under 5t ha^{-1} enriched compost application among all treatments. Uptake N, P and K increased and, Al decreased in grain, husk and straw of rice with organic practices. Exchangeable Al and exchangeable acidity in the soil were negatively correlated with microbial function, while weakly organically bound Al fraction and total potential acidity were positively correlated. Application of enriched compost (5 t ha^{-1}) and compost (5 t ha^{-1}) + biofertilizer consortia were most effective to alleviate Al-toxicity, soil acidity and to enhance microbial function, yield and quality of rice in an acidic Inceptisol.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Shubharanjan Nayak	50052	M.Sc.	Aluminium dynamics and microbial function in an acidic Inceptisol under long-term organic rice cultivation	Dr. Sarvendra Kumar
2.	Debrup Ghosh	50053	M.Sc.	Effect of silicon rich crop residues on available phosphorus in soils	Dr. Mandira Barman
3.	Siyaram Meena	50054	M.Sc.	Immobilization of arsenic in soil using functionalized clays	Mr. Kapil A. Chobhe
4.	Partha Sarathi Ghorai	60052	M.Sc.	Long term effect of fertilization and manuring on soil quality under rice-mustard-sesame cropping system	Dr. Sunanda Biswas

5.	Deepak	60053	M.Sc.	Sorption-desorption behaviour of arsenic on clay-organic complex in an Alfisol and Inceptisol of Jharkhand	Dr. Ruma Das
6.	Sujit Das	60054	M.Sc.	Labile organic carbon and biological soil health indicators under conservation agriculture based rice-wheat cropping system in an Inceptisol	Dr. Sunanda Biswas
7.	Saptaparnee Dey	21355	M.Sc.	Effect of engineered biochar on nutrient retention in an Inceptisol	Dr. T.J. Purakayastha
8.	Sharat Kothari	21356	M.Sc.	Synthesis and evaluation of novel nitrogenous fertilizer products for enhancing nitrogen use efficiency	Mr. Kapil A. Chobhe
9.	Ravi Saini	21357	M.Sc.	Synthesis and evaluation of urea loaded nanoclay biopolymer composites for enhancing nitrogen use efficiency in rice	Dr. K.M. Manjaiah
10.	Ritambhara	21358	M.Sc.	Soil organic carbon dynamics under varying tillage, residue and nutrient management in an Inceptisol under maize-wheat cropping system	Dr. Shrila Das
11.	Chinmoy Roy	21359	M.Sc.	Assessment of heavy metals in contaminated soils using visible and near-infrared reflectance spectroscopy	Dr. Nayan Ahmed
12.	Chinmayee Behera	21360	M.Sc.	Phosphorus dynamics under conservation agriculture based maize-mustard system in an Inceptisol	Dr. Shrila Das
13.	Krishna Kumar Mourya	10534	Ph.D.	Assessment of carbon sequestration potential and stability of soil carbon in rice-wheat cropping systems of Indo-Gangetic plains	Dr. T.J. Purakayastha
14.	Sunil B.H.	10895	Ph.D.	Soil phosphorus fractions and their contribution in phosphorus nutrition of wheat under long-term fertilization and manuring	Dr. S.P. Datta
15.	Khusboo Rani	11126	Ph.D.	Isolation of potential potassium solubilizers and their impact in enhancing the availability of potassium from waste mica treated soil	Dr. D.R. Biswas

Water Science and Technology

14

Prof. Man Singh

The Water Technology Centre (WTC) is an inter-disciplinary facility for research, teaching, training and extension in agricultural water management. The Centre has evolved into a unique institution, addressing a wide range of issues pertaining to water management at farm, large irrigation commands and watershed scales. It has mandate to conduct basic and applied research on all aspects of water management in agriculture and develop technologies for improved water management; to participate in the post graduate teaching programmes of IARI for developing human resources and organize training programmes for the in-service field and research personnel working in the area of water management in agriculture; to disseminate knowledge developed through appropriate documentation. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Wastewater management

Impact assessment and standardization of sensor-based wastewater irrigation scheduling in marigold (*Tegetes patula* L.)

A study was conducted at Water Technology Centre, ICAR-Indian Agricultural Research Institute, New Delhi, during the year 2020-21 to standardize the FDR sensor-based wastewater irrigation scheduling for marigold (*Tagetes patula* L.). The influence of wastewater irrigation scheduled at different MADs (Maximum Allowable Depletion) to know its impact on soil health, water use efficiency, economics and flower quality and productivity of marigold was evaluated in a randomized block design with four replications and eight treatments, namely, T1: groundwater irrigation scheduled at 25% MAD, T2: groundwater irrigation scheduled at 50% MAD, T3: groundwater irrigation scheduled at 75% MAD, T4: groundwater irrigation scheduled according to farmers package of practices (PoP)/ recommendation, T5: wastewater irrigation scheduled at 25% MAD, T6: wastewater irrigation scheduled at 50% MAD, T7: wastewater irrigation scheduled at 75% MAD, T7: wastewater irrigation scheduled according to farmers PoP under an open field condition. The results revealed that wastewater irrigation at 50% MAD considerably improved soil health parameters (EC, pH, OC, NPK, and micronutrients) as compared to groundwater irrigation at same MAD. Further, flower quality in-terms of vase life (3.68 days) & floral turgidity (as higher relative water content 84.52 %), flower yield (9.59 t/ha), flower size (86.41 mm), water use efficiency (7.05 kg/ha-mm) were found significantly higher under wastewater irrigations scheduled at 50% MAD. Moreover, the highest economics in terms of benefit cost ratio (3.41) were also observed in the same treatment. Thus, the study concluded that the irrigation schedule at 50% MAD may improve marigold quality and productivity without degradation of soil health under short-term application of wastewater. However, long-term application of wastewater in marigold needs to be monitored at different soil and climatic conditions.

Impact assessment of heavy metals spiked wastewater irrigation on soil health, productivity and metal translocation in marigold (*Tagetes patula*. L)

A pot experiment was conducted to find out the impact assessment of heavy metals spiked wastewater irrigation on soil health, productivity and metal translocation in marigold (*Tagetes patula. L*) at Water Technology Centre of ICAR- Indian Agricultural Research Institute, New Delhi during *rabi* season of 2020-21 with seven treatments *viz*. T-1: Sole groundwater irrigation without spiking of heavy metal, T-2: Sole wastewater irrigation without spiking of heavy metal, T-3: Wastewater irrigation spiked with Cd (0.005 ppm), Cr (0.05 ppm), Ni (0.1 ppm) and Pb (2.5 ppm), T- 4: Wastewater irrigation spiked with Cd (0.01 ppm), Cr (0.1 ppm), Ni (0.2 ppm) and Pb (5.0 ppm), T-5: Wastewater irrigation spiked with Cd (0.1 ppm), Cr (0.1 ppm), Ni (2 ppm) and Pb (10 ppm) , T-6: Wastewater irrigation spiked with Cd (0.25 ppm), Cr (2.5 ppm), Ni (5 ppm) and Pb (30 ppm) , T-7: Wastewater irrigation spiked with Cd (0.5 ppm), Cr (5.0 ppm), Ni (10 ppm) and Pb (50 ppm). Results indicated that quality of sole wastewater and groundwater for irrigation purpose is safe with regards to pH, EC, SAR, RSC and heavy metals contents. However, wastewater has higher nutrients (NPK) potential and heavy metal contents as compared to groundwater. Temporal changes in quality of treated water due to storage after spiking of heavy metals in wastewater was negligible. Soil health in terms of pH, organic carbon, phosphorous, potassium and micronutrients (Cu, Fe, Mn, Zn) was significantly not changed whereas, significantly higher salinity (EC 0.45 dS/m), nitrogen content (164.17 kg/ha) as well as significantly higher concentration of Ni (0.76 mg/kg), Cr (1.66 mg/kg), Cd (0.18 mg/kg) and Pb (2.78 mg/kg) in irrigated soils were observed in the treatment T7 where higher concentration of metals were spiked in wastewater. Productivity of marigold with reference to vegetative growth, flowering, keeping quality and marketable flower yields was significantly increased with wastewater irrigation as compared to groundwater irrigation and decreased with increased concentrations of spiked metals in wastewater. Concentrations of Ni, Cr, Cd and Pb in the root under consideration varied from 2.05 to 54.48, 13.67 to 86.35, 0.89 to 5.21 and 3.84 to 22 mg/kg, respectively, and in shoot parts varied from 9.3 to 63.05, 29.9 to 97.4, 1.8 to 6.42 and 12.38 to 29.93 mg/kg, respectively. Translocation factors for heavy metals (Ni, Cr, Cd, Pb) were varied from 0.13 to 0.87, 0.47 to 0.9, 0.38 to 0.82 and 0.32 to 0.75, respectively. Bio-accumulation factors for heavy metals (Ni, Cr, Cd, Pb) were varied from 63.8 to 125.26, 39.76 to 72.18, 47.80 to 55.53 and 6.3 to 12.61, respectively. It is concluded that marigold may be selected for phytoremediation of heavy metals from metal contaminated soils.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of student	Roll No.	Degree	Title of the Thesis	Name of Chairman
1.	Aditya V Machnoor	21366	M.Sc.	Impact assessment and standardization of sensor-based wastewater irrigation scheduling in marigold (*Tagetes patula* L.)	Dr. D.S. Gurjar
2.	Vignesh P	21376	M.Sc.	Impact assessment of heavy metals spiked wastewater irrigation on soil health, productivity and metal translocation in marigold (*Tagetes patula* L.)	Dr. D.S. Gurjar

School of Basic Sciences

Discipline	Number of Thesis Submitted	
	M.Sc.	**Ph.D.**
Biochemistry	05	01
Molecular Biology and Biotechnology	07	02
Plant Physiology	05	01
Total	**17**	**04**

Biochemistry

15

Prof. Anil Dahuja

The mandate of the Division of Biochemistry is to undertake fundamental and applied biochemical, molecular biological and nutritional research related to the current problems in the field of agriculture and to conduct teaching and training programmes to develop skilled human resource in the area of plant biochemistry and molecular biology. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Non-destructive nutrient profiling of food crops for their nutritional quality assessment

Evaluation and identification of pearl millet (*Pennisetum glaucum* L.) genotypes based on nutritional quality, biochemical diversity and physicochemical properties using near-infrared spectroscopy (NIRS) prediction models

Pearl millet holds a great potential for food diversification owing to its balanced nutritional composition. A study was, therefore, conducted to analyse the nutritional composition of 87 diverse pearl millet (*Pennisetum glaucum* (L.) R. Br.) genotypes, including landraces and commercial varieties, using standard biochemical protocols. The results of the study indicated a substantial variability in total carbohydrates-measured in terms of starch (50.37–63.25), amylose (19.26–27.90), sucrose (0.58–1.53), glucose (0.32–0.75), resistant starch (RS) (1.49–3.52), total soluble sugars (TSS) (1.53–3.22); expressed as g/100g-, protein (8.07–18.15 g/100g), total dietary fibres (TDF) (7.68–16.18 g/100g), lipids and fatty acids [total lipid (5.24–9.99), palmitic (20.30–32.49), linoleic (32.11–46.91), oleic (21.99–33.43) and stearic acid (3.28–7.91) expressed as g/100g], antinutritional factors [phytic acid (0.54–1.43 g/100g) and RFOs (0.27–2.08 mmol/100g)], phenols (0.04–0.21 g/100g), and minerals.The multivariate data analysis, using hierarchical cluster analysis (HCA) and principal component analysis (PCA) was then applied for deciphering the differences/similarities between multiple nutritional attributes, sample types and also for projecting the object in a two/three-dimensional factor-plane, determined based on various distinct characteristics so as to augment an enhanced understanding of data structure and the distribution of the nutritional traits across 87 germplasm. The findings indicated that PM germplasm displays a great nutritional diversity and the germplasm in the clusters can have diverse applications. Near-infrared spectroscopy (NIRS) using near-infrared radiation sections of the electromagnetic spectrum for precise and speedy determination of biochemical parameters was conducted in the selected 87 germplasmand modified partial least squares regression based NIRS prediction models developed to assess starch, RS, amylose, protein, oil, TDF, phenolics, total soluble sugars, phytic acid for high throughput screening of pearl millet germplasm. Mathematical treatments were executed by permutations and combinations for calibrating the model, where 2nd, 3rd, and 4th derivatives produced the best results. Treatments "4,5,4,1" was finalized for protein, oil, RS, TDF, "3,4,4,1" for phenolics, "2,8,4,1" for amylose, "2,4,4,1" for phytic acid, "4,7,4,1" for total soluble sugars and "2,8,4,1" for starch. Furthermore, RVA (Rapid Visco Analyser) profile wasused to indicate the complex interactions between starch and water, influenced by time and temperature. High pasting temperature (PT) values of 75.78 °C in HHB-299 indicated the presence of starch, which can effectively resist rupturing and swelling. Lower PT values of 54.88 °C in CHANANA BAJRI-1 showed the presence of starchy flours, which can be highly susceptible to rupturing and swelling. A lower breakdown value of 296.2 mPa·s in PC-443 indicated higher stability of starch under elevated temperature, while a higher breakdown value of 814 mPa·s in JAKHRANA suggested otherwise. The final viscosity (FV), which signifies the potential of starch granules to produce a highly viscous paste, varied from 2206 mPa· s in GADHWAL KI DHANI-1 to 3823 mPa·s in JAKHRANA. The high FV (which could result from amylose molecule aggregation) of GADHWAL KI DHANI-1 indicated its increased resistance to shear stress. The texture profile analyzer (TPA) curves indicating the textural properties of pearl millet flour gels showed that the adhesiveness varies between -104.394 g/sec in PC-443 to -25.824 g/sec in 86M86 and the chewiness between 6.004 in 86M86 to 12.871 in PC-443 thereby indicating that PC-443 can possibly endure longer chewing than 86M86. The cohesiveness varied from 0.215 in NANDI-72 to 0.320 in PC-701. The analysis can form the basis for the commercialization and utilization of pearl millet using efficacious breeding strategies.

Theme 2. Deciphering factors controlling quality, bioavailability and functionality of nutrients in different food matrices

Deciphering the influence of food matrix state of composite flour on nutrient quality and bioavailability

Malnutrition, also known as “hidden hunger,” is an invisible menace that evidently affects billions of people worldwide due to insufficient or imbalanced diets with respect to essential nutrients, particularly protein and iron. Lack of intake of protein- (both quality and quantity) and iron-rich diets is one of the major causes for protein malnutrition and anaemia, which often results in impaired growth and development in children. The possible strategy to overcome protein energy malnutrition (PEM) and anaemia is to bring economically feasible nutrimix blends, rich in protein and iron, on consumers’ daily plates. We, therefore, developed six nutrimixes (NM1-6) by combining iron- (8-12mg/100g) and Zn- (4-6mg/100g) rich pearl millet flour with chickpea flour, a prominent protein source (22-26%) with a well-balanced composition and greater bioavailability of essential amino acids, in varying proportions. These nutrimixes belong to two separate groups; sprouted pearlmillet (SPM) and unsprouted pearlmillet (USPM) prepared from sprouted and un-sprouted pearlmillet grains respectively. Besides, the protein and starch digestibility of these nutrimixes along with the microstructure of dough matrix were also studied to analyse their nutritional and dough quality attributes. Among the six nutrimixes prepared, highest and lowest values of the total crude protein (26.15g/100g / 23.15g/100g) and soluble protein (26.01g/100g / 22.15g/100g) were observed in NM6(10% Gluten + 50% sprouted pearl millet flour + 40 % chickpea flour) and NM1 (10% Gluten + 70% pearl millet flour + 20 % chickpea flour) respectively. Further, the results of amino acid profiling showed balanced amino acid score for all the essential amino acids except methionine and cysteine (sulphur containing amino acids.)The highest contents of starch (64.62 to 67.26g/100g), carbohydrates (71.24 to 79.74g/100g), reducing sugar (4.13 to 4.97g/100g) and fat (4.88 to 5.27g/100g) were found in USPNM group as compared to SPNM group. Furthermore, physico-chemical analysis showed higher emulsion capacity (EC), emulsion stability (ES), foaming capacity (FC), foaming stability (FS), swelling capacity (SC) and least gelation concentration (LGC) in USPNM as compared to SPNM. Dough quality parameters revealed higher dough consistency (DC-609BU) and water absorption (WA-65.4%) in NM3 (10% Gluten + 50% pearl millet flour + 40 % chickpea flour), whereas NM4 [10% Gluten + 70% sprouted pearl millet flour + 20 % chickpea flour] showed lowest DC (489BU) and WA

(50.8%). Lowest protein weakening (1.87), starch gelatinization (3.56), with increased cohesiveness (0.34) was found in USPNM-NM3, which further validated better dough quality. Based on the farinograph, mixolab and TPA parameters, USPNM-NM3 was found to have dough quality as superior as wheat dough. Among SPNM, better dough quality was found in dough prepared from NM6. Hence, visco-elastic properties using dynamic mechanical analyzer (storage modulus-G', loss modulus G", loss tangent-tanδ, temperature sweep-G*), and creep-recovery tests were analyzed only in USPNM-NM6 and SPNM-NM3 and compared with wheat dough. Creep-recovery tests showed elastic share of visco elastic compliance (Je/Jmax) of 33.68% and 14.13% in USPNM-NM3 and SPNM-NM6 respectively, whereas viscous share of visco elastic compliance (Jv/Jmax) was found to be higher (85.87%) in SPNM-NM6 as compared to USPNM-NM3 (66.32%). The dynamic mechanical analysis also reconfirmed the dominance of elastic behavior over the viscous one, hence the better dough quality, in USPNM-NM3 nutrimix dough as compared to SPNM-NM6. The results for protein-starch interaction, quantitative and qualitative analysis of gluten network in dough matrix using CLSM and Angio tool respectively revealed highest and lowest gluten area (25.91 x 104 µm / 24.47 x 104 µm) and gluten percentage (27.91% /19.63%) in USPNM-NM3 and SPNM-NM6 respectively, suggesting better dough matrix formation in USPNM-NM3 dough as compared to SPNM-NM6. In-vitro starch digestibility (IVSD) and inherent glycemic potential (IGP) was determined based on starch hydrolysis kinetics (SHK); results showed higher IVSD (%) (48.33 vs 42.69) and IGP (55.18 vs 54.23) values in SPNM-NM6 as compared to USPNM-NM3. Further, the FTIR spectra for starch fingerprinting region was carried out to determine 1047/1022 cm^{-1} and 1022/955 cm^{-1} ratios,which were found to be (0.89 vs 0.87) and (0.96 vs 1.0) in USPNM-NM3 and SPNM-NM6 respectively indicating increased IVSD and IGP in SPNM-NM6 as compared to USPNM-NM3. The *in vitro* protein digestibility (IVPD) and PDCAAS score in SPNM-NM6 and USPNM-NM3 were observed as (76.14 vs 73.01%) and (0.5 vs 0.44) respectively. The higher IVPD and PDCASS score in SPNM-NM6 nutrimix chapatti was further validated by FTIR spectra for protein fingerprinting,which showed increased proportion of α helices (0.012) in SPNM-NM6 as compared to USPNM-NM3 (0.010). In conclusion, the results of this study clearly indicated that USPNM-NM3 is not only nutritionally rich, in terms of iron, zinc and protein availability, but also has a great potential to act as a sustainable alternative to wheat in many baked and cooked preparations.

Starch-lipid interactions and its influence on inherent glycaemic potential

Inherent glycemic potential (IGP) is an index of starch bioavailability in terms of eliciting post-prandial glycemic response of staple cereals which leads to chronic hyperglycemia such as type 2 diabetes mellitus (T2DM), cardiovascular diseases (CVD) and their sequelae. Directed investigation in this direction is thus required to understand the role of explanatory variables governing IGP as well as to develop a model system for limiting high blood glucose of staple cereals. Therefore, a study was carried out to address few basic questions to share a comprehensive understanding on various illustrative variables possessing roles like: does inherent indices like microstructure, matrix compositions/ interactions and molecular configurations affect starch digestibility and ultimate IGP? This study inscribes these questions by considering two starch sources of varying inherent matrix composition viz. pearl-millet (PM) and rice, and five cooking fats (*ghee, coconut oil, sunflower oil, mustard oil, til oil*) selected on the basis of microstructure, fatty acid profiles through gas chromatography (GC-MS), starch-lipid (S-L) complexation (CI and iodine spectra), food matrix interactions via CLSM, *in-vitro* starch dynamics and starch hydrolyzation kinetics (SHK), molecular mechanism like short range and long range molecular organization through FTIR and XRD as well as *in-vitro* glucose diffusion assay (GDRI) to predict *in-vivo* starch bioavailability into the system. Based on results, *in-vitro* oral-gastro intestinal simulation revealed PM to have low IGP (63.71%) compared to rice (65.89 %) and it was well correlated with microstructural parameters [pericarp thickness (22.71

± 0.20 μm), granule size (2.16 ± 0.12 μm), endodermal surface area (1199.64 ± 2.86 μm^2)]. It was also found that dense food matrix components and higher S-L interaction visualized by CLSM contributes to the resistance towards digestive enzymes. The molecular structures were explored using FTIR, XRD to understand the synergistic effects of short range and longer range molecular patterns (R1047/1022: 0.80 and CD % : 21.73%) of PM starch, which revealed the superior crystalline compactness as vital towards low IGP. Further, exogenous addition of cooking fats revealed that PM-mustard oil (PM-MO) and rice-mustard oil (R-MO) complexes were found most promising with least IGP of 57.17 % and 59.65 % respectively. Molecular structural differences (short range and long range) of these two complexes were also found in line with previous results (R1047/1022: 0.85 and 0.80, CD %: 50.13 %, 31.09 %). Therefore, our research for the first time unravelled a perspective relation of IGP with various intrinsic characters and also deciphered the mechanism of modulating IGP of archeological nutri-cereal like PM as compared with staple cereal- rice by formation of a *lipid induced digestive model*, acting as one of significant approaches of lowering IGP against current situation of diabetic and pre-diabetic scenario.

Genome-wide identification, cloning and characterization of gene(s) coding for lipase from pearl millet (*Pennisetum glaucum* L.) and their physicochemical characterization for grain quality

Pearl millet is one of the most important coarse cereals and is called as "Nutri-cereal" due to its rich nutrient profile. This crop is also termed as an orphan crop because of limited information available on public domain. Low keeping quality of the flour due to rancidity is one of the major problems in pearl millet. Lipases are a group of enzymes that produces free fatty acids that ultimately leads to rancidity. Very few lipases have been identified and characterized from pearl millet. Here, we have identified 77 transcripts of lipases from pooled samples (leaf, stem and developing grains) of pearl millet using *de novo* transcriptomic approach. Further, we cloned putative lipase (1.4 Kb) and TAG lipase (1.5 Kb) from pearl millet genotype Pusa 1201. BLASTp analysis showed maximum homology with uncharacterized protein from *Setaria italica* (acc.no. XP_004977061.1) and *Setaria viridis* (acc. no. XP_034605001.1). The gene sequences were submitted to NCBI GenBank (acc. no. MZ590564 and acc. no. MZ590565). ORF analysis showed the presence of 453 and 504 amino acids in the genes respectively. CD search analysis showed the presence of serine-threonine residues in the active site, which is characteristic of lipase family of proteins. We observed abundance of transcripts of both the lipases in developing grains during mealy-ripe stage, as compared to milky stage. Based on the intensity of bands observed on the gel, expression was observed higher in hybrid (Pusa1201) and composite (PC701), as compared to the landraces (Chadi Bajri and Damodhar Bajri). Biochemical markers linked with flour rancidity like antioxidants, antioxidant enzyme activities like catalase and SOD assay, and TAC were observed maximum in landraces, as compared to the hybrid and composite varieties. We also performed physiological characterization of the genotypes. There is a need to characterize other rancidity causing enzymes using both molecular and biochemical tools in order to arrest the lipid rancidity at appropriate time without compromising with the quality of the grains. This will pave the way for further enhancing the keeping quality of the pearl millet flour without compromising with the quality.

Theme 3. Enhancing the nutritional and keeping quality of food products through processing

Understanding the effect of probiotic fermentation and germination on the protein digestibility, bioavailability of isoflavones and mineral content in soymilk

Soybean (*Glycine max*) is being considered a high-quality food source because of its high protein content and quality, PUFA-rich fat and presence of nutritionally-important bioactive phytochemicals viz. isoflavones, tocopherols, saponins etc. Soymilk-one of the major commercial products derived from soybean is a best alternative to dairy products due to its low cholesterol and lactose levels, and for its functional properties. However, the consumption of soymilk is limited due to the presence of nondigestible oligosaccharides and anti-nutritional factors such as trypsin inhibitors and phytic acid. The germination and probiotic fermentation have been previously shown to reduce these anti-nutritional factors. But, the cumulative effects of germination and fermentation on the nutritional profile of soymilk have not been studied so far. The current study was, therefore, aimed to understand this facet as well as to explore the use of mixed culture approach for developing fermented soymilk, using recently recognized probiotic *Weissella* strains, from food grade (FG) and oil grade (Low-KTI) varieties of soybean. Five different strains of *Weissella* sps were screened for their potential probiotic activity. Besides, the β-glucosidase and phytase activity were analysed at different stages of seed germination and based on the data obtained, eight-days old germinated seedlings were selected for soymilk preparation. Results showed that fermentation along with germination increased isoflavone bioconversion, mineral content anti-oxidant activity, titratable acidity and decrease in phytic acid content. Through screening best performing strains, *Weissellacibari*a Sb and *Weissella confusa* 30082a; in case of food grade soymilk (FG) and *Weissella cibaria* Za and *Weissella confusa* 30082a; in case of low KTI soymilk (LKTI) fermentation were selected by cluster analysis and used in mixed-culture approach to study their potential synergistic effects in improving soymilk quality. The mixed culture approach yielded better results than single culture approach, in terms of enhancement in the nutritional/functional value of soymilk; (Isoflavones up to 112.07 µg/10ml Daidzein, 152 .33 µg/10ml Glycitein , 140 µg/10ml Genistein -LKTI) ,Titratable acidity (0.7 % Lactic acid production-FG), Antioxidant activity (87.19 % DPPH inhibition - LKTI), Phytic acid (0.06 g/100g reduction-LKTI) ,Minerals (2.04 µg/ml Zn- FG, 1.84µg/ml Fe -LKTI) along with increased in vitro digestibility(up to 92%-LKTI), PDCAAS value (0.66-LKTI), decreased trypsin inhibitor concentration (0.04 µg/g -LKTI) and increased sugar (1.025 mg/ml -LKTI) and protein content (44 to 49 g/100g-FG). Since, the consumption of soy products is mainly limited by its beany and astringent flavour, the sensory evaluation was also performed by panel of experts to check the overall acceptability of the fermented soymilk in comparison with non-fermented one; moderate liking towards fermented soymilk was observed from food grade soymilk with added sugar (6%). However, the acceptance level of soymilk prepared from germinated low KTI soybeans was found to be considerably low, despite its enhanced functional properties. In future, the benefits accrued from synergistic effect of probiotic fermentation and germination can be optimally realized through development and deployment of technologies for improvement in the sensory/textural properties of soymilk and further optimization.

Arresting the rancidity of rice bran by regulation of lipase and lipoxygenase

Any rise in the economic value of rice crop could have a large impact. Rice bran, a by-product of ricemilling is used to produce rice bran oil (RBO), which is emerging as a major vegetable oil. In spite ofbeing a rich source of nutrients and bioactive compounds (γ- oryzanol, tocopherols, phytosterols and ferulic acids) that aid in the prevention of oxidative stress-related diseases, rice bran is rarely beingutilized for the residual bioactive components because it is susceptible to hydrolytic and oxidative rancidity. Lipase, lipoxygenase and peroxidase contribute mainly to enzymatic rancidity. The lipases, which are endogenously present, cause hydrolysis of neutral bran oil to free fatty acids (FFA), leading to the development of hydrolytic rancidity. The FFAs are highly prone to oxidation, which is likely caused by the action of the inherent lipoxygenases. As a result, the FFAs undergo further oxidative decomposition with the generation of rancid off- flavours in rice bran. In this research, the effects of different stabilization treatments – namely, autoclaving, infrared- radiation, low temperature treatment and dry heating, on the nutritional and stability attributes of rice bran oil was evaluated. Lipase and lipoxygenase activity as well as free fatty acid content, peroxide value, iodine value, saponification value, oil fatty acid compositions, and contents of tocopherol and γ- oryzanol after different treatments were investigated to evaluate the effect of stabilization and oil quality. The results indicated that the activities of key enzymes, including lipase and lipoxygenase decreased after autoclave, infrared and dry heat treatments after 60 days of storage and the rising trend of the free fatty acid content decreased significantly during storage. Autoclave treatment proved to be better than other treatments in reducing lipase and lipoxygenase activitywith 24.7% and 19.3% residual activities respectively. Maximum reduction in free fatty acid content was shown by autoclave treatment, which had the FFA of 8.6 % after 60 days of storage. Autoclave treatment reduced the oxidation and hydroperoxides of rice bran, which can control the rise of peroxide value during 60 days of storage (4.8 meq/ kg). Iodine values of the different treated oils were in the range of 93.2 g I_2/100ml oil (low temperature) to 104.4 g I_2/100ml oil (autoclave). Significant increase ($p < 0.05$) in saponification values was observed in low temperature and dry heat stabilized rice bran oil. Although the autoclave achieved maximum stability, the tocopherol content decreased significantly ($p < 0.05$). Infrared and low-temperature treatments preserved the tocopherol content the best. All the treatments had no significant influence ($p > 0.05$) on the γ- oryzanol content of oils. The various treatments caused significant increase in the palmitic acid, oleic acid and linoleic acid of rice bran oil after 60 days of storage. Infrared treatment resulted in rice bran stabilization while retaining the nutritional and fatty acid profiles of rice bran oil, and hence could be recommended for rice bran stabilization.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the Student	Roll No.	Degree	Title of the Thesis	Name of the Chairperson
1.	Sushmitha J.	21250	M.Sc.	Arresting the rancidity of rice bran by regulation of lipase and lipoxygenase	Dr. Aruna Tyagi
2.	Debarati Mondal	21251	M.Sc.	Starch-lipid interactions and its influence on inherent glycaemic potential	Dr. Veda Krishnan
3.	Kangkan Pandit	21252	M.Sc.	Genome-wide identification, cloning and characterization of gene(s) coding for lipase from pearl Millet (*Pennisetum glaucum* L.) and their physicochemical characterization for grain quality	Dr. Ranjeet Ranjan Kumar
4.	Tamil Selvan S.	21253	M.Sc.	Deciphering the influence of food matrix state of composite flour on nutrient quality and bioavailability	Dr. Vinutha T.
5.	Arpitha S.R.	21254	M.Sc.	Understanding the effect of probiotic fermentation and germination on the protein digestibility, bioavailability of isoflavones and mineral content in soymilk	Dr. Anil Dahuja
6.	Maharishi Tomar	10270	Ph.D.	Evaluation and identification of pearl millet (*Pennisetum glaucum* L.) genotypes based on nutritional quality, biochemical diversity and physicochemical properties using Near-infrared spectroscopy (NIRS) prediction models	Dr. Archana Sachdev

Molecular Biology and Biotechnology

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Prof. Debasis Pattanayak

The National Institute on Plant Biotechnology (NIPB) has been entrusted with the responsibility of developing new tools and techniques and to deliver breakthrough in biotechnology for crop improvement. The mandates of the NIPB are to undertake molecular mechanisms underlying biological processes; to develop capabilities of devising tools and techniques of biotechnology and genetic engineering for crop improvement; to use the knowledge gained and technologies developed for advancing agricultural development; to serve as a national lead centre for plant molecular biology and biotechnology research; to create trained manpower in the area of plant biotechnology. The NIPB is engaged in teaching postgraduate students in Molecular Biology and Biotechnology. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Abiotic stress tolerance

Study of allantoin-mediated salinity tolerance in rice genotype IR-29

Rice is an important cereal crop belonging to the family *Poaceae*. It encounters various abiotic stresses during its entire life cycle. Salinity stress is one of major abiotic stress, causes significant amount of yield loss in rice. IR-29 is an indica rice variety. It is highly salt sensitive. Genetic factors, agronomic practices and different chemical amelioration can reduce the effect salinity stress. Allantoin is a nitrogenous compound, derived from the degradation pathway of purine. Present study focuses on the exogenous application of allantoin to mitigate the salinity stress in IR-29. Based on the phenotype, 5th day of salt (100 mM) as well as allantoin (0.01 mM) treatment has been decided for the experiments of morphological, biochemical and expression analysis of hormonal biosynthetic genes. Root length, shoot length, fresh weight of root as well as shoot and dry weight of root as well as shoot have been increased in the media containing NaCl along with allantoin compared with only NaCl treated condition. Proine content, chlorophyll content and Na^+/K^+ ratio were also improved by exogenous supplementation with allantoin in salt treated condition. Relative expression of auxin (*OsYUCCA1*), gibberellin (*OsGA20Ox2*), ABA (*OsNCED1*) and brassinosteroid (*OsCYP90B2*) biosynthetic genes were upregulated in NaCl along with allantoin containing media compared with only NaCl treated media. Salinity stress for up to 5 days of IR-29 was thought to be improved by allantoin by increasing the accumulation of proline which acts as osmo-protectants by maintaining the osmotic pressure within the cell, decreasing the Na^+/K^+ ratio, increasing the chlorophyll content as well as enhancing the total allantoin accumulation and enhancing the relative expression of hormonal biosynthetic genes.

In silico whole-genome analyses of MBF1 (multiprotein bridging factor 1) gene and phenotypic characterization of heat stress responses in two contrasting wheat cultivars (*Triticum aestivum* L)

Wheat is the second most significant cultivated food crop in India after rice. During 2020-21, India recorded an all-time high wheat production of 108.75 million tonnes. Wheat is adversely affected by climate change and rising temperature specifically at grain filling stage called terminal heat stress and developing climate-smart wheat cultivars is a high priority in wheat breeding today. Towards this, identification of novel stress-responsive genes and their functional characterization is an essential requirement. Here, we structurally characterized the wheat MBF1 (Multiprotein Bridging Factor 1) gene family after a whole genome analysis. The MBF1 proteins are transcription co-factors, associated with TATA box-binding proteins which form a bridge between transcription factors and the basal transcription machinery of stress-responsive genes. Various reports have demonstrated involvement of MBF1 genes in various stress modulation and specifically during heat stress. Phenotypic analysis was also carried out in two contrasting heat responsive cultivars viz. RAJ3765 and HD2967 at anthesis stage after seed priming with heat and raising them in season. The comprehensive computational analysis has identified the most inducible and modulated members of the MBF1 gene family. Phenotypic analyses showed indicators of stress tolerance and involvement of important pathways/processes modulated under heat stress in wheat.

Characterization of gene CaM (calmodulin) from *Pennisetum glaucum* (L.) R. Br for its role in heat stress tolerance

Pennisetum glaucum (L.) R. Br. being a hardy cereal may harbour a repository of genes for heat stress tolerance which can be used for the genetic improvement of crops. CaM (calmodulin) has a role in stress tolerance and is involved in calcium signal transduction pathways. The study involved genetic transformation of *Nicotiana tabacum* with *CaM* from *Pennisetum glaucum* cv. 841B. Callus formation was induced on selective MS media + NAA 0.1 + BAP 2.5 followed by emergence of shoots. The shoots were excised from the calli and placed on rooting medium (1/2MS medium + antibiotics). The regenerated plantlets were transferred to pots with soilrite for hardening. Three plants obtained, were confirmed for presence of transgene by PCR analysis and Southern hybridization technique. For functional validation of *PgCaM*, transgenic T0 seedlings were exposed to heat stress (42ºC for 2 hrs). RWC, MSI and chlorophyll content significantly increased in transgenic plants when compared to wild type plant. qRT-PCR analysis of transgenic lines showed higher expression level of *PgCaM* in response to heat stress.

Molecular and biochemical analysis of traits related to salt tolerance in RIL mapping population of wheat (*Triticum aestivum* L.)

RILs produced from (HD-2851×Kharchia-65) and parental genotypes were grown in hydroponics under optimal conditions in NPF, IARI, New Delhi. Seedlings were grown under control and salt treatment (ECiw, 15 dS m^{-1}) for two weeks. Effects of salt treatment on parents and RILs were tested for physio-biochemical, growth and root traits. Reduction in RWC and MSI was less in Kharchia 65 and RILs as compared to HD 2851. Salinity caused lower decrease in primary root length, root surface area, root volume and total root length in Kharchia 65 and most of the RILs as compared to HD 2851. Total dry weight of the Kharchia 65 and RILs decreased less than that of HD 2851. Dry matter partitioning to roots improved in Kharchia 65 and RILs, but decreased in HD 2851. Reduction in LAR and LA was observed in parental genotypes and RILs. Compared to HD 2851, Kharchia 65 and RILs showed less reduction in AGR, RGR and NAR. HD 2851 had lower Na^+/K^+ ratio in roots than in leaves. Whereas, Kharchia 65 and RILs had lesser Na^+/K^+ ratio in leaves than in the roots. RIL-5, RIL-7 and RIL-17 were identified as tolerant RILs and RIL-13 and RIL-14 as susceptible RILs. Up-regulation of *TaNHX1* and *TaAVP1* genes was observed in root and shoot of RIL-5, however no major change in expression level of these genes was observed in RIL-13 following salt treatment.

Genome-wide discovery and characterization of miRNAs and target genes under water deficit stress conditions in chickpea

Chickpea is the third most important legume grown worldwide, and India is the largest producer and consumer of chickpea. The production of chickpea in India and elsewhere is adversely affected by several abiotic stresses like drought, salinity, low temperature and biotic stresses like insect, fungal and viral diseases. Drought/water-deficit is most severe and the number one abiotic constraint to chickpea production throughout India, as the crop is largely grown as a rainfed crop during the post-rainy season. Drought resistance is regulated by hundreds of genes that control various morphological and physiological responses to drought. MicroRNAs (miRNAs) are non-coding RNAs of 21-24 nt in length and have emerged as major regulatory molecules which regulate gene expression during drought stress. Two genotypes, ICC4958 (drought tolerant) and ICC1882 (drought sensitive) were subjected to drought and tissue was used for construction of four small RNA libraries which were sequenced using next-generation sequencing technology. A total of 146.7 million reads were generated. Bioinformatics analysis revealed 379 unique miRNA sequences including 224 conserved miRNAs, belonging to 51 families, and 155 novel miRNAs from two contrasting chickpea genotypes. In silico analysis suggested differential expression of 98 miRNAs between drought-tolerant and -sensitive genotypes under water-deficit stress. More than one thousand mRNA targets involved in diverse cellular processes were predicted for all the miRNAs using psRNAtarget and miRanda web server. Genomic locus distribution of identified miRNAs was mapped on eight chickpea chromosomes. Poly(A)-based qRT-PCR (Quantitative real-time PCR) was used to validate eleven conserved and six novel miRNAs indifferent genotypes- drought tolerant (ICC 4958 and Pusa-362) and drought sensitive (ICC1882 and SBD377). miR159, miR171 and miR390 emerged out as drought-responsive miRNAs in tolerant genotype. The expression of selected miRNAs in extreme RILs with low and high root biomass was also evaluated and found to be similar to parents. miR166 and miR171 targets homeobox-leucine zipper protein and Scarecrow-like transcription factor, respectively were validated by 5'RLM-RACE. The elucidation of the complex mechanisms underlying drought resistance in chickpea and the identification of key genes and understanding of interactions among them will accelerate the development of new varieties with enhanced drought tolerance.

Theme 2. Biotic stress resistance

Screening of *Bacillus thuringiensis* isolates recovered from different agro-climatic zones in India for the presence of *vip3*-type genes

A collection of 84 *B. thuringiensis* isolates recovered from various sources, sampling sites, and different agro-climatic zones of India comprising 11 states and 2 union territories was screened by using PCR for the presence of partial (608 bp) and full length (2.37 kb) *vip3* type genes. For amplification of partial (608 bp) *vip3* type genes, single pair of primer was used while for amplification of full length (2.37 kb) *vip3* type genes 4 different sets of primers specific to different types of *vip3*- gene namely set I for *vip3Aa*, set Π for *vip3Ab*, *vip3Ae*, *vip3Ag*, set Ш for *vip3Af* and set IV for *vip3Ad, vip3Ah* were used. Out of 84 native *B. thuringiensis* isolates 43 (51.19%) isolates found positive for 608 bp partial *vip3* gene sequence and 29 (34.52%) isolates namely SK-3, SK-5, SK-82, SK-223, SK-232, SK-305, SK-415, SK-700, SK-758, SK-793, SK-870, SK-911, SK-926, SK-933, SK-952, SK-1317, SK-1386, SK-223,SK-664, SK-793, SK-933, SK-944, SK-1386, SK-758, SK-911, SK-793, SK-870, SK-952, SK-1383 were found positive for full length *vip3*- type genes (2370bp). *vip3Aa* type genes (set I) were found most prevalent (17 out of 29). This is followed by Set Π (6 out of 29) and Set IV (4out of 29). The occurrence of *vip3Af* type genes was the least (2 out of 29). In Frequency distribution study of positive isolates for *vip3*- type genes according to agro-climatic zones, Upper Gangetic Plain Region was found to be most abundant for *vip3*-type genes (80%) followed by Southern Plateau and Hills Region (75%) and Gujarat Plains and Hills Region (66.67%). In the Frequency distribution study of positive isolates for *vip3*- type genes according to the source from which native *B. thuringiensis* isolates were collected, the prevalence of *vip3*-type genes were observed in isolates recovered from soil (53.73%) followed by grain dust (50%) and phyllosphere (50%). In Frequency distribution study of positive isolates for *vip3*- type genes according to sampling sites within the soil from which native *B. thuringiensis* isolates were collected, the prevalence of *vip3*- type genes were observed in isolates recovered from field soil and cattle shed soil (61.29%). Out of 17 positive isolates total of 5, *vip3Aa* type genes amplified by using primer set I namely SK-758, SK-793, SK-911, SK-952, and SK-1317 were cloned in pGEM-T easy vector and sequenced. Multiple sequence alignment results suggested that all 5*vip3Aa* type genes carry nucleotide substitution at one or more positions and were found novel alleles of *vip3Aa* type gene. The highest number of nucleotide substitutions was obtained in *vip911* and *vip1317* (7 substitutions each). Similarly, the highest number of amino acid substitutions was 5 and shown by Vip911, Vip952, and Vip1317. Because of their novelty, NCBI accession number was given to all 5 *vip3Aa* type genes *viz.* MZ191100 (*vip793*), MZ191101(*vip758*), MZ191102 (*vip911*), MZ191103 (*vip952*), and MZ191104 (*vip1317*) and new names were awarded to each gene *viz.vip3Aa81, vip3Aa82, vip3Aa83, vip3Aa84,* and *vip3Aa85* for*vip793, vip758, vip911, vip952, and vip1317* respectively. Protein modeling of all 5 newly identified proteins has been done by using Phyre2 and I-TASSER and confirmed and validated by 'ERRAT' and 'Verify 3D'. Family and domain analysis suggested that all 5 proteins belong to the 'Vegetative Insecticidal Protein (VIP)' super family and have 2 conserved domains namely Vip3A_N (12 to 188 amino acids) and CBM_4_9 (536 to 652 amino acids). Ramachandran plot analysis done by PROCHECK revealed that all 5 models had >90% residues in the most favored region and hence considered as best models. The instability index of all 5 proteins was found less than 40 and hence considered stable under *in vitro* conditions. Multiple sequence alignment of all 5 newly identified proteins with *vip3Aa44* (Cloned in our lab and previously found toxic to *H. armigera*) as all proteins show a significant difference in amino acid sequence as compared to *vip3Aa44*, we can say that they may differ slightly in their toxicity toward target pests. All the amino acid substitutions found in all 5 newly identified proteins were classified domain-wise to get further details about their effect on protein function. Amino acid substitutions in domain I and domain Π are found in all 5 proteins. Only 2 proteins, namely Vip911 and Vip952, have substitution in domain Ш. All proteins except Vip952 have amino acid substitutions either in domain IV and domain V. As domain IV and domain V are involved in receptor binding due to amino acid substitutions to these domains our proteins may bind to different receptors in the insect mid-gut. An attempt was made to understand docking interactions between Vip793 protein with insect receptor Sf-SRC (*Spodoptera frugiperda*- Scavenger like Receptor C). Two hydrogen bonds were seen in the Vip protein-receptor complex. One is between residue 243 (Leu) of protein with 489 (Pro) of receptor and the second is between 244 (Phe) of protein with 475 (Arg) of the receptor.

Theme 3. Basic research

Sub-cellular localization of *MIZ1* (MIZU-KUSSEI 1) homologs in wheat

Roots constitute a vital trait for dehydration avoidance. Roots exhibit hydrotropism i.e., differential growth towards higher water potential, which may play important role in drought avoidance. However, the detailed molecular mechanism of sensing and signaling of moisture gradient which ultimately governs the growth and development of root under drought stress remains largely unexplored. *Mizu Kussie1* (*MIZ1)* is a gene essential for hydrotropism in Arabidopsis. To analyze the molecular function of *MIZ1* homologs in wheat, sub cellular localization of *MIZ1* homologs of wheat was carried out in the present study. For this, 4 *MIZ1* homologs in wheat viz. *TaMIZ1*-1, *TaMIZ1*-3, *TaMIZ1*-6 and *TaMIZ1*-7, were amplified and cloned in *pCAMBIA1300:GFP* binary vector and N- terminal *GFP-MIZ1* fusion constructs were developed. The constructs were confirmed by PCR, restriction digestion and sequencing. Subsequently the constructs were transformed into Agrobacterium and transient expression analysis was carried out in onion epidermal peels. The localization of the fusion protein at subcellular level was captured using the confocal microscopy which revealed that four of the *TaMIZ1* protein were localized in cytoplasm and may be localized surrounding the nucleus.

Genome-wide identification and cloning of cytokinin oxidase/dehydrogenase 5 (*CKX5*) gene from *Brassica juncea*

Indian mustard (*Brassica juncea*) is the second most important oilseed crop next to soybean in India contributing about 25-30% of oilseed production. Despite India is being the world's fourth-largest producer of rapeseed mustard, the productivity is comparatively far behind the EU, Canada, and China. The conventional breeding method has been found an effective strategy for increasing the yield but the narrow genetic base and limited germplasm resources have limited its success which can be addressed by adopting genetic modifications or gene-editing strategies to manipulate the candidate genes and pathway. The cytokine in oxidase/dehydrogenase (*CKX*) regulates the cytokinin homeostasis and found a promising gene to manipulate for the yield and stress tolerance enhancement. The *CKX3* and *CKX5* are the key enzymes known to improve yield attributing traits as observed in the *ckx3* and *ckx5* mutants of Arabidopsis, *B. napus,* and barley. The present study was aimed to clone and analyze the *CKX5* genes present in the allotetraploid (AABB; 2n=36) genome of the *B. juncea* using the homologs sequence information. We have cloned the *CKX5* homolog of *B. juncea* and submitted the gene sequence information to GenBank. The local blast of the whole-genome sequence of *B. juncea*cv. Varuna with the cloned *BjCKX5* homolog, Two different *CKX5* paralogs were predicted to be present on A7 and B7 chromosomes. These paralogs were named *BjCKX5*-X1 and *BjCKX5*-X2 isoforms. The FAD_binding_4 domain was found universally present in all the *CKX5* homologs but with the common and varying motifs in the*CKX5* homologs. The gene structure of both the *BjCKX5* isoforms was comprised of 5 exons and 4 introns. The nucleotide discrepancies between these two isoforms have little impact on the amino acid sequence and thus also over the 3D protein structural characteristics. The cladogram distribution showed the *BjCKX5*-X1 could be the ortholog to the *B. rapa CKX5* as they grouped and sharing the same chromosome A7. The *BjCKX5*-X2 isoform present on the B7 chromosome was distantly placed individually in a separate clad and that may probably be the descendent of another progenitor species *B. nigra* with 'BB' genome. In further studies, the *CKX5* paralogs identified in *B. Juncia* need to be cloned and the sequence information obtained will be used for targeted gene editing followed by expression studies in Indian mustard.

Understanding the molecular mechanism of flowering in response to photoperiod in pigeonpea [*Cajanus cajan* (L) Millsp]

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

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the Student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Akash Maity	21308	M.Sc.	Subcellular localization of MIZ1 (MIZU KUSSEI 1) homologs in wheat	Dr. Monika Dalal
2.	Rekha Mahato	21309	M.Sc.	Study of allantoin mediated salinity tolerance in rice genotype IR-29	Dr. Tapan Kumar Mondal
3.	Mutawar Ashfak S.	21310	M.Sc.	Screening of *Bacillus thuringiensis* isolates recovered from different agro-climatic zones in India for the presence of vip3-type genes	Dr. Sarvjeet Kaur
4.	Mahamed Ashiq I	21311	M.Sc.	*In silico* whole-genome analyses of MBF1 (Multiprotein Bridging Factor 1) gene and phenotypic characterization of heat stress responses in two contrasting wheat cultivars (*Triticum aestivum* L)	Dr. Sharmistha Barthakur
5.	Shwetha R.	21312	M.Sc.	Characterization of gene CaM (Calmodulin) from *Pennisetum glaucum* (L.) R.Br for its role in heat stress tolerance	Dr. Jasdeep C. Padaria
6.	Ankita Vilasrao Chinche	21313	M.Sc.	Molecular and biochemical analysis of traits related to salt tolerance in RIL mapping population of wheat (*Triticum aestivum* L.)	Dr. Kanika
7.	Anindita Barua	21314	M.Sc.	Genome-wide identification and cloning of cytokinin oxidase/dehydrogenase 5 (CKX5) gene from *Brassica juncea*	Dr. N. C. Gupta
8.	Lal Bahadur Singh	10696	Ph.D.	Genome-wide discovery and characterization of miRNAs and target genes under water-deficit stress conditions in chickpea	Dr. P. K. Jain
9.	Kishor Uttamrao Tribhuvan	10840	Ph.D.	Understanding the molecular mechanism of flowering in response to photoperiod in pigeon pea (*Cajanus cajan* (L) Millsp)	Dr. Kishor Gaikwad

Plant Physiology

17

Prof. Madan Pal Singh

The Division of Plant Physiology has mandate to conduct basic and strategic research with a view to understand the processes leading to solution of problems in crop productivity; to train Post-Graduate students leading to M.Sc. and Ph.D. degree; to impart training in physiological tools to agricultural scientists of SAUs/ICAR Institutes. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Plant nutrition

Interactive effects of elevated [CO_2] and nitrogen fertilization on yield and nitrogen response of bread wheat

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

Genome wide association study for nutrient use efficiency and its regulation by nitrogen in rice

Rice as a staple meal, provides the majority of dietary nutrients to billions of people around the world. Unfortunately, rice grains are not dense in mineral nutrients, and thus have nutritional shortages for rice-dependent people. This study was planned to identify rice genotypes accumulating high micronutrients (Cu, Fe, Mn, Mo& Zn) in grain even under nitrogen deficit conditions, and their regulation by nitrogen and to identify the involved QTLsfor nutrient use efficiency. The study was planned with 300 rice genotypes raised under climate-controlled greenhouses of Nanaji Deshmukh Plant Phenomics Facility, ICAR-IARI, New Delhi during kharif season 2019 using two nitrogen treatments. Micronutrient content from brown were determined using ICP-OES. Significant decrease in micronutrient content of grain was observed under nitrogen stress conditions, except for manganese. Nitrogen stress could have affected the absorption, translocation and assimilation abilities of these micronutrients. We also identified potential contrast donors for grain micronutrient content.The genotypes 384190 and BAM4797 were found to accumulate both high zinc (52.54 and 81.64 ppm resp.), and iron (48.51 and 49.62 ppm resp.) under control conditions. Under nitrogen stress, Safri-17 accumulated high Zn (47.61ppm) and Fe (35.95ppm). Utilization efficiency of elements under nitrogen stress were increased except for manganese, while the use efficiencies of elements decreased in stress conditions. Partition efficiency also decreased under stress conditions except for manganese. Under control conditions, zinc was positively correlated with nitrogen percent in grain. Under nitrogen stress conditions, nitrogen percent in grain has significant positive correlation with Cu, Mo, Mn and Zn concentration in grain but not with iron, which shows a negative correlation. Population structure analysis revealed the presence of four sub-populations in our panel. Using GWAS, 51 QTLs (40 novel and 11 previously reported) for micronutrient content under control and 39 QTLs (29 novel and 13 previously reported) under nitrogen stress conditions, and several QTLs associated with micronutrient use efficiencies were identified. Further annotation will help to find putative candidate genes explaining mechanisms under grain micronutrient accumulation. Co-localized QTLs for Mn and Zn and for Cu and Zn were identified, which can be utilized to improve these elements simultaneously in rice grain. The novel QTLs identified for association of micronutrient utilization efficiency, micronutrient use efficiency, partition efficiency and relative index for each elements, will give a new way to look into and aid in understanding of the complex mechanisms of nutrient uptake, assimilation and partitioning to rice grains.

Study on grain quality in wheat under different nitrogen conditions

Malnutrition due to micronutrients deficiency (mostly Zn and Fe) affects a large percentage of the world's population. Wheat (*Triticum aestivum* L.) is one of the most widely grown crops worldwide. As a staple meal, wheat grain provides the majority of dietary nutrients to billions of people around the world. Unfortunately, wheat grains are not dense in mineral nutrients, and thus nutritional shortages are widespread among wheat-dependent people. A study was planned to select wheat RILs from the population accumulating high micronutrient in grain even under nitrogen deficit conditions by analyzing micronutrient concentration in wheat grains under nitrogen treatments in parents and their RILs and mapping QTLs/genes for micronutrient concentration in grains by using SNP based linkage map. The RILs population (RAJ 3765 X HD 2329) was raised under climate-controlled greenhouses of Nanaji Deshmukh Plant Phenomics Facility, ICAR-IARI, New Delhi during *rabi* season of 2019, under nitrogen-deficient conditions. By the diacid digestion method, grain samples were digested, and nutrient content were determined using ICP-OES. The phenotypic data showed a significant decrease in grain nutrient content under nitrogen-deficient conditions, but Sr and Na slightly increasedunder nitrogen treatment. Nitrogen stress could have affected the absorption translocation and assimilation abilities of other nutrients. Nitrogen deficiency reduces the accumulation of nutrients significantly, i.e., the nitrogen status of the plants was positively correlated with all elements. Network plot-correlation analysis between nutrients showed a high positive correlation between Na- Sr, Fe-Mg, K-Ca, Fe-Ca in the control condition and Fe-Al, Na-Sr, Fe-Mg in N treatment conditions, and negative correlation between Mo- Na, Fe,-Al, Al-Ni in the control conditions and Mo-Na, Fe-Al, Fe-Ni in N treatment conditions. ICI QTL mapping was done for each trait separately for control and nitrogen stress conditions. We identified 19 QTLs under control and 10 QTLs under nitrogen stress conditions.

Characterization of physiological and molecular responses of maize (*Zea mays* L.) associated with adaptation to nitrogen stress

Nitrogen (N) is one of the most critical elements for growth and development of the plants. N deficiency can lead to a significant reduction in yield and yield related traits in maize. Forty maize inbred lines were assessed at three crop growth stages (i.e. seedling, vegetative and flowering) for nitrogen use efficiency under sufficient and deficient N conditions. Significant variation was observed in the morpho- physiological and agronomical traits. Analysis of morphological-physiological traits formed two distinct clusters i.e. CI and CII based on the response of inbred lines to nitrogen limiting conditions. The CI included inbred lines, viz., DMI 4, DMI 5, DMI 22, DMI 27 and DMI 56 derived from the drought or thermal tolerant parent i.e. HKI 335 and LM 17 with less reductions in growth-related parameters as compared to cluster CII inbred lines derived from sensitive genotypes i.e. MGUD 22 and HKI 1015wg8. Nitrate reductase (NR) and glutamine synthetase (GS) activitieswere observed to be more critical for screening at early growth stage. The identified inbred lines have the potential for developing maize hybrids with improved nitrogen use efficiency in future breeding programs. A comparative transcriptome analysis using leaf and root tissues from contrasting inbred lines, viz., DMI 56 (tolerant to N stress) and DMI 81 (susceptible to N stress) was performed to delineate the differentially expressed genes (DEGs) under low N stress. The contrasting lines were grown hydroponically in modified Hoagland solution having either sufficient- or deficient- N, followed by high-throughput RNA-sequencing. A total of 8 sequencing libraries were prepared and 88-97% of the sequenced raw reads were mapped to the reference B73 maize genome. Genes with a p-value ≤ 0.05 and fold change of ≥ 2.0 were considered as DEGs in various combinations performed between susceptible and tolerant genotypes. DEGs were further classified into different functional categories and pathways according to their putative functions. Gene Ontology based annotation of these DEGs identified three different functional categories: biological processes, molecular function, and cellular component. The KEGG and Mapman based analysis revealed that most of the DEGs fall into various metabolic pathways, biosynthesis of secondary metabolites, signal transduction, amino acid metabolism, N-assimilation and metabolism, and starch metabolism. Some of the key genes involved in N uptake (high-affinity nitrate transporter 2.2 and 2.5), N assimilation and metabolism (glutamine synthetase, asparagine synthetase), redox homeostasis (SOD, POX), and transcription factors (MYB36, AP2-EREBP) were found to be highly expressed in the tolerant line compared to susceptible one.

Theme 2. Abiotic stress tolerance

Hormonal regulation of stay green trait under heat stress in wheat (*Triticum aestivum* L.)

Wheat is one of the most extensively grown cereal crops in the world and is often exposed to a short period of heat stress during anthesis and grain filling. Heat stress at postanthesis induces leaf senescence and forced maturity resulting in poor yield. Delayed leaf senescence atpost anthesis, often referred to as the stay-green trait, which maintains photosynthetic activity for a longer period and produces higher yield. An alternative approach for maintaining stay green is hormone therapy. Stay green traits have been attributed to higher cytokinin levels and or reduced ethylene production or perception. Therefore, in order to study the hormonal regulation of stay-green trait under heat stress in wheat, the present thesis work was carried out with two experiments. In first experiment, 32 diverse wheat genotypes were screened for the stay-green trait under dark stress conditions in the lab and two contrasting genotypes namely Chirya 3 (stay green type) and HD 2329 (non- stay green type)were selected for subsequent experiment II, which comprised of two main treatments i.e. normal sowing (18 Nov 2020) and delayed sowing (18 Jan 2021) for heat stress and five sub- treatments for hormonal manipulation i.e. control (water spray), lovastatin (Lova) (an inhibitor of cytokinin), benzyl aminopurine (BAP), thidiazouron (TDZ) and cobalt chloride ($CoCl_2$) (an inhibitor of ethylene) at anthesis stage to alter the endogenous level of phytohormones. Results of the study showed reduction in SPAD value, NDVI, leaf area, MSI, RWC, CTD, photosynthetic pigments, PN, gs, TR, dry matter partitioning, Fv/Fm ratio, YII, yield and its attributes, and enhancement in senescence score, NPQ, lipid peroxidation, H_2O_2, total soluble sugar, proline content, antioxidant enzymes activity, chlorophyllase enzyme activity under late sown heat stress condition. In general, foliar application of BAP, TDZ, and $CoCl_2$ enhanced SPAD value, NDVI, leaf area, MSI, RWC, CTD, photosynthetic pigments, PN, gs, TR, Fv/Fm ratio, YII, NPQ, total soluble sugar, proline content, dry matter partitioning to ear, yield and its attributes, heat tolerance index and restricted lipid peroxidation, H_2O_2, chlorophyllase activity, heat susceptibility index while the contrasting results were obtained with the application of lovastatin. The study concluded that application of BAP, TDZ, and $CoCl_2$ enhanced stay-green trait, heat tolerance, and yield by increasing photosynthetic pigments, PN, gs, TR, partitioning, Fv/Fm, NPQ, YII, osmolytes, MSI, CTD, RWC, antioxidant enzymes activity, leaf area and by decreasing ROS production, Chl degradation, lipid peroxidation, and CHLase activity.

Physiological characterization of mutants for awn length in wheat

Heat stress is a critical impediment to the yield of wheat. The importance of ear and ear-related traits in conferring yield stability under heat stress has been reported in number of studies. Awns are the most significant organ of wheat ear and play active role in photosynthesis and transpiration. In view of climate change, the awns have more physiological relevance and need to be given more attention with respect to their role in yield stability and thermo-tolerance in wheat. A study was taken up with an objective to study the role and contribution of awns and awn length in selected mutant lines of wheat variety HD 3086. This study was conducted on six selected mutant lines (86-63, 86-156, 86-243, 86-369, 86-387 and 86-425) of wheat variety HD 3086 in comparison to wild-type (referred as control). Various physiological investigations were made on the crop grown in the field under normal sown (18th November) and late-sown (23rd December) conditions. Late-sown resulted in heat stress wherein the crop faced higher mean temperature of about 3.8 ^{o}C during anthesis to crop maturity and 7.6 ^{o}C during ten days prior to anthesis in comparison to normal sown crop. Results revealed that all the mutant lines have reduced awn length in comparison to control under normal as well as under heat stress conditions. SPAD value, Fv/Fm ratio, photosynthesis rate, stomatal conductance, Ci and transpiration rate of flag leaf at post-anthesis stage for mutant lines were also comparable to control. Shortness of awns also caused higher awn temperature at anthesis and thereby overall higher ear temperature. Awn temperature always remined higher by 1.5 to 4.0 ^{o}C than ear temperature for control as well as mutant lines. Shortness of awn also caused negative relationship between grain number and TGW of main ear under heat stress condition. Heat stress caused significant decrease in TGW of main ear in control. So, shortness of awns (in mutant lines) caused reduction in grain number of mainear but had no adverse effect on TGW of main ear under heat stress. Due to shortness of awns, grain number as well as TGW served as the determinants of grain yield of main ear while, it was only the TGW that served as key determinant for control. Grain yield/plant for mutants was found to be linked inversely with ear and awn temperature at anthesis under normal condition. Findings of this study confirmed the significance of optimum length of awns in wheat plant for getting better and stable yield under heat stress conditions. Thus, awn length can be an important physiological trait in future breeding programs ofwheat meant for normal, high temperature and other stress prone environments.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Sinto Antoo	21335	M.Sc.	Interactive effects of elevated [CO_2] and nitrogen fertilization on yield and nitrogen response of bread wheat	Dr. Lekshmy S.
2.	Nidhi Chaturvedi	21336	M.Sc.	Genome wide association study for nutrient use efficiency and its regulation by nitrogen in rice	Dr. Dandapani Raju
3.	Animireddy China Malakondaiah	21338	M.Sc.	Study on grain quality in wheat under different nitrogen conditions	Dr. Sudhir Kumar
4.	Jyoti Mehra	21339	M.Sc.	Hormonal regulation of stay green trait under heat stress in wheat (*Triticum aestivum* L.)	Dr. Pramod Kumar
5.	Gopa Deb	21340	M.Sc.	Physiological characterization of mutants for awn length in wheat	Dr. Vijay Paul
6.	Prabha Singh	10702	Ph.D.	Characterization of physiological and molecular responses of maize (*Zea mays* L.) associated with adaptation to nitrogen stress	Dr. Ishwar Singh

School of Horticultural Sciences

Discipline	Number of Thesis Submitted	
	M.Sc./M.Tech	Ph.D.
Floriculture and Landscape Architecture	05	02
Fruit Science	06	03
Post-Harvest Technology	06	06
Vegetable Science	10	05
Total	**27**	**16**

Floriculture and Landscape Architecture

18

Prof. Kanwar Pal Singh

The Division of Floriculture and Landscaping heralded an articulated and comprehensive research programmes on crop improvement using conventional and biotechnology tools, production in open and protected environments, technology dissemination for the benefit of farming fraternity. The Division has following mandates to carryout basic and applied research for crop improvement and development of production technology in important flower crops; to impart Post Graduate teaching and human resource development; dissemination of information and transfer of technology through outreach programmes. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Improvement of flower crops

Cold tolerance studies in marigold (*Tagetes* species)

Marigold (*Tagetes* spp.) is one of the popular ornamental crop belonging to family Asteraceae. It is extensively grown for production of loose flowers for making garlands, religious offerings, social functions and pigment extraction in addition to its use for garden display as bedding, potplantetc. Cold tolerance is an important genotypic trait to be considered when selecting marigold cultivars for growing under low temperature stress conditions as its growth and flowering are drastically reduced at low temperature.In the present study, twenty marigold genotypes i.e. ten genotypes from African marigold (*Tagetes erecta* L.) and ten genotypes from French marigold (*Tagetes patula* L.) were taken to observe their responses to morphological, physiological, biochemical and image based (high through-put phenotyping) parameters in relation to low temperature stress. The plants of these genotypes were grown in pots during winterseason,in two environments i.e. outside polyhouse and inside polyhouse under twosets of experiment (first set of experiment from mid-November to mid-February and second set of experiment from December end to April end) to study the effect of low temperature prevailing during December and January in Delhi conditions on various morphological, physiological, biochemical and image based (High through-put phenotyping) parameters of young plants (in second set of experiment) and well grown plants (in first set of experiment) of these genotypes grown outside polyhouse andinside polyhouse.

In African marigold genotypes, the morphological parameters likeplantheight, number of primary branches, stem diameter, leaf length, leaf area, flower diameter, length of the petal and flower longevity on the plant were outperformed in genotype Af. /W-4 followed by the genotypes Pusa Bahar, Pusa Basanti Gainda, Af/W-1 and Af./W-7. Among the physiological and biochemical parameters, maximum Relative Water Content, photosynthetic and transpiration rate, chlorophyll a, b & totalchlorophyll content, total carotenoids, Super Oxide Dismutase, Catalase, Guaiacol Peroxidase antioxidant enzymes, Total Phenolic Content, proline content, protein content and minimum Electrolyte Leakage Rate and Malondialdehyde content were also found in genotype Af./W-4. Under non-destructive image analysis studies through high through-put phenotyping, genotypeAf. /W-4 was found to have higher plant area, convex hull, greenness, water content, compactness and caliper length compared to the other genotypes.

In French marigold genotypes, Pusa Arpita genotype outperformed the others in terms of morphological parameters such as plant height, plant spread, number of secondary branches/plants, flowering duration, weight of the single flower, flower yield/plant, number of petals per flower and flower longevity on the plant followed by the genotypes Hisar Beauty and Hisar Jafri. Among the physiological and biochemical parameters, Hisar Beauty genotype had the highest Relative Water Content, Super Oxide Dismutase, Catalase, Guaiacol Peroxidase antioxidant enzymes, Total Phenolic Content, proline content and the lowest Electrolyte Leakage Rate and Malondialdehyde content followed the genotypes Hisar Jafri and, Pusa Arpita. In image-based traits, the genotype Hisar Jafri had higher plant area and greenness while genotype Hisar Beauty had higher water content and compactness and the genotype Pusa Arpita had higher caliper length. When comparing the two sets of experiments, the first set of experiment showed a higher level of cold tolerance based on the assay ofvarious morphological, physiological, biochemical and image based (high through-put phenotyping) traits compared to the second set of experiment in both African and French genotypes.

Development of *in vitro* regeneration protocol in apetalous male sterile lines of marigold (*Tagetes erecta* L.)

Marigold (*Tagetes* spp.) is a popular ornamental crop belonging to Asteraceae family. In recent years, F1 hybrids are gaining tremendous popularity among marigold growers. Male sterile (MS) lines are widely used as female parent for hybrid seed production. Among the three types of male sterility systems reported in marigold, apetalous form is commercially utilised for hybrid development. The apetalous form of male sterility in marigold is controlled by a single recessive gene (msms), and is often maintained by crossing male sterile (msms) plants with heterozygous (Msms) maintainers. The maintenance of these MS lines through conventional method results in both male sterile and fertile plants in a 1:1 ratio in the female line. Hence, only 50% of the male sterile plants form the female line can be exploited for hybrid seed production and the remaining 50% of the male fertile plants needed to be rogued out at the flowering stage. Thus, there is a need to develop high throughput in vitro regeneration protocol for the apetalous male sterile lines of marigold. The explant types, genotypes and the growth regulators are among the major factors influencing the in vitro regeneration in marigold. Further, in vitro regenerated plants, when exposed to outdoor environment, show a very high mortality that necessitates for the standardization of ex vitro hardening strategies. Hence, in the present study we have optimized the explants and growth regulators for rapid regeneration of apetalous male sterile lines of marigold and standardized the ex-vitro hardening strategies for improving the field survival of in vitro regenerated plants. Surface sterilization of different explants with 0.2 % $HgCl_2$ for 7 minutes was found effective in improving the survival of explants and simultaneously reducing the microbial load from the explants. Modified MS medium (MS medium enriched with 125 mg/ l of PVP, 0.2 mg/l of GA3, and 30 g/l of sucrose) supplemented with 1.5 mg/l of TDZ and 0.2 mg/l of NAA, recorded the maximum culture establishment, early shoot initiation and longest shoots in both the explants. Among the two explants, shoot tip explants exhibited better culture establishment than the nodal segment explants. When the effectiveness of two cytokinins was compared for mass multiplication, kinetin was found to be superior over TDZ for in vitro proliferation of male sterile lines of marigold. Among the different media, modified MS medium enriched with kinetin of 0.5 mg/l and 0.1 mg/l NAA was found optimum for mass multiplication of quality shoots in marigold.

While, optimizing GA3 concentrations for shoot elongation, the lengthiest shoots were recorded on MS medium fortified with 1.0 mg/l of GA3. Treatment, TR1- comprising of half strength MS medium fortified with 0.5 mg/l of IBA was found best for in vitro rooting of male sterile lines of marigold. Among the various in vitro hardening strategies, the maximum survival and optimum growth of in vitro raised plantlets was noticed when they were hardened in poly propylene glasses filled with sterilized peat + soilrite mixture and covered with propylene cover. During ex vitro hardening, the highest survival along with the optimum vegetative growth of in vitro regenerated plants was observed in the treatment comprising of soil and Vermicompost at 3:1 ratio enriched with 20 g VAM consortia. Among the three male sterile lines of marigold, MS-5 displayed the highest in vitro establishment and regeneration potentials and exhibited better in vitro mass proliferation, rooting and hardening abilities over the two male sterile. The developed protocol can be efficiently utilized for high throughput in vitro mass multiplication of apetalous male sterile lines of marigold. Large scale use of developed protocol will eliminate the need for roughing of male fertile plants from female parent during F1 hybrid seed production of marigold. Further, the ex-vitro hardening strategy established in this study can be effectively utilized to improve the field survival of in vitro regenerated plantlets of marigold. In long term, this study will facilitate the hybrid seed production in marigold and will prove effective in reducing the hybrid seed production cost.

Studies on crossability and white rust resistance in chrysanthemum (*Dendranthema* x *grandiflora* Tzvelv)

The present investigation was carried out in the research block of the Division of Floriculture and Medicinal Crops, ICAR-Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bengaluru, during 2016-17 and 2017-18. The objectives of the investigation were floral biology studies of selected Chrysanthemum genotypes, identification of compatible chrysanthemum genotypes and screening of half-sib progenies for quality as well as resistance to white rust. Chrysanthemum is popularly called as “Queen of the East”. It belongs to the family Asteraceae and recognized as a potential flower crop for cut, loose flower and also as pot plants in many countries. It is second most important cut flower and fourth as potted plant in global trade. It is a lucrative flower crop, which fetches more income to the farmers compared to other field and commercial crops. A total of 20 genotypes were selected for floral biology studies. The floral biology result revealed that the day to first flower opening was recorded earliest in Local White (65 days) and Sweta Singar (65.50 days), peak time of anthesis from 9.30 h to 10.30 h. and genotype IIHR6-32 (4.11 days) recorded maximum days to anther dehiscence. The maximum pollen viability was recorded in Red Stone (95.02%) followed by IIHR6-26 (88.20%), IIHR9-3 (87.44%) and Sweta Singar (85.59%). The maximum pollen size was recorded in the genotype IIHR9-3 (38.20 µm), while, PEG4000 at 20% recorded maximum pollen germination in 43.57% (IIHR9-3) followed by 19.43% (Kalpana) and 19.34% (IIHR6-29). A combination of 10% sucrose + 15% PEG, recorded maximum pollen germination in IIHR2-7 (42.27%) which was on par with IIHR6-26 (42.24%). However, 15% sucrose + 30% PEG recorded maximum pollen germination in IIHR6-26 (41.76%) followed by IIHR2-7 (38.64%) and Red Stone (31.66%). Maximum duration of stigma receptivity was recorded in genotypes Garden Beauty and Local White (21.67 h). The different concentration media such as sucrose, PEG4000 and in combination were used before pollination to achieve successful cross. The seeds collected from only one successful cross IIHR6-41 x Mixed Pollen (MP) recorded 25.68% (15% sucrose) to 40.74% (10% sucrose) seed setting and IIHR6-41 x MP recorded 26.74% (15% sucrose) to 54.12% (control) seed germination. Among PEG4000 concentrations, the seed setting was ranged from 1.57% (Ajay x MP) to 31.35 % (IIHR6-41 x MP). The seed germination in one successful cross IIHR6-41 x MP recorded 54.48% germination. Among sucrose and PEG4000 concentrations, seed setting was observed in five crosses i.e. Ajay x MP, Arka Chandrika x MP, Arka Kirti x MP, Lal Pari x MP and IIHR6-41 x MP. Seed setting was ranged from 1.69 (Ajay x MP) to 39.32 (IIHR6-41 x MP). Seed germination was recorded in four crosses i.e. Arka Chandrika x MP, Arka Kirti x MP, Lal Pari x MP and IIHR6-41 x MP, found significant seed germination ranged from 3.27% (Arka Chandrika x MP) to 49.02% (IIHR6-41 x MP). Seed setting was observed in five crosses i.e. Ajay x MP, Arka Chandrika x MP, Arka Kirti x MP, Lal Pari x MP and IIHR6-41 x MP. Among crosses and sucrose + PEG concentrations, 10% sucrose + 15% PEG with crosses Arka Chandrika x MP and IIHR6-41 x MP recorded seed set ranged from 3.44% to 52.65%, respectively. Among crosses and sucrose + PEG concentrations, cross Arka Kirti x MP with 5% sucrose + 10% PEG recorded significantly lowest seed germination (6.19%), whereas, cross IIHR6-41 x MP with (10% sucrose + 15% PEG) recorded highest seed germination (60.50%). Evaluation of parents and half-sib progenies for white rust revealed that 11 genotypes namely Sweta Singar, Punjab Gold, Garden Beauty, Red Stone, Punjab Anuradha, IIHR6-32, IIHR9-3, IIHR6-41, Lal Pari, White Dolly and White Andaman were found to be resistant.Out of total 54 half-sib progenies screened, 18 half-sib progenies *viz.*, CH14-1, CH15-1, CH15-2, CH47-1, CH3-1, CH3-10, CH3-27, CH3-41, CH3-51, CH3-70, CH3-74, CH3-81, CH3-121, CH3-128, CH3-150, CH3-155, CH3-156, CH3-162 recorded nil disease index.The half-sib progenies namely CH14-1, CH14-2, CH15-1, CH15-2, CH3-1, CH3-121, CH3-162 does not showed any disease. These seven half-sib progenies also have superior horticultural traits such as flower colour, dwarf and compact growth habit.

Theme 2. Crop production and management in flowering plants

Response of organic manure and inorganic fertilizer on flower and bulb production of LA hybrid lilium

Lily is a non- traditional flower and considered as the king of bulbous flowers, belongs to genus Lilium which comprises of around 100 species, 7 sections and 10,000 documented cultivars. Lily is a monocotyledon belonging to Liliaceae family. Liliums are well distributed mostly in northern hemisphere (i.e., South-East Asia, North America and Europe). Lilies are highly demanded cut flower in international flower trade due to its wide diversity of flower color, attractive flower shape, long multi-flowering stalk, and having long post-harvest shelf life. Lilium is widely used as potted plant, bedding plant and cut flower. Stem bulblets and bulb divisions are very common method of propagation . In India, the area under commercial *Lilium* cultivation is growing day by day. The present study was carried out at experimental field of Division of Floriculture and Landscape Architecture and in the Laboratory of Soil Science and Agriculture Chemistry, Plant Physiology and Agronomy, ICAR-Indian Agricultural Research Institute (IARI), New Delhi during 2020-21 to study the response of organic manure (FYM) and inorganic fertilizer for better quality flower and bulb & bulblet production of LA hybrid lilium. The present investigation was conducted on LA hybrid lilium cv. Masai in a two factors factorial experiment in Randomized Block Design which comprises of 5 levels of organic manure (FYM) 0 t/ha, 10 t/ha, 15 t/ha, 20 t/ha and 25 t/ha and five levels of inorganic fertilizers ($N:P_2O_5:K_2O$) 160:120:100, 120:90:75, 80:60:50 and 40:30:25 and their combination. The findings revealed that among various concentrations of FYM @ 25 t/ha performed better in most of the vegetative growth parameter, better quality flower, bulb & bulblet production and total phosphorous content in leaves. Whereas plants applied with FYM @ 20 t/ha showed Early flower opening and early bud initiation. Among different concentration of inorganic fertilizer, plants applied with $N:P_2O_5:K_2O$ @ 160:120:100 kg/ha performed better over control in most of the parameters viz., plant height, leaf length, leaf width, stalk length, stalk diameter, bulb & bulblet production, chlorophyll, total nitrogen, phosphorous and potassium content in leaves and partitioning ratio. Plants applied with $N:P_2O_5:K_2O$ @ 120:90:75 kg/ha found early color shown and early flower opening. Whereas, plants applied with $N:P_2O_5:K_2O$ @ 80:60:50 kg/ha recorded early bud initiation.

Among different combinations of both organic manure and inorganic fertilizer, plants applied with FYM @ 25 t/ha + N:P_2O_5:K_2O @ 160:120:100 kg/ha performed better over control with respect to most of the parameters viz., plant height, leaf length, early flowering, stalk length, stalk diameter, bulb & bulblet production and total nitrogen content in leaves.

Characterization and management of phytoplasmas in rose (*Rosa* × *hybrida* L.) genotypes

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

Theme 3. Post harvest management in flower crops

Enhancing the storage life of marigold (*Tagetes erecta* L.) flowers using preservatives and packaging materials

Owing to the steady increase in demand of flowers, floriculture has become one of the important commercial businesses in horticulture. Marigold is one of the topmost loose flowers that earns high domestic as well as export value. Postharvest management of loose flowers is crucial to get good remuneration. It is important to enhance the shelf life of loose flowers and keep them attractive for a longer time after consumers' purchase. Application of chemical preservatives helps delay the process of senescence of flowers. Moreover, selection of appropriate packaging material and lining material may be game changers in maintaining quality of loose flowers during storage. Keeping these points in view, the present study was conducted to enhance the shelf life of marigold flowers under three experiments. In the first experiment, efficacy of three chemical preservatives, namely, ascorbic acid, boric acid and salicylic acid was tested to prolong the storage life of loose marigold flowers. Maximum shelf life (6.75 days) of flowers could be achieved by spray of boric acid at 4% when stored under cold storage in comparison to ambient storage conditions (4.50 days). Treatment with 4% boric acid significantly maintained higher colour intensity, flower diameter, moisture content, membrane solubility index (MSI), carotenoid content, superoxide dismutase (SOD) and catalase activity and minimized shrivelling, physiological loss in weight (PLW) and respiration rate. Guaiacol peroxidase activity was found to be maximum in the flowers sprayed with 50 ppm salicylic acid. Second experiment dealt with the selection of packaging material. Maximum shelf life enhancement could be achieved by use of shrink wrap (19.00 days) and HDPE (18.50 days) under cold storage conditions. Shrink wrapped flowers exhibited better freshness in terms of maximum diameter, colour intensity, moisture content, MSI, total carotenoids and minimum shrivelling, PLW and respiration rate. Maximum SOD, catalase, guaiacol peroxidase activity was also recorded in shrink wrapped flowers. Shrink wrapping delayed senescence of marigold flowers by regulating all enzyme activities under ambient and cold storage conditions. Selection of the lining material was done in the third experiment. Flowers kept in plastic basket lined with butter paper and covered with muslin cloth showed the maximum shelf life (12.00 days) under cold storage conditions. Maximum diameter, moisture content, MSI, total carotenoids and minimum shrivelling, PLW, respiration rate was recorded in the flowers kept in lining and covering combination.

Enhancing the shelf life of loose flowers of tuberose (*Polianthes tuberosa* L.) using preservatives and packaging materials

Tuberose (*Polianthes tuberosa* L.) is one of the topmost loose flower having high demand in domestic as well as international market.A study entitled was conducted during 2020-2021to determine the effect of various preservatives and packaging materials in enhancing the shelf life of loose tuberose flowers. In the present study among preservatives flowers treated with boric acid 4% and packed in muslin cloth bag (C_3P_2) was found to be the best with regard to maximum moisture content, floret diameter, shelf life, SOD activity and minimum respiration rate under both ambient and cold storage. Minimum PLW, maximum catalase activity under ambient and maximum colour (whiteness index) under cold storage was found in C_3P_2. Catalase and guaiacol peroxidase activity was found to be maximum in flowers treated with salicylic acid 50 ppm and packed in muslin cloth bag (C_5P_2) under cold storage.Among packaging materials, HDPE (P_2) was found to be the best with maximum moisture content on day, colour (whiteness index), floret diameter, shelf life, SOD activity, minimum PLW and respiration rate under both ambient and cold storage condition. Catalase and guaiacol activity was found to be maximum in flowers packed in LDPE (P_3) under both ambient and cold storage.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Saraswati	21282	M.Sc.	Response of organic manure and inorganic fertilizer on flower and bulb production of LA hybrid lilium	Dr. Markandey Singh
2.	Nandeesh Ganiga	21283	M.Sc.	Development of *in vitro* regeneration protocol in apetalous male sterile lines of marigold (*Tagetes erecta* L.)	Dr. Reeta Bhatia Dey
3.	Ediga Amala	21284	M.Sc.	Cold tolerance studies in marigold (*Tagetes* species)	Dr. Kanwar Pal Singh
4.	Viresh M. Belavanaki	21285	M.Sc.	Enhancing the storage life of marigold (*Tagetes erecta* L.) flowers using preservatives and packaging material	Dr. Ritu Jain
5.	Priya B.B.	21286	M.Sc.	Enhancing the shelf life of loose flowers of tuberose (*Polianthes tuberosa L.*) using preservatives and packaging materials	Dr. Krishan Pal Singh
6.	Sunil Kumar	10619	Ph.D.	Studies on crossability and white rust resistance in chrysanthemum (*Dendranthema* x *grandiflora* Tzvelv)	Dr. Rajiv Kumar
7.	Rihne T.	11033	Ph.D.	Characterization and management of phytoplasmas in rose (*Rosa* × *hybrida* L.) genotypes	Dr. Namita

Fruit Science

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Prof. Manish Srivastav

The Division of Fruits and Horticultural Technology has significantly contributed through research for the advancement of horticulture by ushering in the frontiers of knowledge in fruit crops and providing practical solutions to the problems confronting fruit industry. A strong emphasis is given on human resource development for horticultural research through post-graduate teaching in frontline areas in production, breeding and molecular research on fruit crops. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Genetical studies and molecular characterization

QTL mapping for fruit quality traits in mango (*Mangifera indica* L.)

The present investigation was carried out during 2018-2020 with the objectives to generate genetic linkage map and to identify the quantitative trait loci (QTL) for the fruit quality traits in mango. F_1 bi-parental progenies derived from Amrapali x Sensation cross were used as mapping population and hyper-variable SSR and SNP identified from whole genome sequence of Amrapali have been used as marker systems for genotyping. Significant variation was observed in hybrids for the fruit weight, pulp content, peel thickness. Many hybrids (88.24%) had low fibre attached to the stone compared to Sensation. Most of the hybrids had firmer peel at the middle of the fruit and 51.76% of hybrids had more peel firmness than the male donor Sensation. The fruit peel *a* value was higher in 57.65% of the progenies than the stone parent Amrapali. The pulp *b* values varied greatly and 43.53% of the hybrids had dark yellow-orange coloured pulp than female parent Amrapali. β-carotene content ranged from 16.43 to 185.69 µg/g and hybrids (81.18%) had higher β-carotene content than the male parent Sensation. A total of 558 HMSSRs were used for the polymorphism survey and 160 were found polymorphic. Out of 160 polymorphic markers, three HMSSRs, namely, M109, P125 and M73 were informative in ascertaining hybridity in progenies of open-pollinated seedlings of Amrapali. The polymorphic HMSSRs have been grouped based on polymorphism pattern between parental genotypes and expected segregation among progenies obtained from Amrapali x Sensation cross. The numbers of HMSSR available with the goodness of fit were relatively low (49 markers) and found to be insufficient to construct SSR-based linkage map covering all 20 LGs. Further, a linkage map was constructed using 492 polymrophic SNP markers expected to segregate in a 1:1 ratio among progenies. The cumulative genetic map distance observed was 4974.1 cM with an average marker interval of 12.1 cM. A total of 10 QTLs were identified associated with seven important traits, *viz*., fruit length, fruit width, fruit thickness, stone length, stone width, peel colour brightness (L^*) at the shoulder and pulp colour brightness (L^*) spanning over four chromosomes (7, 11, 15 and 16). Out of the 10 QTL identified, 5 were stable over the years. The QTL fruit length (*qFL15.1*) determined on LG 15 was consistently detected across the years between the markers AX-169939012 and AX-169898879 with the phenotypic variance explaining (PVE) of 17.9%. The fruit width QTL, *qFWD11.1* was identified consistently between the flanking markers AX-169929080 and AX-169902641with 21.5 per cent of PVE. The QTL for stone width (*qSW11.1*) mapped on chromosome 11 was consistent and with a PVE of 15%. The QTL governing peel brightness L^* at the shoulder point (*qPCLS15.1*) detected on LG15 and *qPUCL16.1* for fruit pulp colour brightness (L^*) identified on LG16 were consistent with PVE of 15.8 and 19.3%, respectively. Based on the present study, it can be concluded that F_1 bi-parental population (Amrapali and Sensation) segregated for fruit quality traits and phenotypic polymorphism revealed that the progenies could serve core resource for QTL mapping. The genetic linkage map developed in the present study with 492 SNP markers may be further enriched by adding more SNP markers in future to have a comprehensive linkage map. Mapping the region harbouring QTLs identified in this study would help in developing QTL-based markers. However, these QTLs need to be validated in diverse mango population and could be further used for genomic-assisted breeding in mango.

Evaluation of putative ploidy progenies of guava (*Psidium guajava* L.)

Knowledge about the extent of genetic diversity/relatedness in guava is vital for developing coherent strategies for future gains in productivity and quality. The present investigation was conducted at ICAR-Indian Institute of Horticultural Research (ICAR-IIHR), Bengaluru during 2018-2020 by studying the morphological and biochemical characters to assess the extent of variability and the genetic diversity using SSR markers. Wide variation was recorded among the 551 putative polyploid progenies and these progenies differed significantly for all morphological and biochemical characters studied. Genetic variability studies revealed that the range of PCV was 10.48 to 45.31, while, the range of GCV was 7.26 to 41.66. The estimates for heritability ranged from 19.30 to 98.60 and genetic advancement showed highest for fruit weight and number of seeds per fruit in all the progenies. Among putative polyploid progenies, Arka Mridula progenies developed by seed treatment were grouped highest number of clusters in cluster analysis. The absolute genome size varies from 0.460-1.293 pg/2C (499.88-1204.88 Mb/2C) in Arka Kiran and 0.493-1.333 (482.88-1304 Mb/2C) in Arka Mridula progenies as compared to the mother variety Arka Kiran (0.957 pg/2C) and Arka Mridula (0.960 pg/2C) that reflects the variability present in progenies. The 2C DNA content has significant positive correlation with leaf characters, stomatal size and TSS whereas, significant negative correlation with shoot internodal length and stomatal density. Diversity analysis identified 151 alleles with 6-16 alleles having an average polymorphic value 0.732 (mean of 9.44 alleles/ loci). The polymorphic information content (PIC) value was maximum (0.927) in MPg CIR097 and minimum (0.436) in MPg CIR334. Among all treatments, the seed treated progenies of Arka Kiran recorded highest variability parameter including highest number of alleles (5.563) and Shannon information index (1.283). Clustering and population structure of progenies distinctly separated Arka Kiran and Arka Mridula into two major groups. Principle coordinate analysis (PCoA) showed 37.79% of variation contributed by first three coordinates. Analysis of molecular variance (AMOVA) showed 16%, 75% and 9% variation among population, among individual, and within individual, respectively. This genetic variation in colchicine treated progenies can be further used for improving fruit yield and quality of guava.

Morphogenetic characterization of second generation colchiploids of sweet orange cv. Mosambi

Induction of tetraploidy in citrus is generally aimed for the development of triploid seedless cultivars, which are needed for meeting the requirements of the citrus industry. Suitable tetraploids are not available in Mosambi and have to be developed for future breeding programmes aimed at developing seedless cultivars. The present study was carried out during 2020-21 employing three-year-old 20 second generation colchiploid plants developed from the putative tetraploid branches of the first generation colchiploids of sweet orange cv. Mosambi along with its wild parent. These colchiploids and wild type have been characterized based on morphological, physiological, cytological and molecular variations. Plant height and canopy volume decreased, but stem girth increased in majority of the second generation colchiploids compared to wild type. Shoot internodal length reduced, but number of nodes per shoot and bark: wood ratio increased in colchiploids compared to the wild type. Leaf area, fresh weight and succulence increased, but leaf dry weight and density of foliar tissue reduced in majority of the second generation colchiploids. Flower length and width also increased in second generation colchiploids. Seed number was lowest in M-3 (7.33) second generation colchiploids. TSS and juice contents reduced, but acidity increased in majority of these colchiploids. Chlorophyll fractions and total carotenoids were augmented in majority of the colchiploids. Stomatal density reduced, but stomatal dimensions increased in all the second generation colchiploids. Cytological studies identified five putative solid tetraploids (M-1, M-5, M-6, M-8, and M-13) based on chromosome counting. Genetic diversity of second generation Mosambicolchiploids and their wild type were carried out using RAPD markers. N-J tree constructed based on RAPD loci displayed genetic diversity, where M-1, M-5, M-8 and M-12 were dissimilar colchiploids compared to their wild type. From the overall characterization of second generation colchiploidson the basis of number of acquiring of desirable traits for tetraploidy, eight putative solid tetraploids of Mosambi have been identified.

Morphogenetic characterization of second generation Kinnow mandarin colchiploids

The citrus cultivar Kinnow mandarin is a heavy yielder of good quality fruits which is easy-to-peel and has abundant juice with low acidity. High seediness of its fruits and bitterness in juice due to crushed seeds during juice extraction is a major obstacle in processing and consumer satisfaction for this cultivar. Hence, ploidy manipulation in Kinnow mandarin is targeted to develop triploid seedless cultivars to fulfill market demands. Development of tetraploids is a prerequisite for creating triploid seedless genotypes, and there are a few tetraploids available that can be used for this purpose. The present study was carried out during 2020-21 using three-year-old colchicine treated 21 second generation colchiploids of Kinnow mandarin and one wild type. These colchiploids and wild type have been characterized based on morphological, physiological, cytological and molecular variations. Stem girth increased significantly in K-10 (24.8 cm) colchiploid compared to wild type (17.08 cm). Further, colchiploids had shorter internodal length and a greater number of nodes than wild type. Both bark and wood weight of majority of colchiploids were found to be more as compared to wild type. However, ratio of bark and wood was higher in the wild type. Flower length and width increased in majority of the colchiploids compared to wild type. Colchiploids had larger leaf area, fresh weight and density of the foliage tissue than the wild type, but, leaf dry weight and succulency reduced in majority of the colchiploids as compared to wild type. Colchiploids had longer, wider, and thicker leaves than wild type. Bigger fruits with more weight and thicker rind were recorded in colchiploids. Seed number was lowest in colchiploid K-19 (6.44 seeds/fruit). In the majority of colchiploids, stomatal densities decreased but stomatal dimensions increased. The presence of hyperploidy in colchiploids K-1, K-4, K-10, K-16, K-17 and K-19 was also observed after cytological analysis. Two out of 30 RAPD markers used for molecular study exhibited polymorphism in colchiploids compared to the wild type. Genotypes K-1, K-4, K-10, K-17, K-18 and K-19 were identified as putative solid tetraploids. The overall characterization of colchiploids resulted in the detection of eleven putative tetraploids of which six were solid.

Morphological, physiological, biochemical and molecular characterization of progenies of Olour mango

Mango (*Mangifera indica* L.) is one of the most important, choicest and most popular tropical fruit crops cultivated throughout the tropical and subtropical frost-free regions of the world. Despite of the fact that India leads the world in mango production, but its productivity is lower than other developed countries due to a number of factors including, big tree size, lower planting densities, use of seedling rootstocks with unknown pedigree and irregular bearing behaviour. However, the unavailability of standard rootstocks in mango is often considered as major obstacle, which has considerable impact on orchard productivity. Among rootstocks, Olour has better compatibility with several improved cultivars and having several desirable features such as polyembryony which produce nucellar seedlings which are true to type and uniform in size. In the present study, attempts have been made to confirm the hybridity of open pollinated Olour progenies using molecular markers, and to evaluate the progenies based on morphological, physiological and biochemical parameters. Out of four SSRs primers, two SSRs, *viz*., LMMA2 and LMMA8 were found informative in determining the zygotic and nucellar origin of saplings among Olour progenies. Out of 90 progenies, 28 were found to have suspected hybrids (zygotics) origin based on molecular markers. A significant level of variability was also observed in these 28 suspected hybrids. Morphological markers like height of the plant, stem girth, bark and wood ratio and specific leaf weight were found to be useful markers to select Olour saplings for their vigour. As regards to physiological and biochemical markers, chlorophyll content, photosynthetic rate, transpiration rate, stomatal density, total phenolics, flavonoides and total antioxidant capacity were found useful parameters for determining the vigour of the saplings. On the basis of morphological, physiological and biochemical markers, OP-17-58, OP-17-1, OP-17-34, OP-17-19, OP-17-10 and OP-17-47 were found to be dwarf and OP-17-11, OP-17-26, OP-17-39, OP-17-31 and OP- 17-12 were vigorous compared to Olour maternal sapling.

Understanding the basis of pulp colour in black guava (*Psidium guajava* L.)

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

Molecular studies on shelf-life in mango (*Mangifera indica* L.)

Mango known as the 'King of fruits' owing to its pleasing flavour, high nutritive value and delicious taste. However, most of the popular varieties of mango possess a very short shelf-life. Therefore, the present investigation was carried to identify good molecular markers linked to fruit shelf-life. Present study was carried out using 44 mango genotypes raised on their own roots as well using poly-embryonic rootstocks and *in-silico* mined 95 nucleotide ripening gene sequences. A total of 35 shelf-life specific primers were designed using these sequences. Analysis of the detected SSRs revealed that all of them represented mainly di- and trinucleotide repeats. Out of 35 shelf-life specific markers developed, 27 were found polymorphic, which showed substantial genetic diversity among the 20 mango genotypes. The average number of alleles per locus (An), gene diversity (GD), major allele frequency (Maf), expected heterozygosity (Ho) and polymorphic information content (PIC) of 27 shelf-life markers were 2.25, 0.40, 0.77, 0.20 and 0.61, respectively. In rootstocks (4) and scion/rootstock (20) combinations, 25 markers were found polymorphic. The average number of alleles per locus (An), major allele frequency (Maf), gene diversity (GD), expected heterozygosity (Ho) and polymorphic information content (PIC) of 25 shelf-life markers were 2.20, 0.78, 0.43, 0.32 and 0.55, respectively. Moreover, detailed cluster analysis revealed that these 20 mango genotypes clearly grouped according to their shelf-life pattern (long, medium and short). Moreover, initial studies of scion/rootstock combinations indicated that there is effect of rootstock on scion of mango in terms of shelf-life. Among all rootstocks, Olour was found best for long shelf-life in mango varieties. Therefore, it is concluded that marker system utilized in the present study could be able to identify the genotypes for long shelf-life. Hence, the molecular characterization of important mango genotypes for shelf-life *via* ripening related gene specific primers could be utilized in the design of marker-assisted breeding for longer shelf-life.

Theme 2. Crop improvement and character association

Identification of grape genotypes tolerant to berry cracking

Studies on identification of grape genotypes tolerant to berry cracking were carried out using 29 diverse genotypes. Genotypes having large compact bunch size and round bold berry such as Pusa Aditi, Flame Seedless and Cardinal were found to be more prone to berry cracking incidence. Seed content and its associated traits did not affect the berry cracking, regardless of the grape genotypes. Physiological activities in the grapevines were found to be more in cracking susceptible genotypes (Hy. 72-151 and Flame Seedless) as compared to the tolerant genotypes (Black Muscat, Black Prince and Hur). Biochemical traits like high TSS favoured berry cracking and other traits like pH, ascorbic acid, total phenolics, total flavonoids, DPPH, FRAP and CUPRAC did not affected the severity of cracking. *In vitro* berry cracking ratio and water uptake by berries was found most associated traits related to the berry cracking. A strong correlation was also observed between these two parameters. Based on the berry cracking ratio, genotypes Black Muscat, Black Prince and Hur were found most tolerant and Hy.72-151, Flame Seedless, Cardinal and Beauty Seedless were most susceptible under *in vitro* conditions. However, under open field conditions, the maximum cracking was observed in the Cardinal followed by Hy.16/2A R2P16, Perlette and Bharat Early. In majority of the genotypes the longitudinal cracking symptoms were observed followed by LC + RC. The content of N and K was found higher in susceptible genotypes. Whereas, high leaf Ca and Mg was found in comparatively tolerant genotypes. Principal component analysis based on all traits clearly grouped comparatively cracking tolerant genotypes together in one cluster like Black Muscat, Julesky Muscat, Hy.16/2A

R4P13, Punjab Purple, Hy.16/2AR2P16, Hy.16/2AR4P7 and Pusa Navrang. Strong correlation between berry cracking ratio and the water uptake by berry was also observed. In rest of the genotypes, a low level of correlation was noted for all the traits under study. This is concluded from the present study that berry cracking is directly not affected by the internal composition of fruits, whereas, it is more affected by the sudden changes in the water content in the berries due to rains or irrigation.

Theme 3. Crop regulation

Effect of plant growth regulators on hastening embryo maturation and fruit quality of papaya (*Carica papaya* L.) var. Pusa Nanha

Papaya (*Carica papaya* L.) is an important fruit crops of the tropical and subtropical regions of the world having numerous nutritional and medicinal properties. Papaya is a highly cross-pollinated crop. Varietal improvement work in papaya takes approximately 7-8 generations (15-16 years) to release a variety. Thus, shortening the growth cycle seems to be highly desirable for enhancing the breeding efficiency in papaya. The period from fruit set to fruit harvest may be shortened by culturing embryos *in vitro*. In the present study, seven treatments of different plant growth regulators, *viz*., ethrel (100 and 120 ppm), ABA (10^{-6} M and 10^{-4} M) and MeJA (10^{-5} M and 10^{-3} M) including control were applied at 75 and 90-day-old fruits (DOF) and at 140 DOF to discover the effects of growth regulators on hastening the embryo maturity for shortening the breeding cycle and fruit quality of papaya var. Pusa Nanha. Among treatments, ethrel 120 and 100 ppm at 90 DOF was found most effective for improving seed length (6.46 mm), seed colour (light brown), embryo formation (85%) and colour (pure white), size (2.93 mm), germination (85%), rapid shoot emergence (5.67 days), earliest adical emergence (2.67 days), plantlet weight (83.67 mg) and plantlet regeneration (86.67%) of papaya. The treatment MeJA (10^{-5} M) was also found significant for the maximum number of roots (5.13), root length (63.33 mm), plantlet length (7.56 cm) and regeneration. As regards to quality of fruits, application of 120 ppm ethrel improved the peel (L^* 61.00, a^* 12.50 and b^* 38.23 values) and pulp (L^* 47.70, a^* 25.96 and b^* 33.80 values) colour, TSS (11.36° Brix), reducing sugars (3.14%), total sugars (7.67%), flavonoids (21.18 mg/100 g), CUPRAC activity (4.77 µmol/g) and lycopene content (3.78 mg/100 g) of fruits. Whereas, total phenols (24.01 mg GAE/100 g), ascorbic acid (81.42 mg/100 g), total carotenoids (4.22 mg/100 g) and β-carotene content (3.74 mg/100 g) were increased as a result of application of MeJA (10^{-5} M).

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Rutuparna Senapati	21287	M.Sc.	Understanding the basis of pulp colour in Black guava (*Psidium guajava* L*)*	Dr. Madhubala Thakre
2.	Shivam	21288	M.Sc.	Morphological, physiological, biochemical and molecular characterization of progenies of Olour mango	Dr. Kanhaiya Singh
3.	Sandeep Kumar Badhei	21289	M.Sc.	Morphogenetic characterization of second generation Kinnow mandarin colchiploids	Dr. Awtar Singh
4.	Mukesh Shivran	21290	M.Sc.	Molecular studies on shelf-life in mango (*Mangifera indica* L.)	Dr. Nimisha Sharma
5.	Kiran K.N.	21291	M.Sc.	Morphogenetic characterization of second generation colchiploids of sweet orange cv. Mosambi	Dr. Awtar Singh
6.	Bhupendra Sagore	21292	M.Sc.	Effect of plant growth regulators on hastening embryo maturation and fruit quality of papaya (*Carica papaya* l.) var. Pusa Nanha	Dr. Kanhaiya Singh
7.	Uwisize Marie Grace	10917	Ph.D.	Identification of grape genotypes tolerant to berry cracking	Dr. Mahendra Kumar Verma
8.	Kiran Kumar G. N.	11041	Ph.D.	Evaluation of putative ploidy progenies of guava (*Psidium guajava* L.)	Dr. M.R. Dinesh
9.	Sridhar Ramachandra	11043	Ph.D.	QTL mapping for fruit quality traits in mango (*Mangifera indica* L.)	Dr. Manish Srivastav

Post Harvest Technology

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Prof. Ram Asrey

The Division of Post Harvest Technology with a multidisciplinary approach has mandate of integration of production with post harvest management; development of appropriate storage protocols; valorization through processing; design, development and evaluation of packages, low cost post harvest equipment and machinery; development programme for transfer of technology; advisory consultancy to both public and private sectors. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Post harvest management of fresh fruits and vegetables

Combinational effect of ultra violet radiation and post-harvest elicitors on storage behavior and post-harvest quality of bitter gourd (*Momordica charantia)*

Bitter gourd (*Momordica charantia)* is vegetable crop of immense value widely grown in tropical and subtropical areas of the world. It is rich in several bioactive compounds such as ascorbic acid, phenols, antioxidants and most importantly it possesses anti-diabetic potential used for treating diabetes and other human ailments. Bitter gourd fruit is highly perishable in nature due to short shelf-life of 4-5 days under ambient condition and spoils rapidly due to excessive moisture loss, tissue softening, yellowing, and quality loss. To address these problems, three objectives were formulated. Ultra violet –C (UV-C) radiation at three different treatment times were used as an elicitor for reducing the microbial load and increasing the biochemical parameters of bitter gourd fruit during cold storage. Results showed that UV-C treatment for 40 min has retained 57% higher antioxidant activity, 61% higher total phenols, 61.9% higher total chlorophyll, 51% higher antidiabetic potential and 5% higher saponin content compared to control. Immature green bitter gourd fruits were dipped in different concentrations of salicylic acid (SA 3, 5, 10 mM), putrescine (PUT 1, 2, 3 mM), and calcium lactate (CL 50, 75 and 100 mM) and stored at 10 ºC, and 85–95% relative humidity (RH) for 20 days. Among the treatments, SA 7.5 mM retained 73% higher total chlorophyll, 16% higher total carotenoid, and 80% higher ascorbic acid while SA 10 mM retained 85% higher total phenol, two-times higher anti-oxidant capacity and 19% higher antidiabetic potential compared to control on 20th day of cold storage. Higher fruit firmness, lower PLW and PME activity were also recorded in SA 10 mM treated fruits. PUT 3 mM was best in retaining two times higher fruit firmness, 74% higher total chlorophyll, 45% higher ascorbic acid, 36% higher antioxidant, 35% higher ant diabetic potential and 4% higher saponin compared to control on 20th day of storage under cold condition. CL 100 mM dose was found more effective in reducing the PLW to 6.46% and decay rate to 33.33% on 20th day of storage. Hence, SA PUT and CL could be used as an eco-friendly approach for extending bitter gourd shelfife up to 20 days under cold condition with higher retention of nutraceutical parameters. The charantin content in bitter gourd fruit treated with physical and chemical elicitors. was assessed. Results showed that PUT 3 mM has retained higher charantin content (723.03µg g-1DW) compared to control and other treatments, hence this was subjected to gene expression study of Mc CAS1 and Mc SE gene responsible for charantin biosynthesis which showed that other than these gene some other gene could be responsible for its biosynthesis due to their spatial, temporal and tissue specific expression during storage.

Management of chilling injury, shelf life and post-harvest disease in mango

Mango (*Mangifera indica* L.) chilling injury (CI) is a physiological disorder associated with inadequate low-temperature storage that adversely affects its marketability and postharvest quality. We evaluated the effects of γ-Aminobutyric acid (GABA) and Arginine application on amelioration of chilling injury in 'Amrapali' mango. Results indicated that GABA attenuated CI incidence in mango fruit during low temperature storage by enhancing of antioxidant system. GABA treatment showed lower CI index, electrolyte leakage, malondialdehyde contents and higher firmness and total carotenoid content. It also slowed the rate of respiration, ethylene evolution rate and weight loss. Moreover, GABA not only increased the antioxidant substances such as total phenolic content, total flavonoid content and total antioxidant activity under cold storage, but it also elevated PAL enzyme activity. We also evaluated the effects of alkaloid glycine betaine (GB) in maintaining postharvest quality and improving shelf life of 'Amrapali' mango. Its effect on quality attributes and shelf life were evaluated during storage at 30 ±2 ºC for 12 days. Results suggest that GB (15 mM) showed less weight loss, firmness loss, respiration rate and ethylene evolution rate. GB (15 mM) treatment resulted in higher titratable acidity, total soluble solids, ascorbic acid, total carotenoid content, total phenolic content, total flavonoid content and antioxidant activity. Additionally, it also suppressed pectin methyl esterase (PME) activity. Therefore, GB (15 mM) is considered as best treatment. Anthracnose disease incited by *Colletotrichum gloeosporioides* reduces the yield and marketquality of mangoes worldwide. In the present study, we have explored native-volatiles of *Pseudomonas putida* BP25 and a synthetic-volatile, 2-ethyl-5-methylpyrazine and 2, 5- dimethyl pyrazine, earlier identified in volatilome of *Pseudomonas putida* BP25 for reducing anthracnose in mango cultivars 'Amrapali' and 'Chausa'. The bacterial volatile compounds displayed fungistatic effects on the mycelial growth of *Colletotrichum gloeosporioides* in vitro. The pathogenicity test on *C. gloeosporioides* revealed that spray inoculation of pathogen on mango facilitates better expression of anthracnose symptoms than pin prick method. In vivo prophylactic fumigation of mangoes with native-volatiles or the bacterial origin synthetic 2-ethyl-5-methylpyrazine and 2, 5-dimethyl pyrazine, for 24 h at 25 ºC showed a better control anthracnose severity and incidence on fruit, compared to curative fumigation. Additionally, bacterial VOC fumigation maintained the fruit quality parameters such as higher firmness, low respiration and ethylene production, higher accumulation of phenols, flavonoids, carotenoids, proline, soluble solid content and titratable acidity and high PAL enzyme activity. Anthracnose suppression coupled with the fruit quality enhancement by bacterial and synthetic volatiles (2-ethyl-5-methylpyrazine and 2, 5-dimethyl pyrazine) presents a new opportunity for postharvest management of mango during the storage, transit, and trade.

Extension of storage life of guava using ethylene inhibitors and its integration with modified atmosphere packaging

Guava is one of the most delicious and nutritious fruits, liked by consumers for its refreshing taste and pleasant flavour. It is a climacteric fruit that ripens very rapidly after harvest under ambient conditions and thus highly perishable. Postharvest life of guava fruits can be enhanced by employing different post-harvest treatments followed by storage at optimum temperature or through manipulation of ripening related genes by recombinant DNA technology. In the present investigation different concentrations of three ethylene inhibitors viz. salicylic acid (SA), sodium nitroprusside (NO donor) and 1-methylcyclopropene (1-MCP) were applied on 'Arka Mridula' guava fruits and stored at three different temperatures 8 º, 12 º and RT. Among the different post-harvest treatments, 1-MCP (500 ppb) treated fruits was found to be effective in extending the storage life of guava fruits for three, four weeks at 12 ºC and 8 ºC respectively and seven days at ambient storage conditions followed by SNP (1.5mM) and SA (3 mM). 1-MCP (500 ppb) had exhibited minimum PLW, maximum firmness, with greater retention of green colour and higher quality parameters by the end of storage period at different storage conditions. Concurrently, the effect of different packaging films viz. polypropylene (PP), low density polyethylene (PE) and Cryovac® PD-961 (PD) with and without micro-perforation in extending the shelf life of guava fruits was investigated. The results revealed that, the non-perforated polypropylene (PP-NP) packaging had effectively maintained optimum modified atmosphere conditions and resulted in least PLW, higher fruit firmness and had retained all the quality parameters of guava at 12 ºC and room temperature conditions. In order to reap benefits of both the technologies, they were integrated and applied at three different storage temperatures. Among all the combinations, 1-MCP treatment integrated with non-perforated PP film was found to be significantly effective in extending the storage life and maintenance of different quality attributes of guava fruits. Gene expression studies with two ethylene mediated ripening genes viz. expansin and ACC synthase has revealed the close association between the ethylene production and ACC synthase activity, and due to 1-MCP action ACC synthase expression was down regulated during 14 days of storage. While expansion expression was down regulated till 14 days of storage, a surge in expansin expression was recorded after 21 days of storage which can be directly correlated with the physical texture breakdown noticed under 12 ºC storage.

Post-harvest response modulation of mandarin (*Citrus reticulate* Blanco) fruits to exogenously applied plant hormones

The study was carried out to regulate the postharvest quality of Kinnow mandarin fruits through exogenous application of methyl jasmonate and packaging system at ICAR-Indian Agricultural Research Institute, New Delhi in the year 2018-20. To carry out first objective, Kinnow mandarin fruits were given treatment through two method of application (pre-harvest and post-harvest) with four concentrations of methyl jasmonate (0.1, 0.3, 0.5 and 0.7 mM) and control (distilled water). Pre-harvest spray treatment was given 40 days and 20 days before the commercial harvesting whereas postharvest dipping treatment was given to mature fruits after harvest. Both the lots of treated fruits were then stored at two different temperatures of 2 ^{o}C and 6 ^{o}C with 85-95% relative humidity for 40 days. For the second objective, mature harvested fruits were packed in CFB boxes having anti-microbial sachets (sachet @ 7.0 g KMS, sachet @ 12.0 g KMS, sachet @ 2.5 ml LG oil, sachet @ 5.0 ml LG oil) and control (without sachet) and stored at 6 oC and room temperature with 85-95% relative humidity for 40 days. All the fruits were analysed for physio-chemical attributes at 10 days interval during the storage period. In the first objective, pre-harvest spray at 20 DBH was found most effective method of application than postharvest method of application where 0.5 mM concentration of MeJA showed overall best response in both the conditions i.e method of application and storage temperatures. The fruits stored at 6 ^{o}C showed better quality attributes than the fruits stored at 2 ^{o}C in both the application method. In the second objective, fruits treated with lemon grass oil sachets-5.0 ml and stored at 6 ^{o}C were most effective in maintaining the quality of Kinnow mandarin fruits during storage. Overall, the 0.5 mM MeJA and sachet @ 5.0 ml LG oil treated fruits retained higher moisture content, fruit firmness with increase in TSS, total phenols, total sugars, flavonoids, carotenoids, vitamin C, antioxidant activity, peroxidase and PAL enzyme activities during the storage period. The treatments (0.5 mM MeJA and sachet @ 5.0 ml LG oil) also showed lower respiration rate and acidity content in the fruits with higher sensory attributes on the 40th day of storage period. The fruits treated with 0.5 mM MeJA showed no decay percentage and chilling injury during the storage period. Least decay percentage was observed in the fruits packed with sachet @ 5.0 ml LG oil during the storage period. Therefore, pre-harvest application of 0.5 mM concentration of methyl jasmonate and active packaging with sachet @ 5.0 ml LG oil could be an effective and safe strategy to enhance the quality of Kinnow mandarin fruits with extended shelf-life upto 40 days.

Effect of post-harvest treatment on quality and shelf-life of pointed gourd

With aim to minimize yellowing, shrivelling and postharvest losses, pointed gourd fruits were treated with different concentration of putrescine (0.5,1.0,1.5 mML^{-1}) and spermidine (1.5.3.0,4.5 mML^{-1}) and stored at room temperature (20-25˚C with 60-70 % RH) for 8 days. On the basis of superiority of treatment with respect to PLW and fruit firmness retention, PUT @1.0 mML^{-1} and SPD 3.0 mML^{-1} treatments were found to be the best. In the extended study, fruits were treated with putrescine 1.0 mML^{-1} and spermidine 3.0 mML^{-1} and stored in cold storage at 5-7 ˚C with 85-90 % RH for 20 days. Both the treatments (PUT@1.0 mML^{-1} and SPD 3.0 mML^{-1}) have retained higher fruit firmness, chlorophyll, hue angle (h^{o}), total phenolics and anti-oxidant. Besides, these treatments lower down the respiration rate and percent PLW over control. Among the treatments, spermidine proved superior over putrecine with regard to lowering down the senescence activities. Fruit treated with SPD@3.0 mM L^{-1} and PUT@1.0 mM L^{-1} and stored under cold condition (5-7˚C with 85-90 % RH) could retain the pointed gourd in its better quality and shelf life up to 20 days.

Theme 2. Processing of horticultural crops

Nutritional profiling of common apricots cultivars grown in India and development of osmo-dehydrated products of apricots

An experiment was carried out to develop osmo-dehydrated product from apricot (*Prunus armeniaca* L.) The fruits of six apricot cultivars commercially grown in Himachal Pradesh namely CITH-A-1, CITH-A-2, CITH-A-3, Roxana, Goldcot and Shakarpara were procured and brought to the Division of Food Science and Postharvest Technology, for experimentation. On the basis of physicochemical constituents a significant variation among the cultivars in respect to dry matter, TSS, titratable acidity, minerals, sugars (sucrose, glucose, fructose), sweetness index, organic acids (citric, malic and succinic acids), ascorbic acid, total carotenoids, β-carotene, phenolics, flavonoids and antioxidants activity was recorded. The sucrose in sugars, citric acid in organic acids, β-carotene in carotenoids, and potassium in minerals were predominant, respectively. Among cultivars 'CITH-A-2' found to have high dry matter content, TSS/TA, sugars, sweetness, minerals, carotenoids, and antioxidants activity which render it most suitable for the preparation of dehydrated apricots. To improve the quality of the osmo-dehydrated product a Box-Behnken design (BBD) was employed and the conditions of ultrasound-assisted osmotic dehydration (MUOD) process with independent variables like ultrasound duration (10, 20 and 30 min), the concentration of the osmotic solution (52, 60 and 68 °B) and microwave power (300, 600 and 900 W) were optimized. The increase in solution concentration, microwave power, and ultrasound duration resulted in enhanced quality of the osmo-dehydrated product. However, higher levels of the three variables i.e. concentration of solution, microwave power, and ultrasound duration were not found more effective on the quality of the final osmo-dehydrated product. The osmo-dehydrated apricot product prepared by optimized MUOD process was packed in four different packaging materials namely ALPE (260 gauge), HDPE (200 gauge), LDPE (200 gauge), and SW (150 gauge) and stored at ambient conditions for storage study. The product quality was retained better in the samples packed in ALPE pouches compared to HDPE, LDPE and SW during six months of storage. However, moisture content, reducing sugars and total sugars increased with increase in storage period in all the packages. Whereas rehydration ratio, titratable acidity, ascorbic acid, total carotenoids, β-carotene, phenolic and flavonoid compounds, and antioxidants activity decreased with increase in storage period in all the packages.

Assessment of onion cultivar for dehydration suitability and functional quality

The present study was conducted at the Division of Food Science and Post Harvest Technology, ICAR- IARI, New Delhi during 2020-2021. Eight onion genotypes namely, Pusa Shobha, Pusa Sona, Pusa Riddhi, ORVA 19-

03, ORVA 19-05, ORVA 19-07, ORVA 19-14, ORVA 19-16 were evaluated for their physico-chemical constituents variation and their dehydration suitability. On the basis of physico-chemical constituent variations and dehydration characteristics the genotype Pusa Shobha was found more suitable for dehydration as it retain more pungency, total phenols, antioxidant activity and high dry matter content and dehydration ratio and less browning content as compared to Pusa Sona, Pusa Riddhi, ORVA 19-03, ORVA 19-05, ORVA 19-07, ORVA 19-14, ORVA 19-16. With regards to treatments on the basis of nutritional quality assessment the maximum retention of ascorbic acid, antioxidant activity, total phenols, pungency, better rehydration ratio and low non enzymatic browning, moisture content was found in NaCl 5% treated sample compared to other treatments of NaCl 3%, NaCl 7% and control. Similarly a temperature of 60ºC was found to be good for dehydration of onion slices in comparison of 50 and 55ºC as to took less drying time 7-8 hr to retain up to 5 % moisture in the dehydrated onion slices and better retention pungency, antioxidant, phenol, reducing and non-reducing sugar content in dehydrated onion slices. With regards to packaging and storage temperature, the onion slices packed in 200 g HDPE pouches and stored at low temperature retain better nutritional qualities in respect of ascorbic acid, pungency, total phenol, antioxidant activity, rehydration ratio and sensory score and less moisture content and NEB during storage as compare to slices packed in 200 g LDPE stored at ambient conditions upto 3 months. However in general the nutritional content of pungency, total phenol, antioxidant activity, rehydration ratio and sensory score decreased with increase storage periods and moisture content, total sugar and reducing sugar and NEB increased with increase in storage periods.

Functional stability of beetroot betalains under different processing regimes

Beetroot (*Beta vulgaris* L.) is the richest source of betalains which can be used as natural colourants in foods. Like other natural colours, betalains have limitations of low stability. Understanding these gaps the proposed research work was conducted which included extraction protocol optimization and functional stability enhancement through copigmentation. Beetroot cultivars, namely, Crimson Globe (CG) and Detroit Dark Red (DDR), cultivated by UVDC, ICAR-IARI, New Delhi were used in this study. For execution of this study two objectives were planned. Under first objective, we compared both varieties of beetroot for betalains extraction followed by optimization of betalains extraction protocol. Results revealed that CG was a more feasible matrix for betalains extraction owing to its higher juice yield (50.35% v/s 41.27%), higher redness index (0.0416 v/s 0.0161) and lower firmness (8.05 N v/s 11.91 N) over DDR. However, the betalains content in both the varieties were almost similar (666.22 mg/L v/s 659.98 mg/L). Further from Box Behnken Design, optimization of extraction protocol revealed that at ~70o C extraction temperature, ~4.0 extraction time and ~1:3 solid to solvent ratio, maximum betalains (491.16 mg/L) and phenolics (96.53 mg/L) with maximum antioxidant activity (55.80 µmol/g) and minimum colour change (35.81) could be extracted in water. Second objective comprised the detailed stability study of the pigment under different environmental conditions, additives as well as stability enhancement through copigmentation. Among the temperatures studied, 10 °C showed the minimum betalains degradation (45.91%) after 3 hours of incubation period. Maximum total betalains retention was observed at pH 3.0 under exposure to light (2400 lux). Additives, namely, 1% ascorbic acid, 10% glucose/ fructose, sucrose >45%, EDTA 40 ppm and sodium benzoate 350 ppm were found best for imparting maximum betalains stability, in separate incubations. Betalains retention and total colour change followed similar trend in all the stability studies. Temperature more than 60 ^{o}C, malic acid, light exposure and NaCl (≤10%) were found to be the most detrimental factors for stability of the pigment. Significant stability enhancement was achieved when native pigment was co-pigmented with black carrot anthocyanins at 8% level with noticeable hypochromic and bathochromic shift. The half-life of native betalains pigment at 60, 90 and 120 °C was 107.51, 79.15 and 43.31 min which got enhanced to 270.68, 253.91 and 199.59 min after co-pigmentation. Under light exposure also, the half-life of betalains increased approximately by two-fold after co-pigmentation. In presence of 0.5% malic acid and 15% salt, maximum increase in half-life of betalains was observed after copigmentation. Thus, co-pigmented betalains pigment showed higher stability in comparison with native pigment.

Valorization of pumpkin to calcium enriched crisps

Vacuum impregnation (VI) is a processing operation that permits the impregnation of fruits and vegetables porous tissues with a fast and more homogeneous penetration of active compounds compared to the classical diffusion processes thus acquiring enhanced nutritional and sensory properties of crisps depending on the functionality of the impregnation solution. Vacuum impregnation method combined with microwave drying was used for producing calcium lactate fortified pumpkin crisps. For the study, comparison effect of three pumpkin genotypes such as DPU-K-016, DPU-129 and DPU-150 were selected and was evaluated for three different impregnation alternatives like: I) at atmospheric pressure (0 mmHg) for 10 min II) applying 10 min of vacuum pressure (6 mmHg) to a container with pumpkin samples followed by 10 min of impregnation with fortificant solution at atmospheric pressure and III) applying 10 min of vacuum pressure (13 mmHg) to a container with pumpkin samples followed by 10 min of impregnation with fortificant solution at atmospheric pressure. The impregnating solution concentration used was 0, 1 and 2% calcium lactate solution with 40% maltodextrin and 2.5% salt. The influence of the impregnation method on the calcium uptake, solids gain, flesh firmness and hardness of fresh impregnated slices and calcium content, moisture content, nonenzymatic browning, total carotenoids, textural attributes, oil uptake, colour parameters and sensory evaluation of crisps was determined for all the 3 genotypes with 3 vacuum alternatives. Results showed that among all the 3 genotypes, DPU-K-016 genotype was found best for optimized process conditions (calcium lactate at 1% level and vacuum pressure of 13 mmHg) which fortified pumpkin crisps to 1428.33 mg/100g of calcium level with acceptable sensory attributes followed by DPU-K-016 genotype with optimized process conditions of calcium lactate at 2% and vacuum pressure of 13 mmHg which fortified pumpkin crisps to 1320.33 mg/100g of calcium level. Thus, combination of vacuum impregnation and microwave drying is a suitable way for the production of calcium lactate fortified pumpkin crisps which are porous, crunchy, having lower fat content and with high carotenoids content.

Theme 3. Processing of arable crops

Extrusion processing characteristics of pearl millet

Four cultivars of Pearl Millet viz. Pusa Composite 383, Pusa Composite 701, Pusa Composite 1201 and Pro Agro 9444 were investigated at 10, 15, 20, 25 and 30 % moisture contents. Their size viz. length, width, thickness and geometric mean diameter were measured and presented as the mean values of 2.96-3.26, 2.36-2.70, 1.98-2.26 and 2.42-2.67 mm respectively. The mean values of sphericity, projected area, grain volume, thousand-grain mass, bulk density, true density and porosity were also determined. These properties had respective ranges of 0.79-0.87, 5.6-6.7 mm^2, 5.9-8.4 mm3, 8.3-11.6 g, 846-699 kg/m^3, 1333-1170 kg/m^3 and 36.2-43.3 %. Different surfaces were used for determining the variability in the values for static coefficient of friction against the surfaces. The coefficient value was obtained in the respective ranges of 0.206-0.413, 0.215-0.424, 0.227-0.429 and 0.238-0.442 against the surfaces of food, mild steel, galvanized iron and aluminium. The angle of repose was categorized between emptying and filling with the respective ranges of 28.8-33.6 and 24.3-29.4 degree. This result confirmed the fact for greater values of emptying angle relative to the filling angle of repose. Rupture strength decreased with the moisture content in the range of 53.2-19.8 N. The properties were significantly ($p<0.05$) different with cultivars and moisture content except some of the cases. One of the pearl millet cultivars was selected based on their highest amylase content as it plays significant role in absence of gluten. Thus, grains of Pusa Composite 1201 variety were selected as the highest amylase containing cultivar and milled for preparation of noodles. The pearl millet noodles were obtained with high solid loss, low hydration and insufficient strength to withstand after cooking as observed with cooking time. The hot water treatment along with addition of guar gum could solve the problem upto certain extent. The boiled water was used instead of normal water and mixed with guar gum at 2% dry basis of flours. The treated flour of pearl millet was extruded to prepare noodles after standardizing the methodology. The pre-treatments could improve the cooking quality of pearl millet noodles remarkably. This pre-treated flour was subjected to optimization of extrusion variables. The experiment yielded pearl millet noodles at 74.0°C barrel temperature, 34.7% wet basis moisture content and 178rpm screw speed. It was found with 18.1% solid loss with hydration capacity of 1.89 and cooking time of 429 sec. In view of the BIS: 1485-(2010) recommendation, it was targeted to lower the value of solid losses. Thus, noodle strands were characterized through substitution of pearl millet flour with different ingredients at various levels. The flour ingredients were characterized for physical, functional pasting and phase transition properties prior to characterizing the noodle strands of blends at various levels of substitution. It yielded the best suited quality, especially in terms of solid loss as 11.6% with 50% level of defatted soy flour in pearl millet. So, noodle strands were thoroughly characterized for substitution of pearl millet with defatted soy flour. The cooked noodle of this blend was also found with increased hardness as desirable on addition of defatted soy in pearl millet. The blend of pearl millet and defatted soy flour selected at 50% level was thus used for optimization of extruder variables. It yielded extruder variables as 71°C barrel temperature, 34.4% wet basis moisture content and 178 rpm screw speed. The solid loss, hydration capacity and cooking time were 12.5%, 1.84 and 240 sec, respectively. On storing under ambient condition, the packed noodle strands were found safe when analyzed for moisture content, water activity and microbial quality.

Evaluation of mechanical drying methods for large cardamom (*Amomum subulatum* Roxb.)

A study was undertaken to optimize the microwave and recirculatory air drying of two major varieties (Cv. Ramsey & Varlangey) of large cardamom (*Amomum subulatum* Roxb.) in order to enhance the efficiency of the traditional Bhatti drying which in addition to being inefficient also contributed significantly to environmental pollution. Microwave drying of both the varieties was conducted at 100, 180, 300 & 450 W of microwave power level whereas, Recirculatory air drying was conducted at 35, 45, 55 & 65°C air temperature and a constant relative humidity of 30% of the drying air. Dried product quality was evaluated with respect to total colour change, browning index, oil content, peroxide value of the oil, antioxidant activity of oil and hardness of the dried capsule as well as the seed. Additionally, the moisture and colour kinetics during drying at all experimental conditions were also recorded to understand the same during the entire drying process. Microwave drying time varied between 34 & 300 min. Drying times decreased with the increase in available microwave power. The colour change varied between 6.48 & 11.48 and the browning index between 37.87 & 42.72. However, total colour change reduced with the increase in available microwave power level only between 100 & 180 W. Further increase in microwave power level did not have any effect on total colour change whereas browning index did not change significantly with the available microwave power level barring those between 300 & 450W. Oil content reduced with the increase in the microwave power level for both the varieties. However, for both the varieties, the peroxide value was found to be minimum and the antioxidant activity was found to be maximum when the capsules were dried using 180W microwave power. Hardness of capsule as well as seed for both the varieties were also found to be minimum when they are dried at 180 W. Considering all the parameters, microwave drying using 180 W was found to be optimum for both Ramsey & Varlangey varieties of large cardamom. Recirculatory air drying using dehumidified air required 280 to 820 min. for Ramsey and 310 to 840 min. for Varlangey respectively. For each of the drying temperatures used in the study, Varlangey invariably required a higher drying time compared to Ramsey. For Ramsey total colour change reduced with the increase in drying temperature. However, the decrease is only significant between 35 °C and 45 °C. For Varlangey, the total colour change did not have any significant change when drying temperature increased from 35 °C upto 55 °C. Only when the temperature was raised to 65 °C, there was a significant change in total colour. Browning index in Ramsey was the lowest at 35 °C. At all other temperatures considered for drying, they remained more or less similar. In case of Varlangey there was no significant effect of drying temperature on browning index. Changes in oil content was similar to those obtained in microwave drying i.e. oil content decreased with the increase in drying temperature. However, for both the varieties there was no significant difference in oil content between 45 °C and 55 °C. Peroxide values increased with the increase in the drying temperature. The same varied between 0.78 and 1.44 meq/kg oil for Ramsey and between 0.75 and 1.87 meq/kg oil for Varlangey. Antioxidant activity in Ramsey almost remained unchanged with the drying temperature. For Varlangey the same decreased with the increase in drying temperature but the change between 35 °C and 45 °C was found to be non-significant. Capsule and seed hardness was found to be the minimum when dried at 45 °C. Considering all the parameters under the study drying temperature of 45 °C was found to be the optimum for drying both the varieties of large cardamom.

Over-ripe bitter gourd oleogel for nutritional enhancement of cookie

Shortening is a necessary ingredient in high-quality baked goods. Its impacts on dough structure and desirable final product qualities are mostly determined by its solid fat content and crystalline polymorphs. Shortening contains both saturated and trans fatty acids, both of which are harmful to one's health. As a result, alternative plastic fats with a decreased or nil saturated fat content are being developed. In our study Canola oil oleogel was prepared using ethyl cellulose at 4 to 10% level. The prepared oleogel were used to replace 20%, 40% and 60% of hydrogenated fat for preparing cookies. These cookies were compared with the ones prepared from Commercial shortening and Hydrogenated fat. Overripe bitter gourd pericarp is a major by-product of seed industry but it is very nutritious. Bitter gourd powder was added at three different levels (8, 12, and 16 % of oil) to further stabilize the oleogel. These oleogels were analyzed for their textural and rheological properties with commercial shortening and hydrogenated fat as a reference. The prepared cookies were also compared in terms of textural attributes and physical parameters to assess their texture and sensory attributes. The cookies prepared by using bitter gourd powder stabilized oleogels were found to be rich in phytochemicals like total dietary fibre, total phenolics, total flavonoids, total carotenoids, iron content etc. When selected oleogel was used to replace 40 % hydrogenated fat in cookies preparation, the visual, textural and sensory attributes of cookies were found statistically similar to those prepared from commercial shortening but nutritionally superior. Thus, bitter gourd stabilized canola oleogel can emerge as successful replacement of commercial shortening for preparing cookies.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the Student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Sajeel Ahamad	21341	M.Sc.	Assessment of onion cultivar for dehydration suitability & functional quality	Dr. V.R. Sagar
2.	T.S. Hanunesh Gowda	21342	M.Sc.	Valorization of pumpkin to calcium enriched crisps	Dr. S.G. Rudra
3.	Devesh Kumar	21343	M.Sc.	Effect of postharvest treatment on quality and shelf-life of pointed gourd	Dr. Ram Asrey
4.	Ashwija B.N.	21344	M.Sc.	Over-ripe bitter gourd oleogel for nutritional enhancement of cookie	Dr. S.G. Rudra
5.	Thippeswamy B.	21345	M.Sc.	Functional stability of beetroot betalains under different processing regimes	Dr. Alka Joshi
6.	Jadhav Prasenjit S.	21347	M.Tech.	Evaluation of mechanical drying methods for large cardamom (*Amomum subulatum* Roxb.)	Dr. Abhijit Kar
7	Om Prakash	10345	Ph.D.	Extrusion processing characteristics of pearl millet	Dr. V.R. Sagar
8.	Archana T. Janamati	*10876*	Ph.D.	Management of chilling injury, shelf life and postharvest disease in mango	Dr. Charanjit Kaur
9.	Omar Alajil	10925	Ph.D.	Nutritional profiling of common apricots cultivars grown in India and development of osmo-dehydrated products of apricots	Dr. V.R. Sagar
10	Uma Prajapati	*11103*	Ph.D.	Combinational effect of ultra violet radiation and postharvest elicitors on storage behavior and postharvest quality of bitter gourd (*Momordica charantia)*	Dr. Ram Asrey
11.	Sachin A. J.	11105	Ph.D.	Extension of storage life of guava using ethylene inhibitors and its integration with modified atmosphere packaging	Dr. D.V. Sudhakar Rao
12.	Karan Singh Dhami	11154	Ph.D.	Postharvest response modulation of mandarin (*Citrus reticulate* Blanco) fruits to exogenously applied plant hormones	Dr. Ram Asrey

Vegetable Science

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Prof. R.K. Yadav

The Division of Vegetable Science has the mandate to conduct applied and strategic research on improvement of vegetable crops; to impart postgraduate education and training for human resource development; to disseminate information on recent advances in vegetable crops; to provide advisory and consultancy services on crop and seed production technology and improvement of vegetable crops; to collect, evaluate, purify and preserve the bio-diversity material related to different vegetable crops; to utilize the desirable superior genotypes in the breeding programme. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Genetic improvement and heterosis studies

Assessment of combining ability and heterosis for yield and quality traits utilizing petaloid CMS inbreds in tropical carrot (*Daucus carota* L.)

Forty eight carrot hybrids generated from line × tester crosses (4 CMS lines and 12 Testers) along with one check, PusaVasuda were evaluated. The analysis of variance revealed highly significant difference for all the quantitative, biochemical and quality characters and mineral nutrients. The hybrids DCatH 9848, followed by DCatH 531, DCatH 713, DCatH 9113, DCatH 5313, DCatH 785, DCatH 981, DCatH 71 and DCatH 716 are most promising in terms of root yield and have self-core. Highest GCA for root weight and root yield for lines and testers was observed in DCatCMS-7 and DCat-1, respectively. For root yield, the hybrid DCatH 9848 recorded heterosis percentage of 38.92%, 38.10% and 43.21% over mid parent, better parent and PusaVasuda (check), respectively. The line and tester with highly significant GCA for root yield were DCatCMS-7 and DCat-1, respectively. The genetic components of variance due to SCA was greater than GCA for most of the traits except for days to root maturity and root length. The highest yielding hybrids for invert sugar, juice recovery, total sugars and total antioxidant activity was DCatH 788, DCatH 5300, DCatH 9813 and DCatH 736, respectively. DCatH 9837 was best hybrid for total carotenoids, lycopene and β-carotene and DCatH 5316 for TSS and fructose. Dominant gene action was observed in most of the traits like TSS, invert sugar, fructose, total sugars, total carotenoids, lycopene and β-carotene while additive gene action was found only in juice recovery and total antioxidant activity. The highest yielding hybrids for potassium, calcium and magnesium was DCatH 711, DCatH 536 and DCatH 785, respectively. Similarly, the highest yielding hybrids for iron, zinc, copper and manganese was DCatH 71, DCatH 9888, DCatH 76 and DCatH 5316, respectively. Dominant gene action was observed in most of the mineral nutrients except potassium and manganese. Thus, it is evident that heterosis breeding can be effectively utilized in the improvement of above traits in carrot. The best performing lines and hybrids can be further used in carrot breeding programme.

Heterosis studies on yield and quality traits in temperate carrot (*Daucus carota* subsp. *sativus*) using cytoplasmic male sterile (CMS) lines

Hundred F_1 hybrids ofcarrot were developed in line × tester mating design from 10 CMS lines (pt-CMS) and 10 inbreds used as tester. The resulting 100 hybrids along with 20 parental types and commercial checks were evaluated for thirteen horticultural traits and eight different bioactive compounds consecutively for two years. The pooled estimates of variance analysis over the years revealed significant mean squares of lines, testers and line × testers, which indicated the influence of both additive and non-additive gene effects in the expression. The pooled analysis estimates of per se performance, principal component analysis and dendrogram analysis over the years indicated remarkable genetic variation among the parental types for their exploitation in heterosis breeding. The higher magnitude of σ^2 sca as compared to σ^2 gca highlighted the relevance of specific combining ability in the generation of heterotic crosses for both horticultural and bioactive compounds. The CMS lines KT-8542A (3.54) , KT-98A (1.15) and KT-28A (0.59) were good combiner for root yield .CMS lines viz. KT-8542A (1.92) could be better as female parent for higher root length. CMS lines KT-10A (5.93), for cortex thickness and core diameter KT-8542A (25.33) and could be utilized as parents for developing hybrids with thick flesh and coreless roots. The crosses KT-98 × PN-1, KT-98 × New Kuroda can be recommended for further evaluation trial for developing hybrids with higher marketable roots and its contributing traits. The significant year × genotype interaction for the TCC and β-carotene content revealed therole of few major genes controlling expression of carotenoids in carrot root. The positive association of SCA with heterosis indicated the influence of non-additive gene effects in controlling the expression of traits. The significant genotype × environment interaction variance for total carotenoid and β-carotene indicated the role of both genotype and environment controlling expression of these traits, which necessitated the need of multi-year and multi-environment evaluation for the selection of genotypes for carotenoid content. The pooled analysis results also determined that the carotenoid content in carrot root is under the genetic control of few major genes (oligogenic). The high estimates of h 2 ns over the years for carotenoid and β-carotene indicated that selection would be effective for these traits. GCA effects over the years CMS lines KT-28A (2.75) and KT-28A(2.84) shown good general combiner for β-carotene and total carotenoid content respectively, KT-98A(0.45) for CUPRAC, KT-80A (0.08) for FRAP, and KT-8542A (87.81) for phenols could be used as parents in hybrid breeding programs. The significantly highest heterosis for phenolic content in desirable direction was observed in the 15.38 % (KT-98 × KS-59) to 1546.38 % (KT-62 × KS-21) mid parent. The hybrid6.15% (KT-10 × KS-50) to 320.60% (KT-62 × KS-21) and 8.03 % (KT-39 x PN-1) to 225.10 % (KT-39 × PY-1), respectively exhibited significantly highest heterosis over both mid parent and better parent in desirable direction for beta–carotene content. Significantly high total carotenoid content over the mid parent and better parent heterosis was observed, 6.76 % (KT-62 × KS-20) to 390.38% (KT-28 × KS-59) and 19.18% (KT-80 × PY-1) to 312.88 % (KT-98 × PY-1), respectively. The molecular analysis revealed that Out of 100 microsatellite primers, 67 primers showed high polymorphism among the parental lines. The PIC content ranged from 0.35 to0.86 and genetic distance varied from of 0.46 to 0.89, found significant association of genetic distance based on polymorphic genomic-SSR with heterosis for commercial traits indicated the utility of genetic distances in prediction of heterosis in carrot. Moreover, green petal colour and light green petaloid were predominant in CMS lines, encountered variation in their mid-ribs. Variation in petaloid shape and colour pattern could may be due to influence of genetic background of the transformed CMS lines; however, it needs further investigations. The overall results obtained would be instrumental for carrot breeders, geneticists and food scientists for enhancing potential of carrot for agro-food, pharmaceutical and natural pigment industry.

Studies on heterosis for quality traits in cauliflower

Heterosis studies were done for 12 important agro-morphological traits by involving 24 parental lines (10 CMS and 5 testers in Early group; 5 CMS and 4 testers in Mid group) and 70 F_1 crosses I cauliflower. Wide range of heterosis was revealed by the study of curd yield attributes i.e. curd length, curd width, marketable curd yield and net curd weight. CMS N-2-121, CMS 999-23, DC 67 and DC 71 of Early group and CMS 8401 and DC 401 of Mid group were best combiners for curd yield traits. Further, analysis of nine dietary minerals namely iron (Fe), zinc (Zn), copper (Cu), manganese (Mn), magnesium (Mg), sodium (Na), potassium (K), calcium (Ca) and sulfur (S) content in curd portion at harvest stage indicated wide range of mineral content as well as both mid parent and better parent heterosis. Combining ability analysis indicates for available strong combiners for different dietary minerals in both in Early and Mid groups of Indian cauliflower. Promising combiners for multiple minerals were identified as CMS 999-41-5 (Fe, Mn, Mg, Na, Ca, S), CMS 4348-41-5 (Fe, Zn, Na, Ca, S, K), DC 98-2 (Fe, Cu, Na, Ca, S) and DC 67 (Zn, Mn, Na and S) in Early group. In mid group, CMS 8401 (Fe, Na, Ca, K), CMS 1944-309 (Zn, Ca, S), DC 401 (Fe, S, K) and DC 476 (Cu, Mn, Na) were most promising combinations. Further, the total glucosinolates, sinigrin, glucoerucin and progoitrin content were detected in significant levels in cauliflower parental lines and F1 hybrid of Indian cauliflower. These compounds showed wide range of heterosis. It also revealed potential combiners on the basis of GCA effect and promising F1 combination on the basis of SCA effect. Expression analysis of eight key genes from different branch points from glucosinolates biosynthesis process and amplification of 16 gene specific markers also indicated variable expression pattern in Indian cauliflower. It was first systematic attempt to study the heterosis for dietary minerals and glucosinolates and also for understanding the glucosinolates pathway genes in Indian genotypes of cauliflower. However, the study will be useful for breeding cauliflower hybrids rich in dietary minerals, antioxidants and beneficial glucosinolates.

Assessment of genetic diversity and functional quality in garlic

The genetic diversity through morphological, biochemical and molecular markers and functional quality of 29 garlic genotypes were studied. Significant variability was found among genotypes for different characters. All the morphological and biochemical traits showed higher PCV than GCV revealed the role of environment in trait expression. High to moderate heritability and genetic advance as percent mean was recorded for different traits and low for dry matter and TSS. Correlation analysis revealed highest positive correlation between total yield & marketable yield, FRAP & DPPH. 3 major clusters were identified for morphological and biochemical traits. The genotypes were screened with 214 Microsatellites or Simple Sequence Repeat (SSR) primers with 9 markers showing polymorphism. ACM091 showed high PIC index (0.498) and major allele frequency per locus. AsESSR47, AsESSR 82 detected highest number of alleles (6). Cluster analysis using molecular markers revealed 4 distinct clusters. Black garlic (BG) produced by aging of garlic cloves at constant temperature and relative humidity. . Observations were recorded such as total phenolic content (mg GAE/ 100 g FW), total flavonoid content (mg QE/ 100 g FW), total antioxidant capacity [CUPRAC (µmolTrolox/ g FW, FRAP (µmolTrolox/ g FW), DPPH assay (µmolTrolox/ g FW)], allicin content (mg /100g)**,** pyruvic acid (µMol/ ml) showed higher significant differences. We found higher total phenolics and antioxidant activity until 40th day of aging and decreased thereafter. Total flavonoid content continued to increase throughout the aging process. Allicin content first increased and then decreased throughout the process of aging. Pyruvic acid content tends to decrease in the aging process. High variability observed amongst the 29 garlic germplasm accessions and superior genotype(s) identified from our study can be taken further for crop improvement programme. Evaluation of genetic diversity using more accessions and more markers in order to obtain accurate estimate of genetic diversity. Identified garlic genotypes having high antioxidant properties can be used for commercial production of black garlic.

Genetic diversity and population structure analysis in bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] using morphological and molecular markers

Genetic diversity and population structure analysis was done 82 bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] using morphological and molecular markers at IARI and one experiment on variability analysis with 25 set of genotypes was also carried out at IARI-Jharkhand, Hazaribagh, Jharkhand. Out of 82 genotypes, 50 genotypes had cordate leaf shape; however, JPG-51, IC588084 and JPJ-11 had dark green serrated leaves with visible cut incision. Ten genotypes had penta-lobed leaves while other genotypes had trilobed leaves. Majority of the genotypes (51) had entire leaf margin while other 31 had multifid leaves. Seventy-nine the genotype used in the study showed angular type stem while only three showed round type stem. Pubescence on stem was found in sixty genotypes while in remaining 22 genotypes, it was absent. Morphological fruit characters such as fruit shape, fruit neck type and fruit skin colour showed wide range of variability among the genotypes. All the genotype had triangular seed shape except genotype EC800996 and Market Collection which had rectangular seed shape. Mean sum of squares was highly significant for all 08 quantitative characters, which indicated that presence of high magnitude of variability for yield parameters among the bottle gourd genotypes. At IARI-Jharkhand also, genotypes involved in the study varied significantly for all above horticultural traits. Fruit diameter, fruit weight, fruit length, and number of fruits/plants were significantly positively correlated with yield per plant. According to the path coefficient analysis, fruit weight had the greatest direct impact on yield per plant. D^2analysis revealed six clusters based on quantitative traits under study. The hierarchal cluster analysis also revealed 6 clusters among the 82 genotypes. Quantitative features were categorized into eight PCs of which only six PCs cumulatively contributed 98.25 percent of total variation. According to the PCA the major traits contributing for genetic diversity in PC1 were fruit yield per plant and fruit weight. Out of 100 SSR markers utilized for molecular diversity analysis, 16 were found to be polymorphic in which 48 alleles were amplified, with an average of three alleles per locus. The polymorphic information content (PIC) of the SSR markers ranged from 0.035 to 0.563 with mean value of 0.37. The major allele frequency ranged from 0.476 to 0.982 for markers LASI77 and 37566, respectively. Four SSR markers namely 2825, LASI-75, 44141 and LASI-57 were found highly informative for diversity analysis.
Population Structure Analysis, revealed six populations in the accessions. The overall proportions of membership of the samples in each of the six populations were 0.16, 0.15, 0.17, 0.18, 0.18 and 0.16.

Genetic studies of *Fusarium* wilt resistance in wild pea (*Pisum sativum* ssp. *elatius*)

To study the host plant resistance against *Fusarium* wilt disease in garden pea, 50 genotypes (36 genotypes of *Pisum sativum* var. *hortense*, 10 genotypes of *Pisum sativum* ssp. *elatius*, 4 genotypes of *Pisum fulvum*) were screened in artificially created wilt sick pots under natural conditions. Among the 36 genotypes of *Pisum sativum*var. *hortense* 5 genotypes namely G-2, G-12, G-15, G-17 and G-27 were recorded as resistant to *Fusarium* wilt, two genotypes *Pisum fulvum* G-46, G-49 were showed good resistance and G-37, G-38, G-39, G-40, G-41, G-43, G-44, G-45 of *Pisum sativum* ssp. *elatius* were also noted as resistant to Fusarium wilt of garden pea. Genetics of Fusarium wilt resistance in *Pisum sativum* ssp. *elatius*N-8 using F_2 (VRP-6 × N-8) and BC_1 population. These disease reaction data were analysed using chi square test. In backcross population thirty-four plants that are screened as susceptible to the wilt disease are phenotypically expressed complete wilt symptoms, the forty resistant plants showed light symptoms like yellowing of basal older leaves due to resistant mechanism in the plants, these are segregated in 1:1 expected ratio. In F2 population 36 plants were exhibited full symptoms of fusarium wilt, the remaining 124 plants are screened as resistant. Due to resistant mechanism, these plants expressed less symptoms of wilt disease with normal growth and development. This F2 population for disease resistance segregated in 3:1 expected ratio. Single dominant gene governing resistance against *Fusarium oxysporum* f. sp. *pisi* in wild pea N-8 is found against fop-1. Identified novel sources of Fusarium wilt resistance in *Pisum sativum* ssp. *elatius*, *P. fulvum* and *P. sativum* var *hortense*. Identified single dominant gene in *P. sativum* ssp. *elatius* N-8. It's feasible to transfer via backcross breeding in susceptible varieties of early garden pea.

Genetic analysis of male sterility mediated three-way crosses for yield, quality and resistant to purple blotch disease in onion (*Allium cepa* L.)

Forty-four genotypes including check were evaluated for different quantitative and qualitative attributes at IIHR, Bangaluru. Based on yield per se performance, the perusal of data revealed that the acceptable yield was recorded maximum by L2 × T5 (Arka Lalima F_1×Arka Kalyan) followed by L1 × T4 (Arka Kirthiman×Arka Niketan) in three-way cross hybrids, L2 (Arka Lalima) in lines and T4 (Arka Niketan) in testers. The three-way hybrids namely Arka Kirthiman (F_1) ×Arka Kalyan (7.89), Arka Lalima (F_1) ×Arka Kalyan (8.75) and Arka Lalima (F_1) ×Arka Pitambar (9.78) were found to be resistance under both natural epiphytotic condition as well as artificially inoculated under controlled polyhouse condition against purple blotch disease. Hybrids Arka Kirthiman×Arka Niketan, Arka Kirthiman×Arka Kalyan, Arka Lalima×Arka Niketan and Arka Lalima×Arka Kalyan were observed for less storage losses and suitable for higher shelf-life of bulbs. The hybrids of light green with semi glossy foliage's had very low-level infestation of thrips. Three- way cross hybrid purity was confirmed by using molecular markers from which, onion genomic DNA, screened with SSRs/MK primers, which were specific to S cytoplasm, and male fertile and sterile line screened with ORF primers (designed by using mitochondrial DNA sequence of onion). A significant heterosis over standard check Satara Garva was attained for almost characters, which possesses commercially more importance. Line 2 (Arka Lalima) and tester T4 (Arka Kalyan) has been found best as general combiner for yield and most of the yield attributing parameters. Three-way crosses namely Arka Lalima (F_1) ×Arka Kalyan, Arka Lalima (F_1) ×Arka Niketan, Arka Kirthiman (F_1) ×Arka Kalyan and Arka Kirthiman (F_1) x Niketan were showed overall best performance for yield, storage and resistance to abiotic and biotic stress in terms of SCA effect. These cross combinations were also concluded as superlative to exploit heterosis over standard check.

Incorporation of yellow mosaic disease resistance in pole type french bean (*Phaseolus vulgaris* L.)

Seventy-one genotypes of French bean were screened under natural and artificial epiphytotic conditions against horse gram yellow mosaic virus (HgYMV) at IIHR, Bangaluru. The presence of the viral disease was confirmed through Polymerase Chain Reaction and sequencing of virus genome which indicated 94% identity match for horse gram yellow mosaic virus (HgYMV). Field screening showed that PDI ranged from 13.33 to 75.56 and none of the genotypes were found to be immune to this disease. The commercial varieties like Jade-5058 and Arka Arjun have shown some resistance with PDI 13.33 and 14.44 and 13.33 and 12.22 under in field and artificial screening, respectively, which were much lesser than the susceptible checks Arka Komal (PDI 92.22) and Arka Anoop (PDI 90.00). The highest average rate of infection per unit time period "r" was noted in the susceptible genotypes namely, Arka Suvidha (1.05), IIHR-(19×34)-B (1.03), and least in Jade-5058 (0.64) and Arka Arjun (0.65), as compared to the susceptible checks Arka Komal (0.94) and Arka Anoop (0.88). Both the resistant genotypes, Jade-5058 and Arka Arjun showed less area under disease progress curve (AUDPC) of 350.54 and 359.16 compared to the other genotypes. The maximum disease progress was observed in Arka Suvidha (1363.34), Arka Komal (998.89) and Arka Anoop (776.67). A total of 119 different markers (SSR, RAPD, ISSR, SCAR and RGA) were used for validation of molecular marker linked HgYMD resistance. Fourteen out of all markers 121 screened exhibited polymorphism between the parents viz. Arka Arjun (Resistant), Jade- 5058 (Resistant) and Allama (Susceptible). Bulk segregant analysis (BSA) was done in two segregating F2 populations *viz.,* Arka Arjun × Allama and Jade-5058 × Allama against YMD resistance and it revealed that the YMD resistance in French bean is governed by a single recessive gene. The SSR marker Pvcomp 14 only co–segregated with resistant and susceptible individuals of the F2 populations of Arka Arjun × Allama and was linked to YMV disease resistance loci. Salicylic acid and Jasmonic acid were higher in almost all infected plants of every genotype but it reduced drastically in case of susceptible genotypes after disease inoculation and reduced later on. In case of the resistant genotypes, it was much higher after 15 DAI. The oxygen radical and hydrogen peroxide was present in higher quantities in the infected plants compared to the healthy or control (no disease inoculation) but it was reduced after 7 days. The activity of O-2 was maximum in case of susceptible varieties at 7 days after inoculation (DAI). The peroxidase enzyme activity was maximum after 15 days of inoculation in case of resistant genotypes. In case of total phenol, there was decreased trend across the varieties and treatments. The quantity of total phenol was the highest in resistant genotypes Arka Arjun (146.59 mg/100g fw) and Jade-5058 (151.44 mg/100 g fw) after inoculation.

Theme 2. Mapping of traits and molecular breeding

Breeding for combined resistance to bacterial wilt and root knot nematodes in tomato (*Solanum lycopersicum* L.)

Three tomato lines (IIHR-2610, IIHR-2296 and IIHR-2867) were found highly resistant (HR) against bacterial wilt (BW), whereas three lines (IIHR-2805, IIHR-2963 and IIHR-2964) were found highly resistant against root knot nematodes (RKN) at IIHR, Bangaluru. Three molecular markers (SLM-12-10, SLM-12-2 andSLM-6-118) linked to bacterial wilt resistant were able to distinguish between resistant, susceptible lines for bacterial wilt and the lines with both resistance alleles for Bwr-12 and Bwr-6were the least susceptible and had the lowest disease incidence (3 to 9.18 %), compared to lines with only a single resistance allele from Bwr-12 (11.33 to 18.34 %). Three molecular markers (Mi-23, PMi and W-415) linked to RNK resistance, were able to distinguish between resistant and susceptible lines, in which resistant lines showed the presence of Mi locus, while all susceptible lines were found negative for Mi gene. For development of advance breeding lines having combined resistance to bacterial wilt and root knot nematodes, based on phenotypic and molecular screening six lines viz., IIHR-2296, IIHR-2042, IIHR-2834, IIHR-2867, IIHR-2835 andIIHR-2920, which were found resistant to BW selected as female parents and other six lines (IIHR-2614, IIHR-2786, IIHR-2785, IIHR-2963, IIHR-2964 and IIHR-2965), which were found resistant to RKNs chosen as male parents. Thirty-six F1 hybrids were developed in line × tester fashion and evaluated for yield and its contributing traits for estimating the GCA, SCA and heterosis and based on the performance out of 36 F1 hybrids, five were found superior and selected for further advancement to develop the advance breeding lines. Five different F2 populations and three backcross populations from selected hybrids were developed and evaluated at both phenotypic and genotypic levels. Nine lines (six F2 and three backcrossed lines) with different combination were selected for further advancement based of phenotypic and genotypic selection. At each stage of advancement phenotypic and genotypic selection for BW resistant and genotypic selection for RKN resistant was carried out to insure combined resistance. Finally, nine novel advance breeding lines (six F6 and three BC3F3) lines were developed and evaluated at both phenotypic and genotypic level. Results showed that the developed novel lines were at par for most the horticultural traits with recurrent parent in addition to resistant against both bacterial wilt and root knot nematodes. Effects of root exudates from different resistant and susceptible lines against RKN were examined for relative suppression rate egg hatching (%), J2 mortality and chemotaxis movement of J2. Results showed the significant difference between resistant and susceptible lines for all three parameters (photosynthetic rate, stomatal conductance and transpiration rate) against bacterial wilt and root knot nematodes. In addition to that component analysis (HS-SPME) analysis using capillary GC–MS/MS of root exudates of resistant and susceptible lines was also performed in order to identify the underlying compound(s) responsible for resistance against root knot nematodes and bacterial wilt respectively. Among all the identified compounds, dibutyl phthalate was found directly linked to resistant reaction against the root knot nematodes, as its relative amount increased greatly post inoculation in all resistant lines along with novel developed resistant line, while the decrease was observed in root exudates from both the susceptible lines, after post inoculation of RKN. Whereas, elixene, 2-methyl-1-dodecanol, p-menthone and ethyl 4-ethoxybenzoate were found linked to resistant reaction against bacterial wilt disease, as their relative amount increased greatly post inoculation in all resistant lines along with novel developed resistant line, while the decrease was observed in root exudates from susceptible lines, after post inoculation of Ralstonia solanacearum. Novel advance breeding lines, which were developed in this study, may be used in future breeding programmes related to root knot nematode and bacterial wilt diseases and would facilitate pyramiding of resistance genes for multiple diseases in tomato.

Physio-biochemical traits association and gene expression studies

Thirty-four genotypes of onion were used to identify stage specific expression of morphological traits, mineral content and sugar content and their effect on marketable bulb yield. Besides, the role of *AcFT*gene in bulbing regulation in *kharif* onion was also studied. The genotypes differed significantly for total yield, frequency of marketable bulb (*i.e.*, equatorial diameter >2.5 cm, free from doubles and bolters), average bulb weight, bulb diameter, TSS and dry matter content. Significant differences were also observed for leaf number per plant, leaf length, pseudostem length, pseudostem diameter, leaf area per plant, fresh leaf weight per plant and fresh bulb weight at 60, 90 and 120 DAP. Plant height exhibited significant differences at 60 DAP only. Leaf dry matter exhibited significant differences at 60 DAP and bulb dry matter differed significantly at 60 and 90 DAP. Marketable yield varied from 1.92 - 30.65 t/ha and total yield ranged from 6.27 -4.1 t/ha. Six genotypes produced more than 25.0 t/ha while seven genotypes produced less than 10t/ha. The genotypes were grouped into high (>25.0 t/ha) and low (<10.0 t/ha) yielding groups. The high yielding groups had higher expression of all the morphological traits compared to low yielding group at 60 DAP and lower value at 120 DAP. This suggests higher vegetative growth till 60 DAP plays important role for higher marketable bulb production in *kharif* season. Eight minerals namely nitrogen, phosphorous, potassium, calcium, magnesium, sulphur, iron and zinc were analyzed in 34 genotypes at 60 DAP which revealed significant difference among the tested genotypes. The differences in nitrogen and phosphorous content were not much distinct in the two yielding group but the potassium content was high in low yielding group at 60 DAP and low at 120 DAP. Distinct differences in calcium and sulphur content were observed in all the growth stages with high yielding group having the higher value. Magnesium, iron and zinc content was high in high yielding genotypes at 120 DAP. The association analysis suggested strong correlation of marketable bulb frequency, bulb diameter, total yield and bulb polar diameter with marketable bulb yield. TSS exhibited negative association with marketable bulb yield. Growth parameters at 60 DAP exhibited highly significant positive correlation with marketable bulb yield. At later stages of growth (90 and 120 DAP), the associations were found mostly non-significant and negative. Sulphur103content at 60 DAP had significant positive association and potassium content at 60 DAP had significant negative association with marketable bulb yield. The associations with other minerals were mostly positive but non-significant. The *AcFT*gene expression level suggested their role in bulb formation in *kharif* onion and high expression of *AcFT6* was recorded in leaf tissues of genotype having bulb differentiation stage.

Genome wide association studies (GWAS) for tomato leaf curl New Delhi virus resistance in cucumber (*Cucumis sativus* L.)

Among the 100 genotypes of cucumber evaluated under field condition, three genotypes were found to be highly resistant to ToLCNDV of which DC-61, DC-70 and DC-91 recorded Vulnerability Index (%) values 18.75, 24.95 and 25.35. Seven genotypes viz., DC-77, DGC-104, DC-40, WBC-23-2, DAMPET LOCAL, WBC-5 and DGS-15 were found to be in moderately resistant category. The high-density SNP markers combined with GWAS provide a powerful resource to identify quantitative trait loci (QTL) and possible candidate genes for important horticultural traits. Genotyping by sequencing (GBS) is a technique for identifying candidate genes by detecting single nucleotide polymorphisms (SNPs). Based on the phenotyping data fat three different intervals and genotyping GBS it was found that chromosome 3 and chromosome 5 are the possible source for the QTLs for resistance against the ToLCNDV. The identified SSRs and SNPs associated with QTLs will be used for marker assisted resistance breeding. The information from this study will help in fine mapping of the R genes. Morphological characterization was done for nine important traits namely node to first male flower, node to first female flower, days to first female flower anthesis, numbers of fruits per plant, fruit length , fruit diameter, average fruit weight, vine length and fruit yield per plant under the severe infestation of leaf curl disease predominantly caused by ToLCNDV. Observations were recorded on five randomly selected plants from each entry in three replications for all the morphological characters. The different statistical parameters used for interpretation of data were Analysis of Variance, Genotypic and Phenotypic Variance, Genotypic and Phenotypic coefficient of Variance, Heritability, Genetic Advance, Correlation Coefficient Analysis, Path Coefficient Analysis and Genetic Diversity to study nature and magnitude of variability and diversity. Genetic diversity for all the traits were found significant indicating the extent of diversity present in the population. Based on the result of all major parameters under present investigation, genotype DC-70 and DC-91 appeared to the very good performer even under severe stress condition. Even though DC-61 found be resistance to ToLCNDV but it is less performer under the stress condition. Seven genotypes viz., DC-77, DGC-104, DC-40, WBC-23-2, DAMPET LOCAL, WBC-5 and DGS-15 were found to be in moderately resistant to ToLCNDV but those are good performer under the stress condition so these genotypes were used in the future breeding programmes. Because of the maximum inter cluster distance between them, the genotypes in cluster IV and cluster III showed a significant degree of genetic diversity and used in an inter varietal hybridization programme to produce high yielding recombinants. Molecular diversity analysis revealed significant diversity among the cucumber genotypes and the polymorphic information content (PIC) was highest for UW084908 (0.75) followed by UW08450 (0.74), SSR16667 (0.74), SSR23073 (0.65), UW037969 (0.64) and UW083886 (0.64). However, PIC value ranged from 0.22 (UW085401) to 0.75 (UW084908). Neighbour joining (NJ) cluster analysis revealed the formation of three major clusters. Among the three major clusters, the highest number of genotypes found in Cluster-I followed by Cluster-II and Cluster-III. The relationship of clustering between the morphological and SSR molecular marker is found to be the highest performer genotypes with respect to the yield and other characters found to be same in SSR clustering also.

Studies on physiological traits and identification of QTLs associated with extended shelf-life in cucumber (*Cucumis sativus* L.)

Seven diverse genotypes of cucumber (*Cucumis sativus* L.) were used to study the important physiological and biochemical traits in relation to extended shelf-life and retention of green colour. The plants of these genotypes were grown inside insect proof net during *Kharif* and spring summer season (2020-2021) at the research farm of the Division of vegetable science, ICAR-Indian Agricultural Research Institute, New Delhi. Seven cucumber genotypes were evaluated in Randomized Block Design in three replications. 7 physiological parameters and 5 biochemical parameters were studied and the data was subjected to standard statistical analysis. Different traits such as physiological loss in weight, firmness, pH, photosynthetic rate, stomatal conductance, intercellular CO_2 concentration, transpiration rate, chlorophyll content in leaves, chlorophyll content in fruit peel, catalase, peroxidase, Super Oxide Dismutase were studied. Extended shelf life in DC-48 is mainly attributed to the retention of green colour after harvest and capacity to retain firmness and no shrivelling. Maximum photosynthetic rate noticed in the stay green fruit type genotypes. Among the antioxidant enzymes, catalase, peroxidase, Super Oxide Dismutase concentration was higher in all the stay green type genotypes. In case of DC-48 not much difference in these values at different intervals. For retention of green colour (RGC) two major QTLs *qRgc*4.1 (LOD-150.05) and *qRgc*4.2 (LOD-153.10) with phenotyping variance (R^2) of 17.80% were identified. The common InDel markers, InDel861 and InDel016, were detected near QTLs *qRgc*4.1 and *qRgc*4.2. InDel861 positioned to the QTL *qRgc*4.1 at a distance of 10.5cM and to the QTL *qRgc*4.2 at 12.5 cM. The InDel016 positioned to the QTL *qRgc*4.1 at a distance of 21.5cM and to the QTL *qRgc*4.2 at 8.5 cM. Two QtLs for retention of green colour were identified in the Chr. No. 4.the distance of these markers is far from the QTLs, the QTLs has strong effect on this trait, hence it needs further study to identifying new polymorphic markers flanked to this trait by carry out fine mapping on this locus. This study has demonstrated preliminary research by detecting stable QTLs for RGC can be used in future breeding program and for identifying the flanking marker to this trait using fine–mapping using large scale segregating populations and gene-editing technology to further improve fruit quality.

Identification of host genes involved in recovery phenomenon post leaf curl disease infestation in chilli (*Capsicum annuum* L.)

The present investigation was undertaken to identify host genes involved in recovery phenomenon post leaf curl disease infestation in resistant line DLS-Sel-10 of chilli. The predominant viruses causing leaf curl disease at the experimental site were found to be ChiLCV followed by ToLCJoV. The test genotypes DLS-Sel-10 and Phule Mukta were challenge inoculated with viruliferous whiteflies carrying ChiLCV. After inoculation the viral titre was found to be much lower in DLS-Sel-10 than in Phule Mukta indicating that DLS-Sel-10 tends to inhibit virus multiplication upon infection. To identify the host genes involved in host recovery phenomenon we studied the expression of different genes/transcription factors/host targets of viral genes and host miRNAs identified to be differentially expressing between the between resistant and susceptible genotypes in earlier studies. A total of 8 TFs, 5 miRNAs and 7 host targets of viral miRNAs were studied in the experiment. Along with these, genes involved in RNA interference which includes Argonaute proteins, DCL proteins and RDR proteins were also studied to understand their role in host recovery. For this, a total of twelve Argonaute family proteins, five DCL family proteins and ten RDR proteins were studied. The expression studies revealed the relative expression of TFs belonging to MYB and WRKY family found to be upregulated in resistant genotype DLS –Sel-10 and decreased in susceptible genotype Phule Mukta. Upregulation of these TFs has been found to activate the basal defense mechanism in many crop plants. However, TFs belonging bHLH and GATA Family were downregulated in DLS –Sel-10 in comparison to Phule Mukta. bHLH has been found to negatively regulate defense mechanism in studies of other workers. No specific pattern of expression was observed for miRNAs and host targets of viral RNAs defining their involvement in host recovery. Similar was the results obtained for genes of RNA interference. Majority of AGO proteins, DCLs and RDRs showed lower expression in DLS-Sel-10 the resistant genotype rebutting the role of RNA interference in host recovery phenomenon of DLS-Sel-10. The present study finds a stronger role of basal innate host defense genes in host recovery in comparison to RNA silencing mechanism which has been found to be involved in symptom recovery in many other crops.

Joint multiple family linkage analysis for resistance to watermelon bud necrosis virus and fruit quality traits in watermelon

Citron (*Citrullus amarus*) a wild relative of watermelon having resistance to watermelon bud necrosis orthotospovirus (WBNV) was used for genetic and molecular studies for transfer of desirable traits in cultivated watermelon at IIHR, Bangaluru. Geneticanalysis in two prebred lines *viz.,* BIL-53 and BIL-99 derived from citron suggested that the genetics of most of fruit quality traits are governed by one or two genes suggesting simple inheritance. QTL mapping for fruit shape identifies eleven major QTLs on chromosome 3, 4 and 11. Candidate gene analysis in chromosome (Chr) 3 revealed a novel allele of *Cla011257* gene with two SNPs resulting in oblong fruit shape and predicted *Cla016683* gene as a putative candidate for fruit shape in a novel QTL region on Chr. 11. Similarly, for rind color and pattern consistent QTLs were detected across two populations (F_2 and BC_1F_2) on chromosome 9. Comparative genomics analysis of this region revealed two genes namely *Cla016148* and *Cla016150* as probable potential candidate genes for stripe and interstripe color. QTL analysis for seed traits revealed two QTLs viz., *q_100SW_2.1* and *q_100SW_6.1* for 100seed weight; three QTLs viz., *q_SCC_3.1*, *q_SCC_*5.1 and *q_SCC_5.2* for seed coat color. Results validated the previously reported QTLs viz., *ss2.1* and *qSS6* for seed weight/size and *qsc-c3-1* for seed coat color of watermelon. Similarly, one novel QTL was identified for total soluble solids on Chr. 11; candidate gene analysis in it predicted *Cla016890* and *Cla016891* genes as putative candidates. For flesh color, we made firstattempt to map the genes/QTLs governing flesh color at the different regions of fruit through visual and colorimetric analysis. Results revealed fifteen major QTLs on Chr. 2, 4, 5, 6, 7 and 10 for flesh color at different regions. Candidate gene analysis predicted *Cla020214* and *Cla020121* on Chr.2; *Cla005011* on Chr. 4; *Cla018767, Cla018768, Cla018769, Cla018770, Cla018771* on Chr. 6; *Cla017416* and *Cla017593* on Chr. 10 as a probable candidate genes governing flesh color at different regions. For WBNV resistance, efforts have been made to integrate WBNV resistance QTLs from wide range of populations and screening experiments for a comprehensive analysis through QTL-meta-analysis and joint inclusive composite interval mapping (JICIM). Comprehensive analyses for QTLs suggested *MQTL_WBNV_2.1* on Chr. 2, *MQTL_WBNV_3.2* on Chr. 3 and *MQTL_WBNV_7.2* on Chr. 7 as potential candidate QTL regions for WBNV resistance. The genes identified in these QTLs *viz*., *Cla020173* encoding PR-1, *Cla001733* encoding pathogenesis-related transcriptional factor and ethylene-responsive transcription (ERF), *Cla001590* and *Cla001591* genes encoding acid phosphatase, *Cla019476* encoding TIR-NBS and *Cla011771* belonging to TIR-NBS-LRR gene family may be investigated as putative candidates for WBNV resistance in watermelon. Overall results suggest that the breeders can use citron species as a source of resistance in breeding programs without apprehension of linkage drag on fruit quality traits. The results obtained in present study may provide way for functional validation of putative candidatesand development of suitable markers for marker assisted selection (MAS) to WBNV resistance with improved fruit quality traits in watermelon.

Theme 3. Standardization of seed production technology

Optimization of sowing time and nitrogen level for seed productivity and quality in garden pea (*Pisum sativum* var. *hortense* L.)

The present experiment was conducted during *Rabi* 2020-21 consisting of three dates of sowing (D) and 11 treatments of nitrogen management practices (N) in garden pea variety Pusa Shree. The time of sowing had significant influence on the plant growth parameters. D2 (4th Nov) sowing recorded the significantly higher values for the plant growth parameters like plant height (70.07 cm at 100 days), number of leaves (148.45 at 100 days), nodule count (49.63 at 80 days), root volume ($1.99 cm^3$ at 100 days), shoot dry weight (25.74g at 100 days) and root dry weight (1.21g at 100 days), while D1 (24th Oct) sowing exhibited minimum values. Minimum number of days to 50 percent flowering (37.33) and marketable pod maturity (44.79) was recorded in D1 (24th Oct) sowing. The time of sowing had significant effect on yield and yield contributing characters. D2 (4th Nov) sowing recorded the significantly higher pods per plant (18.03), pod length (6.71cm), 100 seed weight (20.38g), seed yield per hectare (19.29 q/ha) and minimum was observed in D1 (24th Oct) sowing. D2 (4th Nov) sowing showed the significantly higher germination percentage (95.87%), seedling length (23.37 cm), seedling dry weight (36.94 g), Seed vigour index-I (2244.09), seed vigour index-II (3550.12), seed protein content (22.9%) and lowest electrical conductivity was reported in D2 ($22.97\ \mu$ mhos $cm^{-1}g^{-1}$) sowing which indicated the superiority of seeds produced in D2 (4thNov) sowing. Soil parameters differed significantly among different nitrogen management practices. The maximum organic carbon (0.85%), total nitrogen in soil (0.078%) and total phosphorous in soil (0.08%) were reported in N10 treatment. The interaction among the date of sowing and nitrogen treatments were significant for majority of characters except plant height, shoot dry weight, root dry weight, number of seeds per pod, 100 seed weight, germination %, seedling dry weight, seed vigour index-II, electrical conductivity, nitrogen in soil and total phosphorous in soil. The seed higher seed yield with better seed quality could be obtained from D2 with N10treatment. Thus, based upon experimental findings it is concluded that the seed crop of garden pea cultivar Pusa Shree should be sown around 4th November with50% N + Seed treatment with *Rhizobium* + foliar spray of urea @ 40 (1%) and 60 (2%) days to obtained higher seed yield of 21.46 q/ha with better seed quality traits and highest B:C ratio of 1.47:1

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Pallavi BS	21362	M.Sc.	Identification of host genes involved in recovery phenomenon post leaf curl disease infestation in chilli (*Capsicum annuum* L.)	Dr. Arpita Srivastava
2.	Gowthami	21363	M.Sc.	Genetic studies of *Fusarium* wilt resistance in wild pea (*Pisum sativum* sp. *elatius*)	Dr. Brij Bihari Sharma
3.	P Kaishma	21364	M.Sc.	Assessment of genetic diversity and functional quality in garlic	Dr. Anil Khar
4.	Janardhan Reddy	21365	M.Sc.	Assessment of combining ability and heterosis for yield and quality traits utilizing petaloid CMS inbreds in tropical carrot (*Daucus carota* L.)	Dr. A.K.Sureja
5.	Malatesha K	50055	M.Sc.	Genome wide association studies (GWAS) for tomato leaf curl New Delhi virus resistance in cucumber (*Cucumis sativus* L.)	Dr. S.S. Dey
6.	Geeta P Karigar	50056	M.Sc.	Studies on heterosis for quality traits in cauliflower	Dr. Shrawan Singh
7.	Jayanth K	50057	M.Sc.	Physio-biochemical traits association and gene expression studies for marketable bulb formation in *kharif* onion”	Dr. Sabina Islam
8.	Shamantha TR	60055	M.Sc.	Genetic diversity and population structure analysis in bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] using morphological and molecular markers	Dr. J.K. Ranjan
9.	Pyla Suresh	60056	M.Sc.	Studies on physiological traits and identification of QTLs associated with extended shelf-life in cucumber (*Cucumis sativus* L.)	Dr. A.D. Munshi
10.	Bharath P	60057	M.Sc.	Optimization of sowing time and nitrogen level for seed productivity and quality in garden pea (*Pisum sativum* var. *hortense* L.)”,	Dr. B.S. Tomar

11.	Ajay Kumar Pandav	10633	Ph.D.	Genetic analysis of male sterility mediated three-way crosses for yield, quality and resistant to purple blotch disease in onion (*Allium cepa* L.)	Dr. B. Varalakshmi
12.	Vinod Jatav	10713	Ph.D.	Breeding for combined resistance to bacterial wilt and root knot nematodes in tomato (*Solanum lycopersicum* L.)	Dr. A.T. Sadashiva
13.	Siddharood Maragal	10899	Ph.D.	Joint multiple family linkage analysis for resistance to water melon bud necrosis virus and fruit quality traits in watermelon	Dr. E. S. Rao
14.	Hemant Ghemeray	10908	Ph.D.	Heterosis studies on yield and quality traits in temperate carrot (*Daucus carota* subsp. *sativus*) using cytoplasmic male sterile (CMS) lines	Dr. Rajkumar
15.	Arindam Das	10911	Ph.D.	Incorporation of yellow mosaic disease resistance in pole type French bean (*Phaseolus vulgaris* L.)	Dr. Aghora T. S.

School of Social Sciences

Discipline	Number of Thesis Submitted	
	M.Sc.	Ph.D.
Agricultural Economics	04	05
Agricultural Extension	06	03
Agricultural Statistics	09	05
Bioinformatics	05	02
Computer Application	07	04
Total	**31**	**19**

Agricultural Economics

22

Prof. Alka Singh

The Division of Agricultural Economics focused on farm business analysis, efficient allocation of resources, supply response, input demand analysis and marketing efficiency. Research on capital formation, labor employment, farm mechanization, rural credit needs, yield gap analysis, price policy and subsidy issues, efficient management of natural resources, issues related to national food and nutrition security, efficiency and of agricultural production systems, poverty alleviation, research impact assessment and priority setting, export potential of agri-products, etc. were accorded high priority. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Technology, resource and environment

Groundwater-energy nexus in agriculture and its implications on farm economy in western Uttar Pradesh

The intensification path of Indian agriculture is primarily engrained on groundwater resources. Government policy for installation and electrification of wells, enabled farmers to fulfill irrigation water need by extracting groundwater at cheaper cost even from deeper aquifers. However, growth in well density and subsidy support for agricultural electricity resulted into over extraction of groundwater in many parts of the country. Therefore, this study was undertaken to analyze groundwater-energy nexus in Indian agriculture with special reference to western Uttar Pradesh. Primary survey of 238 farm households was conducted in western Uttar Pradesh for crop calendar 2019-20. It was observed that irrigation infrastructure has improved substantially more biased towards groundwater neglecting canal. Groundwater depletion is more serious in north western part of the country and few states government enacted policy to restrict it. In Uttar Pradesh, groundwater is dominant source of irrigation supporting 83 per cent of irrigated area and higher growth found for deep wells whereas, dug wells are on decline. Western zone of Uttar Pradesh is agriculturally more advance and productive compared to other zones of state. At state level, total irrigation water requirement is 64.49 billion cubic meter, 92 per cent of which required for paddy, wheat and sugarcane. In western Uttar Pradesh, higher crop productivity and existence of better procurement policy of government helped in realizing higher physical and economic water productivity. Total available irrigation water at state level estimated to be 65.76 billion cubic meter, which is 1.96 per cent higher than irrigation water demand, but immense disparity exist at agro climatic zones. Analysis based on districts of Uttar Pradesh signify that groundwater depletion will reduce food grain production in the state whereas increase in area under food grain, rainfall and irrigation extent affect positively to food grain production. From survey, it was found that total cost to operate electric wells is much cheaper than diesel operated wells. In addition, proportion of variable cost in diesel operated wells is much higher compared to electric operated wells. In electrification of wells, groundwater depletion played key role in western Uttar Pradesh. Analysis shows that operating cost per hour under flat tariff is cheaper than metered tariff. Farmers' dependent only on groundwater for irrigation have better control in term of timing and quantity of water, which resulted into higher crop yield and generated higher income. Primary survey-based analysis signifies that water productivity (physical and economic) and farm efficiency (technical, allocative and economic) estimate is better for groundwater users compared to farmers who dependent on canal water for few numbers of irrigation. Share of irrigation cost to total cost incurred by farmers, is higher for diesel operated farms compared to electric operated and share of irrigation cost is in accordance with its water intensive nature. Estimated value of economic surplus indicate that about Rs.39032 crores additional income generated with current electrification over diesel operated wells, of which producer surplus is more than 80 per cent.

An economic analysis of production risks in major pulse crops

India is the world's largest pulse producer accounting for 23.40 million tonnes of pulse production covering an area of 29.03 million hectares with a productivity of 806 kg/ha. In India, chick pea and pigeon pea accounts for 36.5 per cent and 15.5 per cent national area and 47.9 per cent and 17.9 per cent of national production respectively. Agricultural production in general, rainfed production specifically is a risky process, and considerable evidence exists to suggest that farmers behave in risk-averse ways. The results of this study revealed that the production and area under cultivation of gram and arhar have increased significantly from period I (1980-81 to 2000-01) to period II (2001-02 to 2017-18), particularly 2007 onwards. The state wise share of area and production of gram and arhar have showed that the share of Rajasthan, Odisha, Bihar and Uttar Pradesh have decreased while the share of Maharashtra, Karnataka and Andhra Pradesh have increased. Madhya Pradesh holds the maximum share in area and production of gram while Maharashtra holds the maximum share in area and production of arhar. The total change in mean production of gram and arhar was mainly due to percentage change in the mean area and the percentage change in mean yield respectively. The analysis on sources of change in instability have showed that the source of variance in gram production in both period I and II was mainly due to area variance, followed by yield variance. In case of arhar production the variance in both period I and II was mainly due to yield variance followed by area variance. The analysis on cost share and net profit have showed that pulses are not profitable as net profit was negative or very small over time period and across states. The analysis of technical efficiency and technological gap have showed that, in gram production, the metafrontier technical efficiency across the states ranged from as small as 0.22 in the case of Karnataka to 0.49 in Andhra Pradesh. There is not much difference between farm groups and the TGR score of Andhra Pradesh (0.77) production potential was much closer to metafrontier followed by Bihar (0.68), Rajasthan (0.58) and other states. In case of arhar production, the metafrontier technical efficiency across the states ranged from as small as 0.09 in Odisha to 0.33 in Gujarat. The study on factors associated with reducing the risk using just and pope production function for gram and arhar have showed that among the independent variables employed in the model, fertilizer, irrigation, seed and labour were found to be the yield risk-reducing whereas the Machinery and technological change were found to be risk increasing.

Theme 2. Agricultural markets and value chain

An econometric analysis of import demand of selected edible oils in India

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

Investment and development of food processing industry: firm-level evidence from India

The contribution of the manufacturing sector to economic development is critical in India. During the developmental transition, the country needs to create more value addition to the commodities produced from the primary sector. In this context, the food processing industry in India has a significant role to play, with diverse production of foodgrains and high value commodities. During the last two decades, concerted efforts have been made to attract investment to expand growth in food processing industry. The encouraging policy support is also reflected in terms of rising capital intensity due to domestic and foreign investment. Despite this, the level of processing and India's global share in the processed food commodities are often reported as sluggish and it lacks competitiveness as compared with the global pioneers. The present study has undertaken for the analysis of the structure, productivity and efficiency pattern of the food processing industry. The results of the study indicated that the food processing industry will continue to play a significant role in the manufacturing sector in terms of output, employment generation and capital investment. Growth patterns across the product groups indicated a tendency of structural change in the industrial composition and there is a rising trend of high-value commodities like fish, meat, dairy, feed and convenience food products. Expansion of the industry output has largely been driven by the combined input growth followed by technical change. The resource use efficiency is although rising, slowly and the potential benefit of the capital investment was found to be very low. The inefficiency of capital use has also been reflected in the reduction of capital productivity. Macro environmental variables in terms of regional policy, openness to access the modern inputs such as embodied and disembodied technology and encouraging the innovations at the industry level will certainly contribute to raising the level of processing. Besides, the cost of raw material was a significant component of the production cost, efforts in materializing the supply chain dynamics of the raw material flow will not only encourage the processing activity, that will also have a significant impact on stabilizing the processed food prices, and helps in position the processed food in the international market at a competitive price. The study has assessed the spillover effect of foreign investment in the food industry. The results indicated that the presence of foreign affiliates largely benefited in rising the domestic firms' productivity and they are mainly channelized through backward vertical linkages. Within the industry also there was an indication of a positive spillover effect, however, it was not uniform across the firms. Further analysis suggested that the firms in the food industry were able to reap the benefit mainly from the developing countries via automatic route. These results suggest that the absorptive capacity of the domestic firms in the food industry has not been sufficient to generate the spillover gain from the technology pioneers. This study found evidence that the strategy for the development of the food processing industry lies in investment growth by attracting foreign capital and rising domestic ventures. Encouraging and incentivizing the R&D activity and expansion of the scale of operation will rise the processing level through higher productivity. Efficiency gain and stabilization of the market prices of agricultural produce are likely to be equally important for the benefits of the food processing sector.

Theme 3. Institutional innovations and rural livelihood

An economic evaluation of soil health card scheme on fertilizer use efficiency and crop productivity: a case study of Andhra Pradesh

Successive Five-Year plans in India have stressed on self-sufficiency and self-reliance in food grains production which has resulted in increase in the food grains production over the years. The increase in fertilizer consumption has contributed significantly to increased production of food grains in the country. However, over application of fertilizers by farmers has resulted in a highly skewed NPK application ratio. To overcome this, the Govt. of India initiated nutrient-based-subsidy (NBS) policy for fertilizers except urea which in turn hiked the prices of P and K. Most recently with the broader aim of integrated nutrient management the govt. of India has launched its ambitious scheme of Soil Health Card (SHC) to diagnose soil fertility related constraints of farmers with effect from December 2015. To assess the SHC scheme, the study used both secondary and primary data. Fertilizer data was accessed from various issues of Fertilizer association of India as well as plot level data from directorate of economics and statistics. Primary data on fertilizer use for Paddy in Andhra Pradesh for 120 SHC adopters and 60 Non adopters was collected to see the impact of SHC. Results revealed increasing imbalance in fertilizer consumption after NBS and impact revealed significant decline in potash consumption with no evidence to show reduced phosphorous and nitrogen application. Composite soil fertility indices (CSFI) were made to categorize the blocks which are representative administrative units in Andhra Pradesh state and the impact of CSFI on yield of Paddy showed significant impact, which can be carried out for other states for macro level planning. Further SHC impact on sampled farmers revealed significant decline in Nitrogen use and also phosphorous use with no significant change in potash consumption, it had shown marginal yield improvement in SHC holders by 3 kg. The trust building with farmers could be enhanced by regular field visits, demonstrations and awareness level. Burden on staff and lack of proper infrastructure at the SHC labs were the main constraints found from the SHC officials in proper and timely implementation of SHC scheme.

Employment diversification and its impact on farm economy: a study on Northeastern Region

Developing countries around the world are undergoing a major structural change in the labour market. India being one of the fastest-growing economies is no exception to this trend. Several studies have observed that there is a transition from the farm sector to the non-farm sector over the years. Although the overall picture suggests that the non-farm sector employs more rural labour, the share of non-farm workers to the total labour force shows considerable variation over regions and among sub-sectors of the non- farm category. This study has been carried out to trace temporal and spatial changes in the rural labour market across gender, sectors, occupations and states; and to assess their implication on the farm and non-farm wages. The latest key indicator from the periodic labour force survey (PLFS, 2018) shows that the non-farm sector is gaining momentum in the northeastern region of the country as well. Almost 50 per cent of the total workforce is engaged in non-farm activities. Hence the study attempts to identify the factors for participation in non-farm activities and analyze the impact on household consumption expenditure in northeastern India. At the national level, structural changes have been observed, as there is an increasing shift of workforce participation rate in the non-farm sector from the farm sector. There is a rapid structural change observed in some states like Haryana, Punjab, Bihar and Uttar Pradesh. While the composition between the sector in some states like West Bengal, Andra Pradesh and Rajasthan are more or less same over the time. Employing a panel vector correction model of 20 major states from 1999 to 2017 in rural India, the study found that the nexus between farm wage and non-farm wage was only one-way causality running from non-farm wage to farm wage. Unit level data from the latest PLFS shows that while age, education and training have a negative and significant effect on farming, they have a positive and significant effect on non-farm activities. Analysis with doubly robust inverse probability weighted regression adjustment model suggests that non-farm household has more monthly consumption expenditure than farm household. A negative link between poverty and employment has been observed in the diversification of economic activities in the non-farm sector. 5-point continuum Likert scale shows that rural youth, in general, has a positive perception towards non-farm as economic activities. In the same line, the survey reflects that 59 per cent of the female and 50 per cent of male aspires for a government job. Using multiple regression analysis, it was observed that mass media utilization has a positive and significant effect on perception towards the non-farm occupation. Whereas, those with more farming experience and land availability had a higher aspiration towards farming. Hence, it is recommended to have skill development and training of the rural workforce in diverse non-farm activities, which would uplift the rural welfare.

An economic analysis of debt and investment by farm household in Semi-Arid Region of India

Semi- Arid Region is described as drought-prone areas that covers 175 districts of India, comprising of 65.3 per cent of the net and 61.7 per cent of the gross cropped area. It accounts for more than one-third of the total geographical area, and contributes almost half of the food grains, and two-thirds of the oilseed production in the country. Credit is one of the most important inputs required for agricultural development in semi-arid region and considered as a catalyst that activates the other factors of production and makes the underused capacities functional for increased production. This study had undertaken to assess the pattern and sources of credit and its determinants, incidence and magnitude of borrowing and its correlates and pattern of farm investment in agricultural households based on household level data from the Village Dynamics Studies in South Asia (VDSA) project, ICRISAT. The results revealed that in 2014, 81.15 per cent of households borrowed from different sources of borrowings among 870 sampled households. The share of households in borrowing for the purpose of agriculture, social functions, repay old debts, marriage and major repairs had increased while share of households in borrowings for the purpose of consumption, medical, education and business had decreased in 2014 as compared to 2009. Out of total sampled households, the share of farm households borrowed only from formal sources had increased from 16.09 per cent in 2009 to 29.89 per cent in 2014. The percentage share of households who invested in farming had decreased from 26.85 per cent in 2009 to 19.19 per cent in 2014. The households who had invested in non- farm activities in the year 2009 were 26.73 per cent which increased to 31.95 per cent in 2014. The overall average of investment-debt ratio was 4.39 in 2009 which decreased to 3.50 in the year 2014. The results from multinomial logit model shows that the increase in landholding size, years of education of the head of household and farming as the sub-occupation of the head of the household increases the probability of borrowing from formal sources only. The result of Heckman selection model indicates that landholding size, farming as the main occupation of the head of the household, household heads with higher education had shown a positive and significant relationship with access to formal credit.

An analysis of performance of custom hiring centre in Rayalseema region of Andhra Pradesh

Agricultural mechanisation is a feasible solution to solve problems of shortage of agricultural labour in India. The government of India launched Sub-Mission on Agricultural Mechanization Scheme to promote farm mechanisation by providing subsidies to establish Custom Hiring Centres (CHCs), Farm Machinery Banks and

Hi-tech hubs. The present status of CHCs in the country was assessed based on the data collected from ministry of Agriculture and Farmers' Welfare and various state government reports. Primary data also collected from 160 farmers by personnel interview from Anantpur and Dharmavaram taluks of Anantpur district. It was found that CHCs has grown at the rate of 45 per cent during 2014-15 to 2020-21 in the country but growth of CHCs is not uniform across the states and regions within the states. The positive net return and more than unity B-C ratio estimates of custom hiring business indicated that investment in CHC is a profitable venture. The mechanization index (MI) for marginal farmers was lower compared to small farmers. The MI for farmers of CHC villages was higher compared to farmers of non-CHC villages due to higher adoption and easy accessibility of farm machineries. Timely unavailability of custom hire services on credit basis was the major problems faced by CHC farmers whereas higher rate, timely unavailability of services, discriminatory rate were the major problems of farmers in non-CHC villages. Total input cost for groundnut cultivation was high for non-CHC village farmers due to high machine labour cost. CHC village farms were relatively more technically and cost efficient as compared to non-CHC village farms. Overall, CHCs were found playing greater role in providing farm machinery services at reasonable charges on time to small and marginal farmers and it helped in enhancing crop yield and reducing cost of cultivation resulting into improved efficiency of crop production and enhanced net income from crop production. Hence there is need to improve access of farm machineries to small and marginal farmers through establishing a greater number of CHCs and providing sufficient number of implements to CHCs for improving availability of services on time.

Economics, institutions and policies influencing adoption and sustainability of solar pump irrigation: a comparative study of Rajasthan and Bihar

Access to timely irrigation services has often been hampered by the inadequate and costly power supply through electricity and diesel pumps. To plug this gap, the solar irrigation pumps (SIPs) offer an innovative solution which can potentially offset the deficit in power supply at substantially cheaper running cost, on timely basis and without leading to environmental degradation. In this context, the present study attempted to assess the requirement and development of SIPs as well as their economic feasibility in Rajasthan and Bihar. The study used secondary data as well as primary data from the districts of Bikaner (in Rajasthan) and Nalanda (in Bihar). Long term trends reveal higher growth in irrigation coverage in Rajasthan as compared to Bihar mainly driven by tube wells, especially during the three decades, viz., seventies, eighties, and nineties. The tubewells were estimated to have the highest productivity among all the other sources. The districts were found to have relatively higher level of absolute disparity in access to irrigation infrastructure in Rajasthan and relative disparity was observed to be higher in case Bihar. The development of SIPs is at the initial stage in India; however, Rajasthan has achieved significantly higher penetration as compared Bihar where it is only 1.2 per cent of the target. The analyses of the state level as well as recently launched national level PM- KUSUM scheme reveals that the allocation of SIPs among the districts appear to be based on irrigation infrastructure related variables. The farm level study shows that SIP has the potential to push the cropping intensities from 130 -200 per cent to as high as 180 to 245 per cent with notable changes in the cropping pattern. Apart from full time access to irrigation supply on the cost of irrigation also significantly comes down for the SIPs, almost half that of the diesel pumps. This was reflected on the financial feasibility of the SIPs with benefit to cost ratio as high as 2.3 in Rajasthan and 1.7 in Bihar. The Chow test and Bisaliah decomposition of the production functions confirm the significant impact of the SIPs. The technical and economic efficiencies were found higher for the SIP adopter farms as compared to the non-adopters. The values pertaining to electric pumps were found marginally less as compared to SIPs, while the diesel pumps using farms were found least efficient. Further, the results of tobit model suggested significant impact of SIP adoption, access to credit, off farm income and higher farm size on technical efficiency. The study also confirms the higher incremental social benefits for the SIPs over the diesel pumps (₹14.2 to 17.7/ha) as compared to the SIPs over the electric pumps (₹5.2 to 7.0/ha). The social benefits were found to be higher in Rajasthan as compared to Bihar. The undulated topography and farm fragmentations were found as the major farm level factors significantly hindering the adoption of SIPs. The findings from ordered logit and Heckman's two stage regression procedure suggested that access to credit and training are significant in pushing up the adoption process. The study suggests that SIP technology needs to be customised in line with the farm size, groundwater availability and other topographical conditions. To enhance the profitability from adoption of SIP, it needs to be complemented with other policy supports like credit and extension services.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Ashish Kumar Verma	21207	M.Sc.	An economic analysis of debt and investment by farm household in Semi-Arid Region of India	Dr. P. Anbukani
2.	Sushma L.	21208	M.Sc.	An economic analysis of production risks in major pulse crops	Dr. Kingsly I.
3.	Ganavi N. R.	21209	M.Sc.	An analysis of performance of custom hiring centre in Rayalseema region of Andhra Pradesh	Dr. N. R. Kumar
4.	Miyir Loyi	21211	M.Sc.	An econometric analysis of import demand of selected edible oils in India	Dr. Shiv Kumar
5.	Prabhat Kishore	10230	Ph.D.	Groundwater-energy nexus in agriculture and its implications on farm economy in western Uttar Pradesh	Dr. D.R. Singh
6.	Rishabh Kumar	10561	Ph.D.	Economics, institutions and policies influencing adoption and sustainability of solar pump irrigation: A comparative study of Rajasthan and Bihar	Dr. Pramod Kumar
7.	Ankhila R. H.	10563	Ph.D.	An economic evaluation of soil health card scheme on fertilizer use efficiency and crop productivity: A case study of Andhra Pradesh	Dr. Alka Singh
8.	Ripi Doni	10735	Ph.D.	Employment diversification and its impact on farm economy: a study on Northeastern Region	Dr. Alka Singh
9.	Nithyashree M. L.	10737	Ph.D.	Investment and development of food processing industry: firm-level evidence from India	Dr. Suresh Pal

Agricultural Extension

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Prof. Rabindra Nath Padaria

The Division of Agricultural Extension has been playing a pioneering role in the growth and development of extension science with specific reference to research, education and training in extension education. It grew leaps and bounds under the dynamic leaders. The Division has been providing the national leadership role in areas of teaching, research and extension. The mandates of the division are to carry out basic and strategic research in the areas of extension education; to carry out post-graduate education programmes; to meet the trained man-power requirements of agricultural universities, research institutes and other development departments; to carry out advanced National and International training programmes to impart knowledge, skills and desired orientation to the persons engaged in teaching, research and transfer of technology so as to improve their efficiency and effectiveness and to the selected farmers to enable them to assume the roles of community leaders; to render expertise support, advisory and consultancy services to extension activities of the institute. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Technology adoption and diffusion network

Perception and acceptance behavior for GM Crops

The stakeholders' risk-benefit perception and acceptance for GM crops were studied using both *ex-ante* and *ex-post* research design. Three GM crops mustard, maize was chosen for their near future approval and already approved cotton. Three states Rajasthan, Karnataka, Maharashtra were selected for higher share in area and production of mustard, maize and cotton respectively in India. The majority of farmers showed their positive attitude for use of genetic engineering in food production, medical use, solving farmers' problems. Maximum farmers had strong benefit perception in getting higher yield and profit at reduced cost as socio-economic gain and lesser risk perception in environmental risk such as loss of biodiversity, harming non-target organism, ill effect on health. They had somewhat higher risk perception in seed dependency and secondary pest problem risk. Farmers strongly preferred traits like yield and drought tolerance in both GM mustard and GM maize crops. Herbicide tolerant GM crops were more preferred than insect resistant GM crops. Seed cost was least concerned if yield would be assured. In partial budget analysis, the extra net benefits for herbicide tolerant GM crops were much more due to higher weeding management cost suffered by farmers than insect resistant GM crops in maize and cotton. The maize farmers' acceptance or purchase intention was significantly affected by benefit perception (β=1.403, p=.015), attitude (β=0.579, p= .025) positively and risk perception (β= - .879, p= .000) negatively. The protestors posed highest risk in "socio-economic impact" theme followed by "health & biosafety", "impact on non-target organism", "loss of biodiversity", "threat to sustainable agriculture & seed system" etc. Protestors had highly association with NGOs, "information seeking & sharing behaviour", "lesser trust in experts and regulations" and "higher trust in media". In socio-economic consideration for GM crops commercialization experts emphasized long term impact of Bt cotton, farmers' profitability based "socio-economic impact" domain; impact on biodiversity and evolving resistance based "environmental safety" domain; "human & animal health safety" domain and "trade & regulatory" with "co-existence" domain to be considered in final SEC framework. The risk communication content analysis during GM mustard consideration showed majority of media coverage had mixed orientation.

Seed source networks

The present study analyzed the seed source networks of wheat and green gram. The districts Palwal (Haryana) and Fatehpur (Uttar Pradesh) were selected purposely and using *ex post facto* research design, data were collected from secondary sources besides, from random sample of 120 farmers through personnel interview and case study of ten seed producers. In both states, seed sources included ICAR Institutes/SAUs, government agencies, private shops, farmers'own seed and farmers' seed exchange. The major *seed source* for Haryana farmers was government agencies whereas it was private shops in case of UP. Higher *seed accessibility* was perceived by Haryana farmers as compared to U.P. The order of *most preferred traits* of wheat for seed production were yield, pest & disease incidence, plant height, water requirement, market rate, grain size and crop duration while for green gram they were market demand, followed by pest & disease incidence, yield, grain quality, synchronized maturity, crop duration and pod size. The motive of small-scale seed producers was to improve quality seed accessibility to their fellow farmers. All the seed producers received several trainings from various institutes to gain the required knowledge and skill for seed production. As all seed sectors have their own strengths, there is need to harmonize them for the benefit of farming community.

Theme 2. Program evaluation

Socio-economic impact of Sansad Adarsh Gram Yojana

The Central Government had launched an ambitious rural development program named *Sansad Adarsh Gram Yojana* (SAGY) on 11th October, 2014 where each Member of Parliament adopts a village and strives to transform it into a Model Village. It was a matter of interest to probe whether the villages adopted under SAGY had reached/exceeded the level of development of already declared Model Villages of their respective states. The study was conducted in 10 villages located in 4 districts of purposively selected states of Maharashtra and Telangana because these states have highest concentration of Model Villages (those declared by MoHRD) which could serve as a comparison for evaluating SAGY villages appropriately. The total sample size for the study was 390 comprising of all categories of stakeholders of SAGY program, viz., residents and farmers of SAGY villages and officials of development departments. For comparative assessment of Model and SAGY villages on various developmental parameters, 7 rural development indices were developed through the NUEPA Method. In Maharashtra, SAGY villages scored more index values in terms of health and farming as compared to already declared Model Villages of the state. In Telangana, SAGY villages scored more index values in terms of education, farming, livestock, ecological status as compared to already declared Model Villages of the state. A multidimensional perception scale constructed for the study revealed that government-public liaison (671.86) was perceived to be the most dominant factor in facilitating the effective implementation of SAGY followed by factors like infrastructure and education (383.14), local political environment (267.42), collective power of villagers and youth (255.98), equality (236.71) and cultural and inherent values (143.03) existing among villagers. Amongst inhibiting factors, the lack of separated funding (-12.88), red tapism by officials to extract personal illegal benefits, presence of factions within village (25.05), lack of coordination amongst Govt. departments (59.65) and faulty policy of village adoption (130.85) were other hindering factors. SAGY had significant impact ($p<0.05$) in terms of increase in monthly family income, number of earning members in family, material possession status, social connectedness, family educational status and satisfaction level of villagers. By using Alfares method the strategy of convergence in funding (W=85.25) was ranked of top priority because the main lacuna in effective implementation of SAGY at ground level was the shortage of fund due to non-allotment of separate fund for this program. Suggestions for promoting effective implementation of SAGY were listed out like ensuring convergence of schemes and its proper implementation on priority basis, leveraging on facilitating factors like community participation and social mobilization of the village community, instilling a spirit of brotherhood and cultural bonding to speed up different developmental activities of the program, correction of faulty adoption policy of the program and involvement of NGOs, community bodies, line deptt officials and less of political involvement to contain political hostility and resentment.

Financial inclusion and skill development through aspirational district programme

Aspirational districts programme was launched by Government of India in 2018 to raise the living standards of citizens by focusing on five major thematic areas viz. health and nutrition, education, agriculture and water resources, financial inclusion and skill development and basic infrastructure in the poor performing 115 districts. The present study was aimed to explore the extent of financial inclusion and skill development in agriculture sector through aspirational district programmes. Three training institutes per district which were actively providing skill-based trainings in agriculture sector were purposively selected from two aspirational districts (Raichur and Yadgir) of Karnataka state a total of 120 trainees selected through stratified random sampling method comprised the sample size. It was found that overall extent of financial inclusion was moderate. Half of the respondents were in the medium level of financial inclusion. Awareness on financial products and services was ranged from moderate to high. Due to lack of financial institutes in the rural areas 37.5 per cent of the respondents reported difficulty in the accessing financial products and services as such the level of usage was low. Around 50 per cent of the respondents had a low level of use of financial products and services. Multiple regression analysis revealed that age, distance to financial institute and lower level of education showed negative and significant contribution towards extent of financial inclusion. Operational land holding, annual income and frequency of visit to financial institutes showed positive and significant contribution to the extent of financial inclusion. The overall effectiveness of skill development trainings was found to be 51 per cent which came under medium effectiveness category. The multiple regression analysis revealed that number of training programmes attended, learning motivation, innovativeness, motivation to transfer learning, self-efficacy and achievement motivation were positive and significantly affecting the training effectiveness. Lack of literacy on financial products and services, low income and cumbersome procedures were most raked constraints to financial inclusion. Lack of hands-on training and lack of access to government benefits were most rated constrains related to training effectiveness. It can be concluded that financial inclusion and skill development in terms of training effectiveness was moderate in aspirational districts. As such it calls for necessary action to increase the accessibility to financial products and services. In case of training attention has to be given to the need assessment, which may further help in scaling up of financial inclusion and skill development in aspirational districts.

Theme 3. Innovative extension approaches

Farmer Producer Organization led extension approach for organic turmeric

A comprehensive study on Kandhamal Apex Spices Association for Marketing (KASAM) was carried out in the Kandhamal district of Odisha employing exploratory and quasi-experimental research designs. KASAM has been engaged with over 11,000 turmeric farmers since 1998 and acts as a marketing partner to 61 producers' groups registered as Spice Development Societies (SDSs). Six officials of KASAM and leaders of 22 SDSs were interviewed to study the Extension and Advisory Services (EAS) offered and to segregate the factors affecting the financial performance of SDSs. For the impact assessment of KASAM, 245 respondents (120 members and 125 non-members) were surveyed using a structured interview schedule. The data were analysed using cluster analysis, Garrett ranking technique, TOPSIS methodology, and Regression Adjustment (RA) model. While analysing the EAS offered by KASAM using Birner's Best Fit Framework and applying Prager's criteria of functional advisory services, the study found that the criteria related to coverage of major advisory topics, linkage with important organizations, the participation level of members in training, etc. were satisfied. However, on parameters like coverage of all client groups and the use of a wide range of methods for EAS provision, the performance was unsatisfactory. The most important factors responsible for success were better prices compared to local traders, good infrastructure, assistance in availing the benefits of government schemes, etc. The most significant constraints were delayed payment, irregular and inadequate supply of inputs, inefficient leadership at SDS, etc. Correlates of a high annual turnover of SDSs were frequency of farm and home visits, frequency of farmers' calls, the participation level of members in training and group meetings, and speed of payment. Regression Adjustment treatment-effect model revealed that there was a significant impact on the members' gross income and price received per quintal. The members earned 36.31 percent more gross income and received 31.45 percent higher price per quintal compared to the non-members. The Study implies that FPOs can play a vital role in offering quality EAS to farmers using effective EAS models. It finds that the major contribution of KASAM to members is providing them a well-established marketing platform to realise better prices. Thus, market-linkage models need to be emphasised while promoting new FPOs. The case of KASAM is a testimony that the government's vision of promoting cluster-based and commodity-specialized FPOs can yield great results for small and marginal farmers.

Perception and extent of usage of social media among extension agents

Andhra Pradesh state was purposively selected due to the prevalence of ICT in governance. Through proportionate random sampling method Srikakulam, Guntur, and Chittoor districts were selected. From the pool of extension agents working in the three districts under the state department of agriculture, KVK, ATMA, private sector firms, and NGOs, proportionate random sampling was used to select 160 extension agents. Among farmers using WhatsApp 63 farmers were randomly selected from these three districts. The *ex-post facto* research design was followed. The findings of the study revealed that the extension agents had a neutral to favourable perception towards social media usage in agriculture extension service delivery. Chi-square analysis showed that education and social participation of the extension agents are associated with their perception. The correlational analysis expressed that innovative proneness, scientific orientation, job perception, technology management orientation, information management orientation, orientation towards extension service profession, and job performance were positively associated and perceived workload was negatively associated with perception. The majority of the extension agents had a medium level of extent of usage of social media. Chi-square analysis expressed that social participation, gender, and training were associated with the extent of usage. Correlational analysis showed that scientific orientation, job perception, job performance, technology management orientation, information management orientation, orientation towards extension service profession, and innovative proneness were positively associated with the extent of usage. Step-wise regression analysis revealed that job perception, technology management orientation, orientation towards extension service profession, social participation, and background contributed 35.7 per cent of the variation in the extent of usage of social media. The majority of the farmers had a medium level of extent of usefulness of messages. Most of the messages were easy to understand by farmers and led to their farm and economic development. The study also emphasized different constraints that were faced by extension agents in using social media by dividing the constraints into social, technical, physical, and communication constraints by using the Garett ranking method. Some of the major constraints that were identified are orientation to traditional dissemination methods in social barriers, lack of technical knowledge and skill in technical barriers, lack of tools and inadequate service in physical barriers, and weak research extension linkage in communication barriers. Concerning the above findings, it is suggested to provide the extension personnel with required technical support such as smartphones and tablets from the organization in which they are working.

Theme 4. Agribusiness: skills and incubation

Effectiveness of agri-business incubators

Three agri-business incubators of ICAR namely IARI, New Delhi; CIPHET, Ludhiana and NAARM were purposively selected based on their performance scores (NAIP, ICAR Report, 2014) for the study and for comparative analysis, the business incubator of RUDSETI (Rural Development and Self Employment Training Institute) was also studied. A total of 160 incubates and 40 institutional stakeholders were selected as sample from these incubators making it a total of 200 respondents as sample size with random sampling method. The results of the study revealed that more respondents were of the young age, between age of 30-35. More than one third of the incubatees were educated to secondary level or below it. Despite having a very limited resource base, about half of the respondent trainees had an annual income of less than 1 lakh. A vast majority of trainees had no previous exposure to any entrepreneurial training programme. Majority of the respondents from the entire four institutes did not find their self-employed parents as role model and preferred government job over entrepreneurship. It was also revealed that a higher number of trainees from RUDSETI more valued the enterprise than trainees from ICAR BPDs. About 65% from RUSTEDI and nearly 54% from ICAR-BPD had high level of entrepreneurial intension. The entrepreneurial capacities of RUDSETI and ICAR-BPD were not separate, and the majority of them possessed a high degree of entrepreneurial ability. There exists no significant difference between RUDSETI trainees and ICAR-BPD trainees interms of perceived support and barriers faced by them. The survey discovered that RUDSETI and ICAR-BPD trainees' achievement motivation, locus of influence, risk taking skill, and resource mobilization capability were not significantly different, while RUDSETI and ICAR-BPD trainees' self-efficacy, pro-activeness, and enthusiasm for work were vastly different. When compared to RUDSETI trainees, ICAR-BPD trainees had higher self-efficacy, innovativeness, and enthusiasm for work. Almost 45 percent of trainees choose their trade based on self-interest. The first reason for using an entrepreneurial profession was a last resort for income. The trainees differed substantially in terms of Formal sources of knowledge, ICT sources of information, Social valuation, Entrepreneurial aim, Perceived supports and obstacles, Achievement inspiration, Leadership, Locus of influence, and Passion for work post training. There has been no major distinction between school and informal knowledge. The trainees also differed significantly in the impact of psychological characteristics such as self-efficacy, innovativeness, risk-taking ability, pro-activeness, resource mobilization, need for achievement, and need for power between the trainees of RUDSETI and ICAR-BPDs. But there was no significant difference in need for affiliation. Both the staff and incubatees ranked first the non-availability of raw materials followed by non-availability of equipments and lack of electricity as major constraints for production and labour.

Multidimensional study on agribusiness incubatees

A Multidimensional study on Agribusiness Incubatees under Business Planning and Development Unit of IIHR Bengaluru was conducted during 2020-21. A total of 32 agribusiness incubatees were selected for study from IIHR

Bengaluru Business Planning and Development unit. The study followed e*x-post-facto* research design and data was collected by conducted personal interviews of the trained incubatees pre-tested structured interview schedule. Appropriate statistical procedures and tools were used to analyse and interpret the data. Entrepreneurial behaviour of agribusiness incubatees was found in medium category for a majority of the agribusiness incubates (59.37%), while it was in high category for about one-fifth of them. Annual income, economic status, rational orientation, self-reliance, media utilization, education and self-concept exhibited significant relationship with entrepreneurial behaviour of agribusiness incubatees. Whereas, variables such as age, age at entry, family type, occupational status, scientific orientation, deferred gratification, vocational diversification, closeness with support system, orientation towards competition and credit orientation were non-significant with the entrepreneurial behaviour of agribusiness incubatees. High price for raw materials, high profit margin for middle man for marketing, high labour cost and high rate of interest were some of major problems faced by agribusiness incubatees. Lesser rate of interest during initial days of enterprise, assured insurance scheme for enterprise and lesser amount of rent for infrastructure by government institution are some of the major suggestions perceived by incubatees to manage the constraints

Agricultural skills among rural youth

Thestudyaimedto understand the attitude of rural youth towards agro based enterprises, the skill gap in various agriculture and allied activities, and training impact of PMKVY. The study was conducted in Hassan and Chikmagalur districts of Karnataka. A multi-staged random sampling technique was followed in order to sample 120 rural youths and 60 trainees from two training institute *Krishi Vigyan Kendras* providing agricultural skill training through ASCI under PMKVY were purposively selected. The rural youth were interviewed personally and trainees' data were collected through Google forms due to COVID-19 restrictions. It was found that overall attitude of rural youth towards agro- based enterprises was moderately favorable. Multiple regression analysis revealed that risk orientation, self-confidence, achievement motivation and hope of success showed significant contribution towards agro- based enterprises. Nearly half (46.67%) of the rural youth had medium agricultural skill gap. Amongst 15 agricultural skills it was found that rural youth had high skill gap in branding skill, procurement and marketing skill, accounting skill, processing and value addition skill, post-harvest handling skill and organic liquid fertilizer skill. The study also revealed that the rural youth had lower skill gap in dairy and livestock farming skill, management skill, personal skills and pesticide spraying skill. The overall impact of agricultural skill development training of PMKVY revealed that amongst the eight core competencies of training self-confidence, economic empowerment, social empowerment and gain in knowledge showed significant impact after training. A majority of trainees perceived that training improved their knowledge and skills but less useful in the taking up new business enterprise in agriculture because of major constraint of youth friendly credit schemes. Less emphasis of practical skill training and lack of financial assistance from banks were the most rated constraints related to agricultural skill development training of PMKVY.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Sagar M.P.	21225	M.Sc.	A multidimensional study on agribusiness incubatees under business planning and development unit of ICAR-IIHR, Bengaluru	Dr. Rashmi Singh
2.	Ankit Mahapatra	21226	M.Sc.	Farmer Producer Organization led extension approach for organic turmeric farming in tribal region of Odisha: The case of KASAM	Dr. Vinayak Nikam
3.	Arun Kumar G.S.	21227	M.Sc.	An assessment of financial inclusion and skill development in agricultural sector through aspirational district programme	Dr. Manjeet Singh Nain
4.	Adupa Shanmukha	21228	M.Sc.	An analysis of perception and extent of usage of social media among extension agents in agricultural extension service delivery in Andhra Pradesh	Dr. V. Lenin
5.	Harshita B.P.	21229	M.Sc.	Multi- dimensional study of agricultural skills among rural youth	Dr. N. Kumbhare
6.	Phelister Adhiambo Were	21198	M.Sc.	A study of seed source networks: a case of wheat and green gram	Dr. Nishi Sharma
7.	Sushil Kumar	10401	Ph.D.	An analytical study of effectiveness of agri-business incubators	Dr. Rashmi Singh
8.	Sangeeta Bhattacharya	10754	Ph.D.	Socio-economic impact of Sansad Adarsh Gram Yojana in Maharashtra and Telangana	Dr. Rajarshi Roy Burman
9.	Alok Kumar Sahoo	10755	Ph.D.	Stakeholders' risk- benefit perception and acceptance behavior for GM crops in India	Dr. R.N. Padaria

Agricultural Statistics

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Prof. Cini Varghese

ICAR-Indian Agricultural Statistics Research Institute undertakes basic and applied research in agricultural statistics, which includes designing of experiment and methodologies for analysis of data, planning and organization of agricultural surveys, statistical modelling and agricultural system modelling and statistical genetics for enriching the quality of Agricultural Research. The research and education conducted are used for improving the quality and meeting the challenges of agricultural research in newer emerging areas. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Designing of experiments and analysis of experimental data

Robust designs for bioequivalence trials

Bioequivalence trials are conducted to investigate the degree to which clinically important outcomes after receiving a new formulation resembles to those of a previously well-established formulation. Evaluation of veterinary medicinal products is one of the important areas where bioequivalence trials are conducted. With emphasis in making test vs. reference formulations comparisons with as much precision as possible, special designs are to be constructed for these trials. Due to constraints in the availability of homogeneous subjects for experimentation, the same set of subjects is used for repeated evaluation. It is natural for experimental subjects to exhibit time trend over periods. A design for bioequivalence trial is said to be trend free, if the sum of squares due to formulations under the model considering trend effects besides direct, residual and subject effects, is same as that obtained under the model considering direct, residual and subject effects ignoring trend effects. General condition for a design to be trend-free has been derived and method of construction of a class of such designs has been developed. Also, if a sequence of formulations are applied to a subject and observations are measured from the same subject over different periods of time, there may be dependency in the observations that are measured from immediate periods of time. Here, variance and efficiency factor of the estimates of contrasts pertaining to test vs. test as well as test vs. reference formulations under different types of correlation structures have been obtained. Another problem commonly encountered in bioequivalence trials is that the subjects under study may not respond similarly after receiving the same formulation. For the detection of an outlying subject in bioequivalence trials, likelihood distance (LD) and estimated distance (ED) test procedures have been developed. Further, the data set sometimes contains either some extremely large or small values. These extreme values may have dramatic effects on the bioequivalence test and therefore, for the detection of such outlier observations, Cook statistic has also been derived.

Trend resistant constant block-sum partially balanced incomplete block designs

In agricultural experiment under block design set up response of a plot in block may be affected by trend effects. Although remote, but trend effects may be incorporated in to the model for proper model specification.

Partially balanced block (PBIB) designs are an important class of incomplete block designs and have found profound application in agricultural research. Constant block sum PBIB designs where block sum w.r.t. treatments for all blocks remain constant, are now a days gaining rapid momentum from research point of view. Here, some aspects of trend resistant constant block sum PBIB designs have been highlighted. First the experimental setup has been defined in terms of model and information matrices. The necessary and sufficient condition for a design to be completely trend resistant i.e. trend free has been discussed. Thereafter, methods of construction trend free constant block sum PBIB designs have been obtained. Statistical properties of the designs obtained under the present investigation have been investigated. SAS macros have been developed for providing readymade solution to the researchers under National Agricultural Research and Education System. Further, efficiencies of existing constant block sum PBIB designs have been calculated in the presence of trend effects. It has been observed that, the existing constant block sum designs don't provide good resistance against trend effects. Catalogue of developed trend free constant block sum PBIB designs for specific parametric combinations have been prepared which will serve as readymade reference to the end users.

Position balanced block designs for sensory studies and consumer experiments

In many experiments it is not possible to allocate all the treatments within a block hence incomplete block designs are used. Allocating treatments randomly within a given block at any position is a common practice in designing experiments. But there are certain situations when these positions of treatments are important. Two such cases are sensory studies and consumer experiments. In both the cases panelists are required to rate and give scores to different products according to various attributes and/or overall acceptability. Rating given to a product may depend on whether it is being given at the beginning, middle, or end of the session and hence there may be position or order effect. Thus, it is important to consider designs which are balanced for position or order effects. Similar considerations also apply for consumer experimentation. Generally, in consumer experiments all samples are given to each panelist in single session, this will lead to use of complete block design since blocking factor is panelists. However, there are significant benefits of using incomplete block designslike more number of products can be evaluated, reducing consumer fatigue etc. For such experimental situations, an algorithm for obtaining position balanced BIB designs has been developed. For a ready reckoner, the catalogues of position balanced BIB designs for $v \leq 20,\ b \leq 40,\ k \leq 10v \leq 20,\ b \leq 40,\ k \leq 10$ along with their layouts have also been prepared. Further, in some BIB designs position balance is not possible, in that case an algorithm for obtaining nearly position balanced BIB designs is developed. The plans for nearly position balanced BIB designs for $v \leq 20,\ b \leq 40,\ k \leq 10v \leq 20,\ b \leq 40,\ k \leq 10$ are generated and catalogue for the same is given at the end of the investigation. R codes for generating the position balanced and nearly position balanced BIB designsare also included.

Row-column designs for two-level factorial and fractional factorial experiments

Row-column designs are useful for the experimental situations in which there are two cross classified sources of heterogeneity in the experimental material. Due to practical considerations it may not be possible to accommodate more than two experimental units in a column of a row-column design. For example, row-column designs with two rows are very useful in two-colour microarray experiments. Row-column designs with two rows and with factorial treatment structure have also been found useful in many other agricultural experiments. When the design is non-orthogonal in a row-column set up, it would be desirable that it permits orthogonal estimation of all factorial effects with high efficiency. This may require a large number of columns. Due to cost and time considerations, it may not be possible to run a design in number of runs that are required for orthogonal estimation of all the factorial effects. The experimenter may, however, be interested in orthogonal estimation of all the main effects and two factor interactions. Another main issue in constructing designs for multifactor experiments is that the factorial effects are commonly defined via an orthogonal parameterization. In agricultural experiments, situations may also occur where experimenter is interested in baseline parameterization rather than orthogonal parameterization where null state or baseline may exist. In such experimental situations as well, it is important to obtain efficient row-column designs in two rows. To deal with the above experimental situations, the present study was undertaken (a) to obtain row-column designs for 2-level factorial experiments for estimating the main effects and two factor interactions in fewer number of runs based on orthogonal parameterization, and (b) to develop general methods of construction of row column designs for factorial experiments based on baseline parameterization. A general method of construction of row-column designs with two rows has been given for orthogonal estimation of all main effects and two factor interactions under orthogonal parameterization. A catalogue of row-column designs for 2^n $(2 \leq n \leq 9)$ factorial experiments in fewer number of replications has been prepared. Similarly, to deal with the situations of baseline parameterization a general procedure of obtaining row-column designs in two rows for n-factor mixed level factorial experiments has been developed. Web application for generation of row-column designs in two rows for orthogonal and baseline parametrization has also been developed.

Construction of response surface designs with mixed levels of factors incorporating neighbour effects

The relationship between numerous explanatory variables and one or more response variable(s) is determined and quantified using response surface methodology (RSM), which is then utilized to optimize an underlying process. In agriculture and allied subjects,the treatment combination administered to one experimental plot may affect the response on neighboring plots as well as the response on the plot to which it is applied. These effects are known as neighbour effects and integrating them in the response surface model improves the experiment's precision.A response surface with n_1 factors at s_1 levels each, n_2 factors at s_2 levels each and n_3 factors at s_3 levels each resulting in $s_1^{n_1} \times s_2^{n_2} \times s_3^{n_3}$ combinations has been considered here. The methodology for response surface with mixed levels of factors incorporating neighbour effects has been described for particular cases. The model considered is a $(s_i\text{-}1)^{th}$ order model without interaction terms, where s_i is the level of the i^{th} highest factor. The conditions required for the near orthogonal estimation of coefficients of response model and also for the constancy of variances have been obtained. Further, conditions for rotatability under these models have also been obtained. The design satisfying these properties are called as Mixed Level Response Surface Design with Neighbour Effects (MLRDNE). Method of constructing MLRDNE for $s_1^{n_1} \times s_2^{n_2} \times s_3^{n_3}$ has been developed. Particular cases of the type $s_1^{n_1} \times s_2^{n_2}$, $s_1^{n_1} \times s_2^{n_2} \times s_3$, $s_1^{n_1} \times s_2 \times s_3$, $s_1^{n_1} \times s_2$, $s_1^{n_1}$, $s_1 \times s_2 \times s_3$ and $s_1 \times s_2$ have been discussed. The developed designs are either rotatable or partially rotatable depending on the model considered. A list of the designs developed has been prepared along with the variance of the estimated response. It is seen that in the presence of neighbour effects, variance of estimated parameters and variance of estimated response reduces as the value of neighbour coefficient increases. R codes have been developed to generate the designs along with the variance of parameter estimates and estimated response under second and higher order models incorporating neighbour effect.

Theme 2. Sample surveys

Prediction approach estimator using auxiliary information under two-phase sampling

Sample survey is a cost-effective mean to collect reliable information about a finite population. There are various sampling methodologies, out ofthem, two-phase sampling is generally used for estimating population mean or total under two different situations. First, when the information of the auxiliary variable is not readily available and second condition is when it is very expensive to gather information on characteristic under study, but it is comparatively cheaper to gather information on the variables which are highly correlated with the characteristic under study. In large scale surveys, two-phase sampling approach is proposed in order to reduce the number of sampled units which require more expensive objective methods. Prediction approach is applied to predict the non-sampled units in surveys. In the large preliminary sample (first phase sample) of two-phase sampling, there are total n′-n non-sampled units having auxiliary information, so there is a need to develop an estimator based on prediction approach under finite population. In the present study, we have proposed a new estimator of finite population total based on prediction approach in the context of two-phase sampling.Although, we have obtained an approximate variance of the proposed prediction-based estimator, it can be observed that the variance expression is very complicated and tedious to obtain.Therefore, we have also proposedProportionate Rescaling Bootstrap without replacement (PRSBWOR) for variance estimation of the proposed prediction-based estimator. In order to measurethe performance of theproposed prediction-based estimator and proposed bootstrap variance estimation techniques, different statistical measures have been used. As missing values are common phenomenon in census as well as survey data. Such incomplete data may arise when some or all of the responses are not collected from a sampled element. Non-responses affect the estimates by introducing both bias and increase in sampling variance due to reduction in effective sample size. To compensate for non-response at the estimation stage, various imputation procedures have been used in practice which may tackle the bias and variance. Under this study, we have proposed the Proportional bootstrap without replacement in the context of variance estimation of the proposed prediction-based estimator under two-phase sampling in presence of missing values. In order to measure the performance of the Proposed Proportional Bootstrap Method of variance estimation in presence of missing values, different imputation techniques (zero, mean, random substitution, ratio and regression method of imputation) along with various measures viz. percentage relative Bias (% RB), Mean departure (MD), Standard Deviation Departure (SDD) and Relative stability (RS) have been considered.

Rescaling bootstrap technique for variance estimation in dual frame surveys

Multiple frames are preferably used when it is difficult to obtain a single sampling frame that covers the whole population or two or more cheaper sampling frames are available from different sources covering whole population. Sometimes, even it is possible to use single frame but it may be very costly to prepare the same, thus, use of additional frames to cover the whole population may be economically advantageous. Dual Frame (DF) surveys are a special case of MF surveys considering two frames covering the entire population. Dual frame surveys are applicable in those situations, where, one frame may covers the entire population but is very expensive to sample, so an alternate frame may be available that does not cover the entire population but it is easily available. In situation, when there are two sampling frames i.e. A and B, covering the population under consideration, there are three possible sets (domains) of sampling units . If a sampling unit belongs to frame A only, then it may be categorized in domain (a). If a sampling unit belongs to frame B only, then it may be categorized in domain (b). If a sampling unit belongs to both frames, then it may be categorized in domain (ab). Unbiased variance estimation for estimation of various population parameters is difficult and complicated for multiple frame surveys as compared to sample from single frame. Therefore, under the study, an attempt has been made to develop three different rescaled unbiased variance estimation procedures for estimation of variance of population total unbiasedly under different cases of dual frame surveys namely, (i) Stratified Rescaling Bootstrap with Known Domain size (StRBKD), (ii) Post-stratified Rescaling Bootstrap with Known Domain size (PstRBKD) and (iii) Post-stratified Rescaling Bootstrap with Unknown Domain size (PstRBUD) method. Under these proposed procedures, resamples are taken domain-wise as well as frame-wise respectively and rescaling factors are obtained for each case under a dual frame survey. It has been proved theoretically that the proposed variance estimation procedures are almost unbiased for the variance of the estimator of population total under dual frame survey. Further, a statistical properties of the proposed bootstrap variance estimation procedures was done through a simulation study. It was found that, due to the use of proposed rescaling factors, the % RB and RS of proposed StRBKD, PstRBKD and PstRBUD methods are reduced significantly from their standard versions without considering any rescaling factors. The proposed procedures show very less amount of %RB and RS in the estimation of the variance of the dual frame estimator of population total. It is observed that the % RB in the PstRBKD method is relatively more than that of the StRBKD method for all different combinations of sample sizes. Therefore, it can be concluded that the variance estimation procedure following the StRBKD method is more efficient and stable than the PstRBKD method with respect to % RB and RS for different sample sizes. Thus, the StRBKD method is preferable to the PstRBKD method due to obious reasons. Furthermore, we developed a Proportional Stratified Bootstrap Method for the case of missing observations in the study. The StRBKD technique was rescaled to estimate the variance of the dual frame estimator in the presence of missing observations in multiple frame surveys, called the Proportional Stratified Bootstrap method has been proposed. A simulation study was used to compare the performance of different imputation techniques, and it was found that the proposed Proportion Stratified Bootstrap method using regression imputation is more successful than other imputation techniques in compensating for bias in variance estimation when dealing with missing observations. It was found that the zero imputation method provides the maximum departure (M.D.) hence may not be very appropriate in this situation, but the other methods are almost comparable. However, if the non-response rate rises, the departures for all imputation procedures rise as well. For all imputation approaches, the best results have been obtained at a non-response rate of 5%. Further efforts can be made in the future to obtain unbiased variance estimation resampling processes utilizing Jackknife and Balanced repeated replication (BRR) for two or more frame estimators of population total in the case of known as well as unknown domain sizes.

Estimation of crop yield using calibration approach under stratified two stage two phase sampling design

In this study, a methodology for estimation of crop yield at district level using calibration approach under stratified two stage two phase sampling has been developed. A separate regression type calibration estimator and a combined regression type calibration estimator of the population total and population mean under stratified two stage two phase sampling have been developed when size of all psu's is known. Also, calibration approach in case of stratified two stage two phase sampling has been developed when size of psu's is unknown. Approximate variance and estimate of variance of the developed estimators have been derived. An empirical evaluation of the proposed calibration estimator using real data application for estimation of cotton yield has been carried out. Cotton yield has been estimated along with percentage standard error (% S.E.) at district level for two districts each of Maharashtra and Andhra Pradesh states using the developed methodology as well as using different existing approaches and the proposed method has been compared with the existing approaches. The estimate obtained using the developed methodology is more efficient, reliable and almost at par with the estimates obtained using General Crop Estimation Survey (GCES) methodology and an alternative methodology using double sampling regression procedure under stratified two stage sampling design framework. The developed methodology will save cost of the survey significantly and will also be operationally more convenient than GCES procedure. The developed calibration approach under stratified two stage two phase sampling design framework results in significant reduction in number of CCEs for estimation of yield of cotton. If the developed approach works well for other crops also, this can be used for crop yield estimation under Pradhan Mantri Fasal Bima Yojana (PMFBY) for obtaining more efficient crop yield estimators and optimizing the number of CCEs.

Crop yield estimation using random forest spatial interpolation technique

General Crop Estimation Surveys (GCES) based on CCEs are conducted for estimation of crop yield following random sampling approach for almost all major crops. About 13 lakh CCEs are conducted every year which has now increased to more than a crore due to the Pradhan Mantri Fasal Bima Yojana (PMFBY) which is yield based insurance scheme. As suggested by MoA&FW, this number needs to be reduced drastically by developing sampling procedures based on the use of advanced technologies and advanced survey techniques for crop yield estimation. In this study, attempt has been made to develop crop yield estimation procedures using spatial random forest technique including the spatial variables like distance and nearest neighbour as covariates. The study was conducted in Barabanki district of UP which consists of six tehsils. For this, initially the original complete dataset consisting of the yield of all the CCE plots in each tehsil was considered. The estimate of average yield under wheat crop was computed for each of the six tehsils. In this dataset, the yield of 30% plots was randomly missed in order to generate dataset with missing yield values which was predicted using Random Forest Spatial Interpolation technique. Similarly, 50% and 70% yield values were missed randomly and were predicted using RFSI. In order to compare the performance of RFSI technique, predictions were also made using kriging and IDW techniques following similar approach. Estimates of yield of wheat were obtained for all the six tehsils using the estimator of stratified two stage sampling technique. The district level estimates were also obtained by pooling area under wheat crop in each tehsil along with the district level estimate of crop yield, estimate of variance, estimate of standard error (SE) and percentage SE of these estimates were also computed in order to made comparison. It can be concluded from this study that for prediction of yield at unknown locations using distance and nearest neighbour, the estimates obtained using RFSI were found to be at par with kriging and better than IDW. RFSI was found to be faster particularly for large training datasets. It is also one of the most flexible and easy to use interpolation technique. The proposed methodology will save cost of the survey significantly and will also be operationally more convenient than GCES procedure. The proposed methodology is also likely to reduce number of CCEs to large extent in case of PMFBY maintaining the same level of precision of the estimates. However, the proposed methodology needs to be tested and validated further to observe its performance in other districts of different States and for some other crops also. Besides RFSI, other machine learning technique like Support Vector Machine, Neural Network etc. may also be tested. The study could be further extended for obtaining improved estimators using prediction approach considering sampled and non-sampled parts.

Theme 3. Statistical modeling

Bayesian estimation for time series models with exogenous variables

Bayesian technique is one of the most powerful methodologies in the modern era of statistics. Bayesian technique has a lot of advantages over the traditional frequency or point estimation. Indian economy depends to a great extent on the production and marketing of agricultural commodities. For planning a new scheme to develop the condition of the Indian economy, the Government needs a reliable forecast of various aspects viz. agriculture, health, economy, etc. Time series analysis is very efficient to meet this need. As traditionally time series model does not have any inclusion of exogenous variable, it unable to capture the effect of extraneous factors. Time series model with exogenous variables has the capacity to identify the underlying patterns in time-series data and to quantify the impact of environmental influences. Time series analysis with explanatory variables encompasses methods to model and predict correlated data taking into account additional information. Seasonal Auto-Regressive Integrated Moving Average (SARIMA) is one of the important models in the class of univariate time series models. To quantify seasonality and external effects, the main statistical model approaches envisaged is SARIMA with intervention-X variable (SARIMA-X model). But the significance of parameters is one of the major lacunae of this model. Non-significant parameters leads to faulty planning and these forecast values are not reliable. One of the important models for volatility modeling is the Generalized Autoregressive Conditional Heteroskedasticity

(GARCH) model. One major problem in including market volatility into the GARCH framework is the appropriate choice of it. In this aspect GARCH-X model, a modified version of the GARCH model has been introduced. The above models perform satisfactorily in their own context, if all the assumptions of the underlying model are fulfilled and are applied to an adequate number of data points. In practical situations when underlying assumptions cannot be satisfied and the available datasets are small, one encounters with the problem of parameter estimation and its interpretation. To improve both the models, we incorporated prior knowledge through Bayesian technique and investigated the superiority of these models under the Bayesian framework. In this study, we developed Bayesian framework for SARIMA-X and GARCH-X models, hence increasing their applicability under various practical scenarios. We examined the performance of the Bayesian SARIMA-X model under the hybrid framework. We discussed different types of priors (informative priors, non-informative priors, conjugate prior). We also elaborated on the MCMC method briefly for the estimation of parameters under the Bayesian framework. We compared the traditional models with the models under the Bayesian framework. From this study, we conclusively infer that the models estimated under the Bayesian framework provided superior results as compared to the models estimated under the classical approach.

Forecasting crop yield using feature selection and machine learning algorithms

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

Study on multiple component models for forecasting price volatility for agricultural commodities

In the present era of globalization, management of food security in any agriculturally dominated developing countries like India needs efficient and reliable food price forecasting models more than ever. Agricultural commodity prices tend to be more volatile due to seasonality, inelastic demand, production uncertainty and also because many agricultural commodities are perishable. An increase in price volatility implies higher uncertainty about future prices, a fact that can affect producer's welfare. OECD (2009) has emphasized that agriculture remains exposed too many risks like production, market, institutional, personal and financial risks. Market risk, which is related to uncertainty about the prices that farmers will obtain for their products or pay for their inputs, is amongst the most important. Therefore, understanding the nature of agricultural commodity price volatility and the ability to accurately forecast the price volatility are important concerns among both policy makers and farming community. Price volatility provides a measure of the possible variation or movement in the price variable. Wide price movements over a short period of time are considered as high volatility. The importance of volatility has led to the development and applications of many significant time series models in the literature. Large many non-linear parametric and non-parametric models have been developed for estimation of volatility. The most widely used among them is the popular generalized autoregressive conditional heteroscedasticity (GARCH) model. The GARCH class of models considered additive volatility components and did not allow for explanatory variables in the conditional variance. Due to this limitation, recently the focus has shifted to multiple component models. In particular, the class of generalized autoregressive conditional heteroscedasticity mixed-data sampling (GARCH-MIDAS) models have been proven to be useful for analyzing the link between financial volatility and the macroeconomic environment. In GARCH-MIDAS model, a unit-variance GARCH component fluctuates around a time-varying long-term component which is a function of (macroeconomic or financial) explanatory variables. By allowing for a mixed-frequency setting, this method fills the gap between daily (high frequency) volatility and low-frequency (e.g., monthly, quarterly) explanatory variables. Thus, in this study an attempt will be made to develop appropriate GARCH-MIDAS model for forecasting volatility of the agricultural commodities by identifying the key explanatory variables. Further, comparative analysis of the models will also be done with standard GARCH models.

Improvement of time varying smoothing models using hybrid machine learning techniques

Time series modelling and forecasting is a vibrant research field that has attracted the interest of the scientific community in recent decades. Forecasts of agricultural production and prices are proposed to be useful for farmers, governments and agribusiness industries. In this study, a hybrid time varying smoothing model was proposed for forecasting agricultural prices. In moving average model, equal weights were allotted to all the observations of the time series. In exponential smoothing, weights are assigned in exponential manner as recent observations getting more weights than the older ones. So it doesn't capture entire pattern in the time series and the entire characteristics of time series can't be explained properly. Hence, exponential smoothing model with time varying parameter is developed with weights as minimum by maximum values, minimum by simple moving average and minimum by weighted moving average of two lagged observations. This study shows that the sudden fluctuations of the time series can be predicted by the proposed model. The monthly price series of Tea of Kolkata market was used for this study. These three cases of time varying models were compared with ARIMA and Holt's linear trend method using accuracy measures like RMSE, MAPE and MAE. Based on forecast accuracy measures, it is showed that minimum by simple moving average of two lagged observations performed better than all other models. The residuals of selected time varying smoothing model is fitted with time delay neural networks for predicting nonlinear pattern in the time series. Finally, the hybrid time varying smoothing model is compared with simple time varying smoothing model and achieved better results. The results of the study show that the hybrid time varying smoothing model performed well than all other used time series models.

Theme 4. Statistical genetics and genomics

Development of empirical approaches for estimating breeding values in genomic selection under incomplete data situations

In the field of DNA sequencing, Genotype-by-sequencing is meant for discover SNPs in order to perform Genotyping studies. A most commonly occurring problem in GBS is the presence of missing observations. Quite often, the standard statistical models may not be able to handle such missing data also known as incomplete data. In GBS is, to impute missing data for further downstream GS analysis. Hence a study on "Development of Empirical Approaches for Estimating Breeding Values in Genomic Selection under Incomplete Data Situations" is conducted with the objectives: 1) To identify a suitable imputation method against varying levels of missing marker genotypes in genotyping-by-sequencing data, 2) To identify a robust genomic selection model against varying levels of missingness, 3) To develop an efficient empirical procedure to estimate GEBVs in presence of varying levels of missing observations, and 4) To compare the efficiency of the proposed empirical procedure with existing approaches based on simulation as well as real data situations. The imputation accuracy of six imputation techniques viz., RFI, EMI, MNI, SVDI, k-NNI and LWI was assessed based on correlation coefficient (r), mean square prediction error (MSPE) and imputation time (in minutes),the results revealed that these RFI, EMI and SVDI performed with high imputation accuracy under varying levels of missing observations i.e., 5%, 10%, 15% and 20%. The prediction accuracies of several GS models viz., RR, Lasso, EN, BA, BB, BC, BRR, BL, GBLUP, EGBLUP, SVM, RKHS, MKRKHS and RF predicting GEBVs were compared at different levels of missing values in the GBS data with MNI imputation technique. The results revealed that prediction accuracies of GS models based on machine learning algorithms (RF, RKHS and MKRKHS) are out performed models based on Bayesian approach (i.e., BA, BB, BC, BL and BRR) followed by BLUP based approaches. Besides the 3 best imputation techniques: RFI, EMI and SVDI integrated with several GS models were also tested for their performance in estimating GEBVs. It was found that RFI with prior fitting of GS models outperformed the EMI and SVDI with all GS models at different levels of missingness. Whereas RFI with GS model based on RF regression that shown highest prediction accuracy while dealing with missing data at different levels. Also, the consistency in performance of the identified combination of imputation technique and GS model was tested under both simulated data at different levels of heritability (0.3, 0.4 and 0.5) as well as real data with 20% level of missing values. Here, the prediction accuracy of the said combination increased with the increase in the heritability value of the trait. From the findings, it is suggested to use RFI for imputing missing values and RF based regression for predicting GEBVs at different levels of missing values in GBS data.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Anushka Garg	21096	M.Sc.	Study on multiple component models for forecasting price volatility for agricultural commodities	Dr. K.N. Singh
2.	Satyam Verma	21236	M.Sc.	Trend resistant constant block-sum partially balanced incomplete block designs	Dr. Arpan Bhowmik
3.	Katore Pramod Balkrushna	21237	M.Sc.	Position balanced block designs for sensory studies and consumer experiments	Dr. B.N. Mandal
4.	Manoj Verma	21238	M.Sc.	Forecasting crop yield using feature selection and machine learning algorithms	Dr. K.N. Singh
5.	Krishna	21239	M.Sc.	Estimation of crop yield using calibration approach under stratified two stage two phase sampling design	Dr. Tauqueer Ahmad
6.	Kaushal Kumar Yadav	21240	M.Sc.	Row-column designs for two-level factorial and fractional factorial experiments	Dr. Sukanta Dash
7.	A. Praveen Kumar	21241	M.Sc.	Improvement of time varying smoothing models using hybrid machine learning techniques	Dr. Wasi Alam
8.	Ashtosh Dalal	21242	M.Sc.	Construction of response surface designs with mixed levels of factors incorporating neighbour effects	Dr. Seema Jaggi
9.	Naveen G.P.	21243	M.Sc.	Crop yield estimation using random forest spatial interpolation technique	Dr. Prachi Misra Sahoo
10.	Sumeet Saurav	10585	Ph.D.	Robust designs for bioequivalence trials	Dr. Cini Varghese
11.	Nitin Varshney	10586	Ph.D.	Prediction approach Estimator using Auxiliary Information under Two-Phase Sampling	Dr. Tauqueer Ahmad
12.	Rajeev Kumar	10587	Ph.D.	Rescaling Bootstrap Technique for Variance Estimation in Dual Frame Surveys	Dr. Anil Rai
13.	Srikant Bairi	10724	Ph.D.	Development of empirical approaches for estimating breeding values in genomic selection under incomplete data situations	Dr. A.R. Rao
14.	Md. Yeasin	10974	Ph.D.	Bayesian estimation for time series models with exogenous variables	Dr. K.N. Singh

Bioinformatics

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Prof. Anil Rai

The Centre of Agricultural Bioinformatics at ICAR-Indian Agricultural Statistics Research Institute aims to understand the biological phenomenon through innovative applications of statistics and computer science. The mandate of the centre is to undertake research, teaching and training in the field of computational biology and agricultural bioinformatics. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Genome bioinformatics

A study on gene regulatory network for rice blast disease

Study of gene regulatory network (GRN) helps in understanding complex biological processes. Inferring GRN is very challenging task as it involves computationally complex steps. The consensus GRN has been constructed using Fisher's weighted method which combines the results obtained from correlation, principal component regression (PCR), partial least squares (PLS) and ridge regression-based scoring methods. The consensus GRN has been constructed using the gene expression datasets of rice leaves under blast infected condition to understand the resistance mechanism in the crop occur during blast fungus infection. Differentially expressed genes (DEG) have been identified using one-way analysis of variance (ANOVA). The DEGs have been considered for computing pair wise connectivity score using correlation, PCR, PLS and ridge regression. The significant edges have been combined by Fisher's weighted method. A total of 74 significant edges and 40 nodes (genes) have been found in the consensus GRN at 1% level of significance with 8 degrees of freedom of chi-square distribution. Evaluation of GRN has been performed using Hamiltonian distance-based criteria, hub genes in the network and QTL analysis. The performance of consensus GRN is better than the individual methods correlation, PCR, PLS and ridge regression. The consensus GRN construction combining the results obtained from correlation, PCR, PLS and ridge regression will be helpful for biological research for understanding pathways of diseases. An interactive and user-friendly web tool has been developed for consensus GRN construction. The web tool can take gene expression data as input and the outputs are provided as downloadable format in result window. The interactive web tool can be very useful and less time-consuming for constructing GRN.

Identification and characterization of Lnc RNA in ricebean (*Vigna umbellata*)

Ricebean, Vigna umbellata is a Kharif-season annual legume. Its seeds are consumed as pulse. It is considered as a minor legume as it is grown in limited areas as an intercrop with maize and sorghum. It is mostly grown in Northern part of India (mainly Uttarakhand) and North-eastern part of India (mainly Assam). Its seed contains a good amount of protein and other nutrients. These protein-coding RNA of developing stages of seed largely regulated by non-coding RNA specifically long non-coding RNA. Long non-coding RNAs (lncRNAs) are a large and diverse class of transcribed RNA molecules with a nucleotide length of more than 200 bp and ORF<100 bp that do not encode proteins. It is one of the types of regulatory non-coding RNA. LncRNAs are important regulators of gene expression by DNA methylation and chromatin remodeling, and in some cases, they act as miRNA (Micro RNA) sponges to enhance the expression of mRNA targeted by miRNA. LncRNAs are thought to have a wide range of functions in cellular and developmental processes. LncRNA may be positioned beside protein coding genes or in between genes even it overlaps with coding genes. There has been hardly any work reported for the identification of lncRNA with respect to the Ricebean crop. This study aims to identify lncRNA and annotate its targets for the developing stages of Ricebean seed. A total of 906 novel lncRNAs have been identified. Out of these 906 novel lncRNAs, 82 lncRNAs have targets of 15 miRNAs. It was observed that different lncRNA could have similar miRNA targets. These 15 microRNA had targets of 15 mRNA. Lastly, annotation of 15 mRNA was carried out and it was found that these mRNA regulated different biological, cellular, metabolic processes of the developmental stages of Rice bean seed. ‘RbLncDB’, a web resource has also been developed under the present study to help future researchers in regard to Ricebean seed transcriptome.

Identification and characterization of bZIP and Dof gene families from developing seeds of *Vigna umbellata*

Ricebean (2n=22) belongs to Fabaceae family and it is one most important legume crop on the global scale due to its high protein content and grows on less fertile soils. It is extensively cultivated for its seeds as staple food as well as feed for livestock population across the world. To overcome the stresses, there are many methods available such as physical, chemical, biological method etc. But biological method plays significant role to overcome these stresses because they are most economical and environmentally friendly. Basic leucine zipper (bZIP) gene family is one of the largest transcription factor gene families in plants and plays crucial roles in various biological processes, such as light signalling, seed maturation, plant growth, development as well as biotic and abiotic stresses. Currently no information is available regarding bZIP gene family in ricebean. In this study, 46 bZIP genes were identified from draft genome of *Vigna umbellata*. All the members of VubZIP family were divided into 9 subfamilies based on phylogenetic relationship with *Arabidopsis thaliana* bZIPs. This was further supported by analysis of their conserved motifs and gene structures. VubZIP genes were characterized in terms of subcellular localization, primary structure analysis, secondary structure prediction and topology prediction. Promoter sequence analysis showed that VubZIP genes harbour many cis-elements related to stress responses (LTR, MeJARE, GARE, ABRE, DTRE etc). Subfamilies share same characteristics within group but vary between group in terms of intron-exon analysis, conserved motif analysis and PTM site prediction. Together, these results provide the way for future studies of VubZIP-mediated various stress response in ricebean. DNA binding with one fingers (Dof) proteins are plant specific transcriptional factors, which play important role in plant growth, development and various stress responses like drought, salt, osmotic and cold stress. Currently no information is available for this gene family in ricebean. In this study, bioinformatics analyses revealed 35 VuDof genes were identified in the draft genome. All VuDof genes were characterized in Vigna umbellata, which includes analyses of genome sequences, conserved protein domains, conserved motif analyses, subcellular localization, intron-exon analysis, primary structure analysis, secondary structure prediction and topology prediction. Although these VuDof genes are variable in their length, molecular weight, iso-electric point etc. all the VuDof genes contain a conserved structure called zf-Dof domain. All the members of VuDof gene family are divided into 5 subfamilies based on phylogenetic relationship with Glycine max, Phaseolu svulgaris Dofs. The promoter sequence of VuDof genes were analysed for cis-elements, which are responsible for tolerating stress condition in plants. These results will help in future studies for expression profiling of genes and other gene families in ricebean.

Theme 2. Computational biology

Development of a deep learning based methodology for functional protein classification

Cereals, belonging to poaceae family, are staple crops widely cultivated across the world. These are highly nutritious, rich in vitamins, minerals, carbohydrates, fats, oils, proteins and fibers but are low in essential amino acids like lysine. They have wider applications in production of flour, bread, rice, cakes, corn, beverages, wine etc. Consumption of these crops are reported to reduce coronary heart disease, diabetes, colon cancer, diverticular disease etc. India is the third largest cereal producer after China and USA. Production of these crops is highly affected by biotic and abiotic stresses, adversely affecting the crop growth and development, leading to economic loss, thus warranting the study of such genes. The genes start adapting under stress factors and produce proteins that can tolerate such changes by changing signalling pathways in protein-protein interaction. Finding these proteins are highly expensive, time consuming and require skilled person. In overcome these constraints, rapid classification and prediction of such proteins using computation approaches is required. In this study, different machine learning techniques, namely, support vector machine, random forest and deep learning (long short-term memory (LSTM)) were applied for development of classification models for protein sequences associated with four major abiotic stresses (heat, cold, salinity and drought). Besides, an activation function, *i.e.,* Gaussian Error Linear Unit with Sigmoid function (SiELU) was developed for deployment in the deep learning model, which showed an increased accuracy and performance of the model. Lastly, a web-based tool, "*DeepAProt: Crop specific abiotic stress protein classification tool using Deep Learning"* available at http://login1.cabgrid.res.in:5000/ was developed for prediction of these abiotic stress associated proteins from poaceae family implementing the proposed LSTM deep learning methodology with *SiELU* activation function and tuning of other hyper-parameters. This tool can classify the functional proteins associated with abiotic stresses which would be useful for breeders in endeavor of better management and improvement.

Deep learning for predicting breeding value using high-throughput (HTP) genotyping and phenotyping

Accurate estimation of the breeding value in a crop breeding program is of key importance. Traditionally, statistical methods have been widely utilized for predicting breeding values using genotypic effects. These statistical methods usually assume that genotypic effects are independently distributed and follows a prior distribution such as Gaussian etc. These statistical assumptions may play limiting role in predicting the breeding values using high throughput genotyping data, which has very precise information of genotypes. At the same time, harnessing the potential of this precise information of genotyping equally precise phenotyping is also warranted. Precise phenotyping is laborious, expensive and sometime impossible in case of conventional phenotyping. Therefore to overcome these limitations, the present work proposes the use of deep learning in prediction of breeding value by exploiting the full potential of high-throughput genotyping in conjecture with high throughput phenotyping. Hence, deep learning-based CNN Model has been trained for the prediction of breeding Value using High Throughput Genotyping and Phenotyping data of wheat dataset, which consist of 184 RILs and each RILs contains 3121 filtered SNPs. Altogether, data of six traits were taken, under two environments (controlled and drought condition), for the prediction of breeding value. First, the whole dataset was randomly divided into two parts, one is training dataset and other is testing dataset. The CNN models were trained on training dataset, which contains 80% of total dataset and remaining 20% of the total data was used for testing. Two parameters were used for testing and evaluation of the deep learning model training. The trained and tested deep learning model was compared with the existing statistical models i.e., GBLUP (Genomic best linear unbiased prediction), rrBLUP (ridge regression best linear unbiased prediction) and Bayesian LASSO (Bayesian Least Absolute Selection and Shrinkage Operator). The result shows that deep learning model performs better as compare to statistical methods undertaken.

Theme 3. Metagenomics

Phylogenetic marker genes based approach for binning of metagenomics data

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

Prediction of enzymes involved in bioremediation using aquatic metagenomes

The increasing use of pesticides, heavy metals, synthetic dyes and other chemicals is a major environmental concern. Water containing these hazardous chemicals, extensively released from small- and large-scale industries cause problems to animals, plants and by entering into the food chain cause serious health impairments in living systems. Removal of these pollutants from water is very important. The arrays of technologies are implemented to date to remediate both inorganic and organic contaminants from wastewaters. Among which, bioremediation is the most attractive method as it is eco-friendly, sustainable and cost-effective. Use of bio-based remediation method is advantageous over the conventional method. Many enzymes and microorganisms are extensively used for elimination of dyes, heavy metals, adsorption of toxic industrial effluents, removal of fertilizers/pesticides, atmospheric pollutants and nuclear waste from the environment. And the major question is how to find out these bioremediating enzymes. Many NGS technologies and metagenomics have been extensively used to find out bioremediating enzymes. Metagenomic is considered as a powerful method to study the bacterial diversity in environmental samples without using any cultural techniques. Metagenomics has changed the microbial world completely. It has provided new insights to analyse microbial genes and metabolites. It offers an outstanding way to characterize the microbes, their genes, proteins, abundance and metabolic pathways, which can be explored in the bioremediation of various contaminants. In this study we have identified dye, hydrocarbon and plastics degrading enzymes using metagenomics data from 4 different sites of river Ganga such as Nawabganj, Kanpur; Jajmau, Kanpur; Below Farakka bridge, West Bengal and Paharghati, West Bengal with the help of RemeDB tool. We have also Identified the abundance of these enzymes using MG-RAST pipeline (https://www.mg-rast.org/) and have also inferred which place is more polluted and which is less. We have identified metabolic pathways of these enzymes using and KEGG pathways (https://www.kegg.jp/kegg/pathway.html). We have developed a web-based search tool containing all the enzymes, organism name, pollutant they degrade and identity percentage of 4 different sites of river ganga. And this web-based search tool contains four bottons such as, Home page, Search, About and Contact us. We can search by entering enzyme name, place name, pollutant they degrade or identity and result can be viewed accordingly.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Bibek Saha	21255	M.Sc.	Identification and Characterization of Lnc RNA in Ricebean (*Vigna umbellata*)	Dr. D.C. Mishra
2.	Laldhari Patel	21256	M.Sc.	Deep learning for predicting breeding value using high-throughput (HTP) genotyping and phenotyping	Mr. Sanjeev Kumar
3.	Shivdarshan Shrishail Jirli	21258	M.Sc.	Identification and characterization of bZIP and Dof gene families from developing seeds of *Vigna umbellata*	Dr. Monendra Grover
4.	Asif Ali V.K.	21259	M.Sc.	Phylogenetic marker genes based approach for binning of metagenomics data	Dr. Anu Sharma
5.	Chandana V.	21260	M.Sc.	Prediction of enzymes involved in bioremediation using aquatic metagenomes	Dr. S.B. Lal
6.	Chiranjib Sarkar	10434	Ph.D.	A study on gene regulatory network for rice blast disease	Dr. Rajender Parsad
7.	Bulbul Ahmed	10780	Ph.D.	Development of a deep learning based methodology for functional protein classification	Dr. Anil Rai

Computer Application

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Prof. Alka Arora

The Division of Computer Application at ICAR- Indian Agricultural Statistics Research Institute has the mandates to develop data bases and information systems for agricultural research; to conduct post-graduate and ad-hoc training courses in computer applications; to provide advisory and consultancy services in data processing; to provide computer services in the institute. The research findings of post graduate students have been grouped under the following themes:

Theme 1. Artificial intelligence/machine learning application in agriculture

Nature inspired algorithms for optimization of crop plan

Agricultural crop planning makes a significant contribution to increase production, income, and the quality of life in the farming community. Proper policy planning and scientific tools are essential for turning agriculture into a profitable profession. This study investigated the development of optimal crop plan using nature-inspired optimization techniques such as genetic algorithms (GA) and differential evolution (DE). Variants of differential evolution algorithms are investigated to discover an optimal crop plan. The results from each algorithm are analyzed, and revealed that DE techniques are more profitable than existing patterns. The multi-objective differential evolution (MODE) method is used to construct and solve problems with two objective functions: maximization of profit and minimization of groundwater utilization, both of which are constrained. MODE's Pareto fronts are compared to NSGA-II, a popular multi-objective evolutionary algorithm based on genetic algorithm, and MODE performed better than NSGA-II. The crop plans generated using multiple nature-inspired algorithms, linear programming (LP), and the existing pattern showed that nature-inspired methods outperformed the existing crop plan. For single-objective and multi-objective optimization, a web-based user interface is developed and validated using real data set. This study can be useful for policymakers, researchers as well as for farmers.The crop plans generated using multiple nature-inspired algorithms, linear programming (LP), and the existing pattern showed that nature-inspired methods outperformed linear programming and the existing crop plan.

Image-based diagnosis of disease severity stages in maize using deep convolution neural networks

In India, maize crop is quite vulnerable to several diseases. The diseases are needed to be identified accurately as well as in the early severity stages for reducing production losses. In recent years, deep learning techniques have become very popular in the field of agriculture. This research work was aimed at proposing a noveldeep learning based approaches for identifying the Maydis Leaf Blight (MLB), Turcicum Leaf Blight (TLB) and Banded Leaf & Sheath Blight (BLSB) disease and for identifying the severity stages of MLB disease of maize crop. In this work, around 5,939 digital images of maize leaves were captured in real in-field conditions in a non-destructive manner from experimental fields of ICAR-IIMR, Ludhiana. In this work, two Deep CNN models were developed: Firstly, a deep CNN model (Inception-v3_ GAP) was proposed for identification of three diseases of maize crop. This model achieved the testing accuracy of 95.71% on separate test dataset for classifying the images into respective classes. Secondly, another deep CNN model (improved InceptionResNet) was developed based on the 'InceptionResnet' architecture, for identification of disease severity stages of MLB disease. The proposed improved Inception ResNet model achieved the testing accuracy of 92.49% on testing dataset. Next, an AI-enabled mobile application (Severity Checker) has been developed by integrating the developed Deep CNN models for facilitating the automated identification of diseases and their severity stages. This mobile application can be a handy tool for identifying the diseases and their severity stages through the mobile phones in agricultural fields.

Development of particle swarm optimization based model for crop planning

Crop planning is one of the methods for increasing crop production. In earlier times, farmers used to plan the crops based on their own estimates. However, due to severe changes in climatic situations and the continued depletion of available resources, crop planning at a broad scale with optimizing the resources and utilizing computational techniques is required. Evolutionary computation performs well in single as well as multi-objective optimization problems. However, there have been few attempts in the literature in this area due to a lack of experience in agriculture, crop planning, and evolutionary algorithms and no online agricultural planning tools are available. In this study Particle Swarm Optimization is used to develop a crop planning model for single objective and multi-objective function at regional level. Developed models validated with two different regions i.e. rainfed and irrigated. Sensitivity analysis is done with respect to some % of changes in water availability and working capital, which denote the increase of the water and working capital at a certain level will enhance the net returns. A multi-objective approach was designed using the MOPSOCD algorithm to obtain the more optimal solution using the crowding distance mechanism. The diverse scenarios with combinations of objective functions are described and results are compared with each other. The multi-objective PSO results outperform the other similar evolutionary algorithm i.e. NSGA II. Finally, an online software is developed as a teaching aid or a research tool for planning the crops at the regional level.

Ontology driven context aware recommender system for maize cultivation

Recommender systems are software solutions which can deliver suggestions to users in areas where a large number of product alternatives are available. These automated recommendations are much more useful to the users if the system is aware of the user's varying needs. With mobile and ubiquitous computing it is now possible to capture user's current situation as context and use it as an additional component for generating new recommendations. Thus context aware recommender systems came into picture and gradually becoming popular. However, the quality and impact of the recommendations on users majorly rely on the correct choice of the context in making these recommendations. To successfully grow a crop up to its maximum yield potential, farmers also require suggestions about which variety to grow, where to buy seeds from, where to sell the produce, weather information and the correct cultivation practices to be followed. Farmers either reach out to their nearest KVKs, other government organizations or contact their fellow farmers for information. The major drawback in the process is not only its time taking but mostly farmers are given a generalized and broader advisory which does not suit their individual requirements. This creates a major gap in adoption of new technologies to farmer's field. Keeping this in mind, a recommendation algorithm has been developed which recommends management practices to the farmers based on their current context (e.g., farm conditions, soil status, budget availability, labour affordability, season of cultivation, purpose of planting, availability of water sources, power availability etc).A multi agent based mobile application has been developed to identify and capture the relevant context parameters for each and every management practice followed for maize cultivation. Farmer's preferences of a particular management practice under certain context have been gathered as ratings to so as to help recommend suitable management practices to other farmers having similar contextual conditions. An ontology has been developed for mapping the context and their suitability to various cultivation practices of maize. The developed context aware system provides better recommendations to farmers than the currently available crop advisory services.

Development of a deep learning-based classification model and web-based application for prediction of LncRNA in crops

The nucleic acid sequence, which provides the 'ladder-step' ordering of nucleotides within the molecules of RNA and DNA, contains and conveys the encoded information. Ribonucleic acid (RNA) is a polymeric molecule that plays numerous biological roles including gene coding, decoding, control, and expression. Along with lipids, proteins, and carbohydrates, nucleic acids are one of the four major macromolecules required for all known forms of life. RNA, like DNA, is built up as a chain of nucleotides, however unlike DNA, RNA is found in nature as a single strand folded over itself rather than a paired double strand. RNA is mainly of two types, coding RNA and non coding RNA. Coding RNAs are messenger RNAs (mRNAs) that encode proteins. A non-coding RNA (ncRNA) molecule is one that is not translated into a protein. There are various types of non coding RNAs in which long non-coding RNA is also a type of non coding RNA. Long non-coding RNAs (LncRNAs) are a form of RNA that are commonly characterised as transcripts with more than 200 nucleotides that are not translated into protein. Plant LncRNAs regulate embryogenesis, root organogenesis, reproduction and gene silencing through DNA methylation. So, there is a need to uncover the function of LncRNA in crop plants. For this purpose firstly we need prediction tool, which can predict sequence as LncRNA or other type of RNA. There are many tools available for classification between LncRNA and coding RNA but most generally they were related to humans and other organism. Also these tools were alignment based, so they were very hard to use. But, in this research we made a web application named as "PLNC-Predictor" by using deep learning based binary classification model CNN. By using 1D CNN we classify LncRNA from cRNA. It predicts given sequence that, weather it is LncRNA or cRNA. The Python language, Google colab notebook, Keras, TensorFlow, Pandas, Sklearn and Keras-tuner etc. libararies and platforms were used for development of classification model. The ROC curve, accuracy score, precision, specificity and f1 score was calculated for evaluation of model. The accuracy of model is 93.40%, precision 96.20% sensitivity 90.90%, F1-score 93.47%, specificity 96.10%, and area under in ROC curve is 93.40 %. The given parameters can be increased by increasing input size for model or by using other type of deep learning model. The developed model is deployed as web application by using anvil software, which provide platform for Python for making web application. The web application is named as "PLNC-Predictor". The most beautiful thing about PLNC-Predictor is that user can directly predict the type of fasta sequence, by just pasting it, in input box of this web app.

Development of web-based application for predicting market price of agricultural commodities using machine learning techniques

Agriculture is backbone of Indian Economy as well as farmer's primary source of income. In India, farmers are facing fluctuations in prices agricultural commodities and it affects the farmers socio economic status as well as an adverse effect on GDP of large population country like India. For farmers, Agricultural commodities market price information is essential for smooth and active operation of marketing system. In this study, an attempt has been made to develop a web-based application named as "ICAR-IASRI: TSW" for Indian farmers. This application is aimed to predicting of agricultural commodities market price can help to safeguard the farmers from market fluctuation and mitigates the risk of loss in profit. Hence the farmers can plan better for releasing their agricultural commodities to market. In this thesis, web-based application "ICAR-IASRI: TSW" developed for predicting of agricultural commodities market price. This web application is based on 3-tier architecture. The front-end interface development carried out using front end technology tools such as HTML, CSSand JavaScript. Sever side implemented python programming language, Django framework. For prediction purpose implemented 4 machine learning techniques such as Autoregressive integrated moving average (ARIMA), Artificial Neural Network (ANN), Support Vector regression (SVR) and Random Forest Regression (RFR). ARIMA model imported from Pmdarima package and supervised learning models ANN, SVR and RFR imported from scikit-learn package. Then all model's performance evaluated by performance parameters such as R^2, RMSE and MAPE. Web application tested by using sample data and collected from Ghaziabad market rice crop arrival price as well predicted market prices with all the models. Developed web application "ICAR-IASRI: TSW" would be of great use to the farmers and safeguard from market fluctuation and mitigates the risk of loss in profit.

Theme 2. Decision support system/mobile based application in agriculture

Mobile based decision support system for nutrition and health assessment using anthropometry techniques

Farmers are the assets of any country in the globe since they generate food for the people, but what if they become unwell or malnourished which will stifle the country's progress. As a result, both farmers and government agencies must keep track on the nutritional health of their constituents in order to provide the best possible service to them. In this context, this research focuses on the creation of an Android-based mobile application that will assist in evaluating the nutritional state of farmers using several anthropometric measurements that are effective in providing a basic overview of their health status and guiding them. This Android-based mobile application was created using a variety of software tools, including the Android Studio development environment, Java programming language, eXtensible Markup Language for application user-end development and a MySQL server as a backend database to store the farmers details data and the various index values of all the farmers. A mobile-based decision support system called '*NutriGuide*' was created for this purpose, and it will assist them in assessing their physical fitness and nutritional state, as well as provide them with a quick note on the value of different types of foods for different age groups. It also has the function that allows you to download the data in excel file for additional examination. Other than all this the application provides a brief details containing suggestions regarding food requirement for nutritional sufficiency.

Mobile app based management of grape cultivation in subtropical region

Agriculture remains the most important sector of the Indian economy, and for millions of farmers, agriculture is more or less a necessity for survival. Mobile apps are potential digital tools that can be used to reach a large number of farmers in a short period with agricultural information. They can be used to boost farm income and productivity by providing accurate information, better input and farm management, easy marketing, and connecting with government agencies to provide policy support to farmers, among other things. In this study, an attempt has been made to develop a mobile application named "GrapeCulture" for Indian farmers. This mobile application is aimed to provide valid and detailed information on vineyard management practices like spacing, planting, training, pruning, maturing, and fertilization, irrigation. It suggests the varieties suitable for the subtropical region. It gives information on pests and diseases along with management practices and recommends suitable pesticides for particular pests and diseases. It provides information on the physiological disorder and nutritional deficiencies.

This application suggests the number of vines that can be accommodated in a given spacing. 'GrapeCulture' mobile application was created using the Android Studio IDE, Java programming language, and XML for application user-end development and SQLite as a backend database to store the information of the subtropical grapes. This mobile application aids in farm management, resulting in increased agricultural yield and farm maintenance, propelling agriculture to new heights.

Development of mobile app for management of cole crops

Cole crops such as Cabbage, Cauliflower, Broccoli, Brussel Sprouts, Kale, and Kohlrabi are rich source of vitamin A, Vitamin C, beta carotene, antioxidants and phytochemicals which can help in preventing cancer and heart diseases. Infestation by insect pests and damage caused by diseases are the major factors responsible for the low productivity of cole crops. Therefore, there is need to develop mobile application which provides detailed information about cultivation practices, different varieties, insect-pests, diseases, physiological disorders and weeds in major cole crops. Thus mobile app on Cole Crops 'ColeApp' has been developed with the objectives "To develop a mobile app for cultivation practices and management of major cole crops", "To populate the database for management of major cole crops". The 'ColeApp' mobile application was created using the Android Studio IDE, Java programming language, and XML for application user-end development and SQLite as a backend database to store the information of package of practices of major cole crops. This 'ColeApp' application contains features such as description of cultivation practices, different varieties which are resistant to particular disease or pest and which are not resistant to disease and pest, different types of the insect-pests, diseases that cause damage through decrease in yield as well as productivity, available measures to control pests and diseases such as Integrated Pest Management (IPM) and Integrated Disease Management (IDM) practices at each stage of crop, nematodes which cause damage with their control methods, different weeds which cause damage to decrease yield and their management practices of major cole crops. The developed mobile application 'ColeApp' would be helpful to the farmers to reduce the crop losses and also to increase the yield and making the farming a profitable venture.

Development of mobile application on integrated farming system

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

Development of mobile app for Kinnow crops

Mobile apps are potential digital tools that can be used to reach a large number of farmers in a short period with agricultural information. MobileApp can be used to boost farm income and productivity by providing accurate information, better input and farm management, easy marketing, and connecting with government agencies to provide policy support to farmers, among other things. In this study, an attempt has been made to develop a mobile application named "Kinnow cultivation" for Indian farmers. This mobile application is aimed to provide valid and detailed information on Kinnow management practices like spacing, planting, training, pruning, maturing, fertilization, irrigation, disease and pest management. It gives information on pests and diseases along with management practices and recommends suitable pesticides for particular pests and diseases. This application provides the calculation of number of plant population, calculation of initial fruit set percentage and calculation of yield per plant.

List of contributing Students and Chairperson of their Advisory Committee

S. No.	Name of the student	Roll No.	Degree	Title of the Thesis	Chairperson
1.	Shubhasish Sarkar	21261	M.Sc.	Mobile based decision support system for nutrition and health assessment using anthropometry techniques	Dr. Mukesh Kumar
2.	Bhavesh Kumar Choubisa	21262	M.Sc.	Development of a deep learning-based classification model and web-based application for prediction of LncRNA in Crops	Dr. Anu Sharma
3.	Apoorva B.M.	21263	M.Sc.	Mobile app based management of grape cultivation in subtropical region	Dr. S.B. Lal
4.	Bharath Kumar N.	21264	M.Sc.	Development of mobile app for management of cole crops	Md. Sameer Farooqi
5.	Pratiksha Subba	21265	M.Sc.	Development of mobile application on integrated farming system	Md. S.N. Islam
6.	Sushma K.	21266	M.Sc.	Development of Mobile app for Kinnow Crops	Dr. Sangeeta Ahuja
7.	Lalsab Momin	21372	M.Sc.	Development of web-based application for predicting market price of agricultural commodities using machine learning techniques	Md. S.N. Islam
8.	Sanchita Naha	10597	Ph.D.	Ontology driven context aware recommender system for maize cultivation	Dr. Sudeep
9.	Kamalika Nath	10599	Ph.D.	Nature inspired algorithms for optimization of crop plan	Dr. Rajni Jain
10.	Md. Ashraful Haque	10783	Ph.D.	Image-based diagnosis of disease severity stages in maize using deep convolution neural networks	Dr. Sudeep
11.	Shbana Begam	10784	Ph.D.	Development of particle swarm optimization based model for crop planning	Dr. Rajni Jain


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