



Sixty Second Convocation

Significant Post Graduate Students' Research

February 4-5, 2024

Abstracts

Chairperson

Prof. (Dr.) Arvind Kumar

Founder Vice-Chancellor, RLBCAU, Jhansi &
Former DDG (Edn.), ICAR

Convenor

Dr. Anil Dahuja

Professor, Division of Biochemistry

Co-Convenor

Dr. Atul Kumar

Associate Dean (PG), ICAR-IARI



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





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Index

M.Sc.

S. No.	Discipline	Name of the Student	Roll No.	Page No.
1.	Agricultural Chemicals	Riya Kundu	21563	1
2.	Agricultural Economics	Pavan Kumar Kumawat	21570	2
3.	Agricultural Engineering	Mohanaselvan T.	21579	3
4.	Agricultural Extension Education	Pasupuleti Sahithi	21589	4
5.	Agricultural Physics	Souramita Chakraborty	21595	5
6.	Agronomy	Satyam Rawat	60099	6
7.	Biochemistry	Shuvarghya Chakraborty	21615	7
8.	Bioinformatics	Abhik Sarkar	21621	8
9.	Computer Application	Sakshi Rawat	21558	9
10.	Entomology	Jagadam Sai Rupali	21636	10
11.	Fruit Science	Raushan Kumar	21655	11
12.	Genetics and Plant Breeding	Jenia Roy	21663	12
13.	Microbiology	Barnana Maitra	21667	13
14.	Molecular Biology and Biotechnology	Usha M.S.	80022	14
15.	Plant Genetic Resources	Jyotsna Verma	21686	15
16.	Plant Pathology	Poulami Basak	21694	16
17.	Plant Physiology	Chanumolu Hari Gopala Krishna	70016	17
18.	Post Harvest Management	Vathsala V.	21706	18
19.	Seed Science & Technology	Tuhina Ghosh	21710	19
20.	Soil Science	Alapati Nymisha	21712	20
21.	Vegetable Science	Luhana Sohamkumar Chetandas	21720	21
22.	Water Science and Technology	Keerthana Maveril M.	21726	22



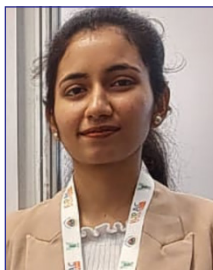
Ph.D.

S. No.	Discipline	Name of the Student	Roll No.	Page No.
1.	Agricultural Chemicals	Anindita Paul	10726	25
2.	Agricultural Economics	Jaiprakash Bisen	10562	26
3.	Agricultural Engineering	Aseeya Wahid	11398	27
4.	Agricultural Extension Education	Aiswarya S.	11195	28
5.	Agricultural Physics	Ram Narayan Singh	10968	29
6.	Agricultural Statistics	Sandip Garai	11710	30
7.	Agronomy	Kamlesh Kumar	11452	31
8.	Biochemistry	Simardeep Kaur	11464	32
9.	Bioinformatics	Sharanbasappa	11739	33
10.	Entomology	K Chandrakumara	11759	34
11.	Environmental Sciences	Gayathri J.	11494	35
12.	Floriculture and Landscaping	Uzma Mehraj	11254	36
13.	Fruit Science	Theivanai M.	11038	37
14.	Genetics and Plant Breeding	Ashvinkumar Katral	11275	38
15.	Microbiology	Aswini K.	11542	39
16.	Molecular Biology & Biotechnology	Sheel Yadav	11291	40
17.	Plant Genetic Resources	Siddhant Ranjan Padhi	11829	41
18.	Plant Pathology	Pankhuri Singhal	11567	42
19.	Plant Physiology	Sandeep Adavi B.	11095	43
20.	Seed Science and Technology	Archana H. R.	11598	44
21.	Soil Science	Avijit Ghosh	10888	45
22.	Vegetable Science	Dhananjay A. Hongal	11619	46
23.	Water Science and Technology	Rashmi Yadav	11641	47

M.Sc.
Thesis Abstracts



Agricultural Chemicals



Riya Kundu

Name of the Student : Riya Kundu
Roll No. : 21563
Chairperson : Dr. Parshant Kaushik



Dr. Parshant Kaushik

Title of the Thesis

Synthesis and evaluation of indazolychromones against plant pathogenic fungi

The world agriculture faces an estimated loss of 18% annually amounting to approximately 1,300 billion INR due to plant diseases. *Sclerotium rolfsii* is an important soil-borne fungus which affects over 500 agricultural and horticultural crops resulting in significant crop losses (10-100%). In the case of tomatoes, the fungus typically targets the lower stem near the soil surface and causes southern blight. *Fusarium oxysporum lycopersici* is another important soil and seed -borne fungal pathogen, causing wilt disease in tomatoes.

Over the past ten years globally, numerous instances of fungicide resistance have resulted in the loss of several important fungicides. Consequently, the synthesis of novel compounds has acquired paramount significance in addressing plant diseases. In our pursuit of new effective fungicides, we synthesised a series of twenty 2-indazol-1-yl-chromen-4-one derivatives (6a- 6t) in the yield range of 76.35-93.86%. The synthesized compounds were characterized using various spectroscopic techniques including IR, ¹H NMR, and ¹³C NMR. Out of 20 synthesised compounds, 19 (6b- 6t) were reported for the first time in literature. All synthesised indazolychromones (6a- 6t) showed good antifungal activity against *S. rolfsii* and *F. oxysporum*. Among the tested compounds, 6t and 6f exhibited very good antifungal activity against *S. rolfsii* with an ED₅₀ of 10.10 ppm and 16.18 ppm, respectively. In case of *F. oxysporum* compound 6f displayed good activity with an ED₅₀ value of 27.82 ppm. Based on *in vitro* results, two most effective compounds, 6f and 6t were taken for pot experiment against *S. rolfsii* in tomato. The pot study revealed that compound 6t (PDI=26.66%) performed at par to that of hexaconazole 5% SC, (PDI=25%). In case of *F. oxysporum*, the tested compound 6f (PDI=35%) was found less active as compared to carbendazim 50% WP (PDI of 24.00%). So, the suitable formulations of compound 6t can be developed for effective management of *Sclerotium rolfsii*.

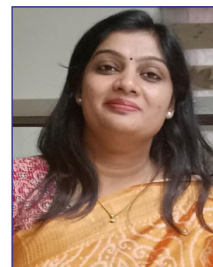


Agricultural Economics



Pavan Kumar Kumawat

Name of the Student : Pavan Kumar Kumawat
Roll No. : 21570
Chairperson : Dr. Akriti Sharma



Dr. Akriti Sharma

Title of the Thesis

A study of determinants of performance of agribusiness start-ups in India

India emerged as the fastest-growing agrarian economy with the 3rd largest start-up ecosystem in the world regarding the number of unicorns made and is now home to more than 27,500 agri-start-ups (DPIIT, May 2023). To provide them a better and adequate supporting ecosystem, a strong stream of research is required. Hence, it becomes essential to identify the factors that are responsible for the performance of start-ups. The research study had three objectives out of which first and second were based upon secondary data and third was based upon primary data. The study was exploratory and qualitative in nature. The research firstly drew a landscape of the start-up ecosystem of India with a focus on agribusiness which gave a clear picture of the whole ecosystem and its actors. The secondary data was collected from Startup India website (startupindia.gov.in) for preparing a report on start-ups' growth trends in the agribusiness sector and overall sector from 2016 to May 2023, and other relevant parameters. In the second objective, a systematic literature review was conducted from the global startup state of the art to identify a list of performance determinants and a primary study was performed in the third objective to assess and develop a performance determinants matrix for agri startups. For a systematic literature review, PRISMA 2020 methodology was used, and for characterizing and mapping agri-start-ups' performance determinants, content analysis was done using Nvivo-14 software. To identify performance determinants of start-ups, performance indicators were identified through a Focused Group Discussion (FGD) which provided a benchmark for startups to look upon and made a base for startup selection for primary study. As the results indicated, funding for agri-start-ups increased continuously even with external constraints in the ecosystem in the previous years. The major funding source for start-ups was venture capital funding. A year-on-year growth of more than 25% in turnover, 30% in profits, increase in employee base, 30 % increase in customer base/ farmers reached and product/geographical diversification were found to be the performance indicators. The determinants were classified into three categories of personal, organizational, and external factors, and the most important performance determinants were product market fit and effective business model. There is a need to inculcate innovation and entrepreneurial culture in Higher Educational Institutes (HEIs) to develop better technologies. Incubators shall be focused on providing mentoring support regarding making a good product market fit and building appealing business models. Various pre-incubation programs shall be organized to sensitize the youth to conduct environmental scanning before getting into product development. A bottom-up approach shall be introduced while assessment of the needs of the market.



Agricultural Engineering



Mohanaselvan T.

Name of the student : Mohanaselvan T.
Roll No. : 21579
Chairperson : Dr. Shiv Pratap Singh



Dr. Shiv Pratap Singh

Title of the Thesis

Study of sugarcane mechanization and health hazards in Erode district

Sugarcane is an important industrial crop of India after cotton, contributing around 6% of the agricultural GDP. Farm mechanization levels in the country increased many-fold (9.9 times) since 1961 and equipment for most of the unit operations of sugarcane have been developed in the country. Under the backdrop of the present scenario, a study was undertaken to analyze the sugarcane mechanization in the selected area of Tamil Nadu state to identify the injury-related operations in sugarcane cultivation and to suggest interventions to prevent the identified injuries. Seventy-two farmers from three villages of Erode district were taken for this study. A structured schedule was used to get the information on mechanization level, adoption of equipment, injury, cultural practices etc. Data analysis indicated that farmers cultivated sugarcane crops in 36.26 to 48.09% of their available lands. An increasing trend of 30 to 35 kW tractors was observed with 76.3% of farmers. Out of 18-unit operations, five-unit operations were fully mechanized, while irrigation was partially mechanized and practiced as drip irrigation. The farms have enough power sources of 4.13 kW/ha, but most of the operations were done manually, reflecting the overall mechanization indicator of 0.162. This is indicating for making strategies to penetrate the developed technologies in villages. Sugarcane leaves constituted 88% of the total injuries and 12% of the injuries were tools related. The causation factor included leaf blades that caused cuts while moving into the fields, deep cuts due to pulling and plucking leaves from a cane and slippage of tools (spade) while hitting some obstructions. These injuries affected the productivity and efficiency of the workers. The tangible injuries can be prevented by wearing footwear, suitable face shields and cotton hand gloves. The farmers are keen to use small and manually portable tools and equipment for sett cutting. So, foot-operated sett cutter was developed. The overall dimensions ($l \times w \times h$) of the cutter were $600 \times 500 \times 940$ mm, respectively. The capacity of the cutter was 830 and 673, and 700 and 620 setts per hour in standing and sitting postures with male and female workers, respectively. The number of setts cut per hour was 10.84% and 9.80% higher with developed sett cutters with male and female workers compared to the traditional sett cutting method.



Agricultural Extension Education



Pasupuleti Sahithi

Name of the Student : Pasupuleti Sahithi
Roll No. : 21589
Chairperson : Dr. Vinayak R. Nikam



Dr. Vinayak R. Nikam

Title of the Thesis

Evaluation of the mango value chain of farmer producer organizations

Farmer Producer Organizations (FPOs) are one of the solutions to reap the benefits of economies of scale, collective post-harvest operations, and marketing. A comprehensive study on ten FPOs and 300 farmers was carried out in Andhra Pradesh and Telangana states and data were collected using a structured interview schedule and open-ended interviews; analyzed using porters' value chain model, regression adjustment, Pro-WEAI, and mixed method analysis. The porter's value chain analysis identified ripening, storage, spoilage and handling and freight expenses as the major areas of cost minimization and the marketing channel with FPOs fetched higher prices to the farmers. FPOs involved in export gained higher prices compared to all other channels. Regression adjustment results indicated that nearly 35.8 percent increase in productivity, 21.9 percent increase in price, and 67.7 percent increase in the value of the output of members compared to non-members. Pro-WEAI and Porters model results showed that women who were empowered at the household level were also empowered at the value chain level but restricted only to a fewer nodes. Training the women on autonomy in decision making and financial literacy helps to better manage the income. A gender-sensitive approach in extension services, such as hiring women extension agents and placing more emphasis on developing and supporting women-led FPOs, will have a multiplier effect on agriculture, farm families, and the rural economy. Farmers should be made aware of the importance of connecting FPOs to digital platforms like Kisan rath, Kisan rail, and Krishi udaan, which offer organised services with negotiable prices. Collaborating with ATMA, KVK, or research institutes to provide training, knowledge, and information on numerous issues and engaging the FPOs in secondary value addition activities helps to overcome the constraints. Better prices for produce, a large number of shareholders, adequate extension and advisory services, etc. were the major success factors identified.



Agricultural Physics



Souramita Chakraborty

Name of the Student : Souramita Chakraborty
Roll No. : 21595
Chairperson : Dr. Deb Kumar Das



Dr. Deb Kumar Das

Title of the Thesis

Hyperspectral remote sensing of wheat yellow rust (*Puccinia striiformis* f. sp. *tritici*)

Wheat serves as the primary food source for approximately 35% of the global population. Yellow rust or stripe rust causes annual average losses of up to 50 per cent in wheat yield and higher losses is possible if the infection commences early. Unfortunately, there is a lack of fundamental information on the spectral signature of wheat yellow rust disease, hindering its real-time detection and management. The current study was aimed at characterizing the spectral reflectance of wheat affected by yellow rust to detect the sensitive spectral range. Field experiment at IARI New Farm area was conducted for the winter wheat crop with different level of yellow rust infection. Spectral observations were taken at canopy level in field condition in the spectral range of 350-2500 nm. Yellow rust severity level was graded from 0-9 score as per standard procedure. The 1st derivative spectral analysis of disease severity levels was conducted to distinguish the sensitive bands. Two newly proposed indices were formulated and evaluated as Normalized Yellow Rust Index 1 (NYRI1), Normalized Yellow Rust Index 2 (NYRI2) with identified wavebands at 675 nm and 1100 nm for NYRI1 and 1750 nm and 2000 nm for NYRI2. Utilizing the spectral data and the sensor response function of the Sentinel-2 sensor, broadband indices were calculated for the Sentinel-2 MSI band information. Among the existing indices, EVI yielded superior results with an R^2 of 0.89 in predicting disease levels. Different multivariate and machine learning algorithms such as partial least square regression (PLSR), multiple linear regression (MLR) and random forest (RF) were also evaluated to predict disease severity levels. All the models were found to be good predictors. However, PLSR yielded the highest R^2 of 0.977, RPD of 0.08 and least RMSE of 0.439. The research affirms the capacity of hyperspectral remote sensing to evaluate and differentiate the various degrees of severity in wheat yellow rust disease.



Agronomy



Satyam Rawat

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Roll No. : 60099
Chairperson : Dr. Rajiv Kumar Singh



Dr. Rajiv Kumar Singh

Title of the Thesis

Effect of nano-urea on maize productivity and nitrogen use efficiency in acid soil of Jharkhand

To validate the efficacy of nano-urea under field conditions, an experiment was conducted at ICAR-IARI, Jharkhand, during the *Kharif* season of 2022. The objectives of the experiment were to assess the impact of various nitrogen doses with nano-urea on maize growth, productivity, nitrogen use efficiency, and economic viability. The soil in the experimental field was classified as alfisol, characterized by red colour and mild acidity with a pH of 6.3. Implemented in a Randomized Block Design, the experiment comprised 12 treatments, including four nitrogen doses (0, 50, 75, and 100% of recommended N) and three spray combinations (no spray, nano-N, and prilled-urea) with three replications. The recommended nitrogen dose was applied in split, with 1/3 as basal, 1/3 at 32 DAS as the top dressing, and 1/3 at 50 DAS as the second top dressing. Nano-N and prilled-urea spray coincided with top dressing at 32 DAS and 50 DAS. Results revealed significantly higher grain yield (6.89 t/ha) under 100% recommended N + 2 nano-urea sprays compared to other treatments, on par with 100% recommended N (6.24 t/ha) and 100% RDN + 2% prilled-urea sprays (6.26 t/ha). Application of 75% recommended N with 2 nano-urea sprays recorded grain yield at par (5.79 t/ha) with 100% recommended N. Net returns and B:C ratio were significantly higher under 100% recommended N + 2 nano-urea sprays, remaining on par with 100% recommended N and 100% RDN + 2% prilled-urea sprays. Application of 75% recommended N with 2 nano-urea sprays recorded net returns and B:C ratio at par with 100% recommended N. In conclusion, the experiment demonstrated the positive impact of nano-urea on maize productivity, nitrogen use efficiency, and economic returns, highlighting its potential as an environmentally friendly alternative in acid soil conditions.



Biochemistry



Shuvarghya Chakraborty

Name of the Student : Shuvarghya Chakraborty
Roll No. : 21615
Chairperson : Dr. Veda Krishnan



Dr. Veda Krishnan

Title of the Thesis

Isolation, structural characterization and hypoglycemic effects of functional polysaccharides from Shiitake (*Lentinula edodes*)

The government of India is actively promoting the “*One District One Product (ODOP)*” initiative to revive niche crops and stimulate balanced regional development. North East India, an untapped region, is identified for its potential to cultivate medicinal mushrooms, particularly Shiitake (*Lentinula edodes*). Shiitake has gained international attention for its nutraceutical benefits in managing type 2 Diabetes Mellitus, with a focus on the therapeutic compound lentinan (LNT), a β -glucan. The study aims to explore indigenous Shiitake strains for their total and conformation-dependent β -glucan forms as well as to validate their anti-diabetic potential. The research identifies DMRO-623 as a Shiitake strain with the highest reported β -glucan content globally, specifically 47% (37% triple helical and 9% single helical). An extraction-enrichment pipeline is established, selecting the acid-alkali method for its efficiency in recovering bioactive triple helical β -glucan (THG). Further enrichment involves membrane-based dialysis and gel-filtration chromatography. Biophysical characterization confirms the unique fingerprint of LNT using various techniques, including FT-IR, MALDI-MS, XRD, ^{13}C , and ^1H NMR. The enriched bioactive THG demonstrates dose-dependent anti-hyperglycemic effects, reducing carbohydrate hydrolysis. The study suggests the inhibitory effect of LNT on carbolytic enzymes as a potential reason for the observed reduction in hydrolysis. Enzyme inhibition assays validate the inhibitory effect, and *in silico* tools such as docking and molecular dynamic simulations reveal LNT’s interactions and inhibitory effects on pancreatic amylase, sodium-glucose cotransporter-1, and glucosidase. In conclusion, the study is the first attempt to characterize LNT from Indian Shiitake and validate its anti-diabetic potential. It emphasizes the need to bridge the gap between *in vivo* and *in vitro* studies to facilitate the transfer of knowledge from the laboratory to practical application in diabetes management.



Bioinformatics



Abhik Sarkar

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Chairperson : Dr. Dwijesh Chandra Mishra



Dr. Dwijesh Chandra Mishra

Title of the Thesis

Development of tool for selective Sweep analysis using artificial intelligence

Natural selection is the key process of evolution. Natural selection especially directional selection plays pivotal role behind genetic hitchhiking mechanism which induces the occurrence of selective sweep. Selective sweep is a biological phenomenon which increases the frequency of the alleles closely linked to the beneficial alleles and non-linked alleles shows decrement in their frequency. From evolutionary aspects to adaptation of newly developed varieties in the environment selective sweep plays crucial role and so analysis of selective sweep has wide importance in evolutionary and population genomics. But most of the existing tools do not provide satisfactory results due to lack of applied approaches as well as lack of implementation of advanced technologies. So, in this research work artificial intelligence-based machine learning algorithms have been implemented as classifier starting with simulated population genomic dataset. Among all machine learning classifiers Random Forest has performed best by ranking through TOPSIS analysis based on evaluation measures like Accuracy, Precision, Recall, Sensitivity etc. and it has performed better than the already existing tools like Sweep Finder, Omega Plus, SweeD, diploS/HIC also. Utilizing this as best model an interactive selective sweep analysis tool has been developed namely “Sweep Discovery Tool” and it had been deployed to the hosting platform “<http://cabgrid.res.in:5599/>”. This tool has the ability to predict selective sweep status among three classes viz. Hard Selective Sweep, Soft Selective Sweep and No Selective Sweep through VCF files as input and this is a user-friendly tool where user can choose the chromosome and region of interest in the specific chromosome to obtain the selective sweep status. The Sweep Discovery Tool will enlighten a new pavement of selective sweep analysis as well as genomic research with optimistic future prospects.



Computer Application



Sakshi Rawat

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Roll No. : 21558
Chairperson : Dr. K. K. Chaturvedi



Dr. K. K. Chaturvedi

Title of the Thesis

Development of web based bibliometric analysis tool for agriculture

The global adoption of digital technology has accelerated the daily data gathering, which has an impact on academic research through rising paper submissions to online databases. Scholars, organizations, and politicians must prioritize identifying and assessing influential research. To manage extensive scholarly data, we employ a technique that originated in library sciences but has now carved out its own distinct place in the realm of research: bibliometric analysis. Bibliometric analysis involves examining and assessing scientific literature through the extraction of vital information, primarily emphasizing quantitative evaluation of publications, citations, and co-authorship networks. This approach aims to pinpoint emerging research domains and trends within articles, while also evaluating journal performance, studying collaboration patterns among research components, and uncovering gaps within the chosen subject domain. However, bibliometric analysis specific to agricultural studies lacks comprehensive coverage. Many major scholarly databases do not encompass most Indian agriculture journals, and a performance indicator that incorporates The National Academy of Agricultural Sciences (NAAS) journal score is absent.

In this study, we developed the Author Performance Indicator (AuthorPerIndic), a score that evaluates an ICAR scientist's productivity based on journal NAAS scores and their authorship. Additionally, we created a novel web tool using Django framework facilitating bibliometric analysis at the author level for ICAR-IASRI scientists. Data is sourced from the ICAR-initiated KRISHI publication repository and processed to meet analysis requirements. The tool employs AuthorPerIndic for performance analysis alongside collaboration and keyword analyses. This tool provides researchers with a systematic way for tracking and evaluating their progress, as well as a chronological picture of their accomplishments. Institutions are capable of selecting financing sources and making informed decisions about promotions. A culture of increasing publication in high-impact journals is also fostered by the tool.



Entomology



Jagadam Sai Rupali

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Roll No. : 21636
Chairperson : Dr. Sagar D.



Dr. Sagar D.

Title of the Thesis

Studies on postmating transcriptional changes in female moths of fall armyworm, *Spodoptera frugiperda* (J.E. Smith)

Fall armyworm (FAW), *Spodoptera frugiperda*, is a highly destructive insect pest causing significant economic losses due to its wide host range, strong dispersal ability, and high reproductive fitness. Current control strategies for managing FAW are challenging due to its high fecundity, mobility, and rapid development of insecticide resistance. Studying the mating-induced gene expression changes enables us to understand the molecular responses that drive adaptations in female reproductive processes. In response to mating in *S. frugiperda*, a total of 13,207 transcripts exhibited differential expression. Among these, 846 (89 upregulated, 757 downregulated) transcripts showed significant expression at 24 hours post-mating. However, at 0 hours post-mating, only four transcripts were notably expressed, all of which were found to be upregulated. GO analysis indicated the majority of the differentially expressed genes were involved in biological processes followed by cellular components and molecular function. Key upregulated genes like cathepsin B, cytochrome P450 6B1, ecdysone oxidase, and ribosome-binding protein 1 play crucial roles in egg development, detoxification, hormone synthesis, and protein production, crucial for successful reproduction. Conversely, immune-related genes such as serine protease inhibitor dipetalogastin-like, attacin, and lysozyme were downregulated, suggesting a strategic balance between resource allocation for reproductive success and immune defense. This phenomenon highlights the dynamic prioritization of energy resources to support reproduction while potentially compromising immune responsiveness. Targeting these key genes and pathways could hold promise for innovative approaches that disrupt reproductive success and population growth, potentially curbing the economic losses caused by this destructive pest.



Fruit Science



Raushan Kumar

Name of the Student : Raushan Kumar
Roll No. : 21655
Chairperson : Dr. Nimisha Sharma



Dr. Nimisha Sharma

Title of the Thesis

Characterization of a set of interspecific citrus hybrids Orangelo (*Citrus maxima* × *Citrus sinensis*)

Twenty-four interspecific citrus orangelo hybrids were characterized based on the DUS guidelines. More than 80% hybrid population had ovate leaf lamina shape. However, two hybrids expressed obovate and SCSH 13-13 and CRH 20-11 showed orbicular and elliptic leaf lamina shape. The largest pedicel length, petal length and diameter of opened flower were observed in SCSH 3-10, while petals were widest in SCSH 9-20. Majority of the hybrids (54.17%) showed spheroid fruit shape, while more than 75% hybrids witnessed green- yellow (RHS N-144A) peel at maturity. The seeds per fruit varied from 8 to 60. Grouping based on morphological traits showed that most of orangelos (21 hybrids) and their parents were clustered together. PCA analysis showed that morphological quantitative traits leaf lamina length, leaf lamina width and their ratio, leaf lamina thickness and pedicel length, accounted for 77.76% of the cumulative variability. Based on the physico-chemical data, all the 24 orangelo along their parents showed two major clusters A and cluster B at similarity value of 0.56. Out of 24 orangelo hybrids, five hybrids namely SCSH 3-10, SCSH 9-20, SCSH 11-15, SCSH 21-10 and CRH 20-11 had better qualitative characters. A total of 50 *de novo* EST-SSR were validated, and 19 primers were polymorphic with a total of 38% polymorphism. The amplicon size ranged from 100 bp in NRCH3 to 300 bp in NRCH49. The trait specific marker NRCH21 had the highest allelic frequency (0.96), while it was lowest (0.52) in NRCH6 and NRCH8. Further, of the 19 primers, highest and lowest PIC values were found in NRCH9 based primers (0.48) and NRCH21 (0.07), respectively. The gene diversity ranged from 0.07 to 0.55, being highest (0.55) in NRCH9. The phylogenetic tree provided the important information regarding genetic relationship in 24 orangelo hybrids with their four parents.



Genetics and Plant Breeding



Jenia Roy

Name of the Student : Jenia Roy
Roll No. : 21663
Chairperson : Dr. Muraleedhar S. Aski



Dr. Muraleedhar S. Aski

Title of the Thesis

Unfolding the complex regulatory network of rust (*Uromyces viciae-fabae*) resistance in lentil (*Lens culinaris* Medik.) using comparative RNA-seq analysis

The study investigated the intricate molecular mechanisms underlying lentil resistance to the harmful rust infection caused by *U. vicia-fabae*. Utilizing RNA-Seq, we examined two genotypes that had been inoculated with rust spores: rust-resistant L4147 and rust-susceptible LLS 18-109. The RNA-Seq method produced useful insights by comparing resistant control (RC), susceptible non-inoculated (SNI), resistant inoculated (RI), and susceptible inoculated (SI) samples. In six comparisons, differentially expressed genes (DEGs) were found, totaling 12,316 DEGs in all possible combinations. In rust-infected plants, functional gene classes related to defense were noticeably impacted. Highlighting metabolic pathways, biosynthesis of secondary metabolites, and plant-pathogen interactions, enriched KEGG pathways shed light on functions of DEGS across all combinations. Notably, several histone-coding genes, R genes, and genes related to ionic activity and metabolic processes showed differential expression, possibly strengthening defense. The number of DEGs was reduced to 34, which included LRR receptor-like kinases, transcription factors (WRKY, TIFY, AP2-EREBP, etc.), pathogenesis-related proteins (PR1-like protein), hormone signaling proteins (GH3 family protein, auxin-induced protein, ethylene-responsive factors, ABA receptors), R proteins (CC-NBS-LRR class), etc. Our protein-protein interaction analysis uncovered intricate connections among these proteins, encompassing cell cycle regulation, hormone signaling, MAPK signaling, suberin biosynthesis etc. and some other non-interactive genes putatively associated with defense responses. The significance of the genes identified in response was highlighted by the validation of 16 genes between RNA-Seq and qRT-PCR results, which confirmed credibility. The study has shed light on the molecular basis of lentil rust resistance.



Microbiology



Barnana Maitra

Name of the Student : Barnana Maitra
Roll No. : 21667
Chairperson : Dr. Minakshi Grover



Dr. Minakshi Grover

Title of the Thesis

Exploring seed endophytic bacteria of pearl millet for plant beneficial traits and abiotic stress tolerance

The present investigation aimed at prospecting the seed endophytic bacteria of pearl millet (*Pennisetum glaucum*) for plant beneficial traits. Seeds of eight Pearl millet cultivars (included popular open pollinated varieties, hybrids, and landraces representing three agro-climatic zones (A1, A and B) were surface sterilized and macerate plated on five different media nutrient agar (NA), R2A, tripticase soy agar (TSA) and two pearl millet flour based media. Highest bacterial population was observed on TSA and NA (copiotrophic media) followed by R2A (oligotrophic media). Highest bacterial population was observed on copiotrophic media. MPMH 21 showed highest population followed by MBC 2, PILI, PC 612, Pusa 1201, HHB 299, MOONCH and PC 701. Eighty-six bacterial colonies were purified characterized for *in vitro* Plant Growth Promoting (PGP) traits, biocontrol potential, osmotic stress tolerance, and extracellular hydrolytic enzymes. The endophytic bacteria exhibited multiple PGP traits with 95%, 43%, 90%, 19%, 34%, 33%, 65% isolates showing IAA, siderophores, ammonia, P, Zn, K solubilization and antifungal activity respectively. The isolates could produce esterase (42%) and pectinase (42%) followed by chitinase (34%), amylase (31%), lipase (30%), protease (27%) and cellulase (26%). These features indicate the seed as a hub of agriculturally and industrially important bacteria.

Based on *in vitro* traits, 38 endophytic bacterial isolates representing eight pearl millet varieties when identified based on 16S rRNA sequence represented 13 bacterial genera including *Acinetobacter*, *Atlantibacter*, *Bacillus*, *Brucella*, *Pantoea*, *Pseudomonas*, *Staphylococcus*, *Stenotrophomonas*, *Exiguobacterium*, *Kosakonia*, *Enterobacter*, *Achromobacter* and *Cronobacter*, indicating structural diversity. *Acinetobacter* was observed in six cultivars indicating its close association with the crop. Twenty-four selected isolates evaluated as seed inoculants in pearl millet cv. PC 701, under moisture deficit (75% FC). Inoculation improved shoot, root length, biomass, chlorophyll, RWC, MSI, antioxidant status under stress conditions. To conclude, endophytic bacteria exhibited potential to alleviate the abiotic stress effects in pearl millet crop.



Molecular Biology and Biotechnology



Usha M.S.

Name of the Student : Usha M.S.
Roll No. : 80022
Chairperson : Dr. Vinay Kumar



Dr. Vinay Kumar

Title of the Thesis

Isolation and characterization of bacterial endophytes having antimicrobial potential against *Sclerotium rolfsii* in chickpea.

Collor rot, caused by fungal pathogen, *Sclerotium rolfsii*, is causing huge economic loss to chickpea (*Cicer arietinum* L.). Bacterial endophytes have emerged as eco-friendly alternative approach to chemical management for mitigation of such diseases. In this study, total 108 bacterial endophytes were isolated from five plant tissues of chickpea namely root (20), stem (39), leaf (35), flower (6) and nodule (8). Morpho-biochemical tests and 16s rDNA sequencing was employed for identification of isolates. Gram staining showed 77 isolates as Gram positive and 31 as Gram negative. The isolates were evaluated for Plant growth-promoting (PGP) traits viz., phosphate solubilization, production of siderophore, IAA, urease, cellulose, nitrate reduction activity, citrate utilization and protease production in which 7, 35, 36, 22, 29, 35, 30 and 76 were positive, respectively. In dual culture assay, 21 isolates showed antagonistic activities against *Sclerotium* with fungal growth inhibition ranging from 25 to 60%. These isolates were found to harbor genes for lipopeptides viz., iturin, surfactin, fengycin, and bacillomycin D. Based on PGP and *in-vitro* antagonistic activities, five isolates namely NIBSM_CpR8, R20, NIBSM_CpS5, S25 and NIBSM_CpL12 were selected for *in-planta* validation. Chickpea plants bio-primed with selected endophytes showed better survival rate against *Sclerotium* pathogen with protection of 25-75% over control. Isolate NIBSM_CpS5 was found best in imparting protection against *Sclerotium*. During differential expression of genes in tripartite interaction (Chickpea- *Sclerotium*- Endophyte) study, there was increased expression of genes viz., NAC transcription factor, CDPK, linoleate 9S-lipoxygenase (LOX) and chitinase in endophyte bio-primed and pathogen-inoculated plants during the early stages (24-48 h) of pathogen infection indicating role endophyte-mediated resistance through enhanced plant's immunity through modulating phytohormone, signalling pathways and secondary metabolite production. The findings suggest that bacterial endophytes identified to have antimicrobial could be integrated into disease control strategies.



Plant Genetic Resources



Jyotsna Verma

Name of the Student : Jyotsna Verma
Roll No. : 21686
Chairperson : Dr. Kuldeep Tripathi



Dr. Kuldeep Tripathi

Title of the Thesis

Assessment of genetic variability of diverse blackgram (*Vigna mungo* (L.) Hepper) germplasm conserved in Indian National Genebank for pre-harvest sprouting tolerance

Blackgram seeds are susceptible to pre-harvest sprouting (PHS) due to absence of fresh seed dormancy (FSD). PHS degrades the quality of seeds even though they are protected inside pods. Loss of adequate seed dormancy during domestication is the primary reason behind PHS under humid weather conditions. Therefore, it is crucial to develop blackgram cultivars with short (10–15 day) FSD periods to reduce PHS loss. To characterize PHS, 112 blackgram accessions were analyzed for different seed and pod morphological traits viz., pod length, pod width, seed length, seed width, water imbibition by pods and seeds, seed germination in pod, fresh seed germination, alpha-amylase activity and hard seededness. α -amylase enzyme activity was used as the indicator of dormancy level. A wide range in PHS tolerance and FSG was observed, and 13 accessions were found to be PHS-tolerant (PHS value <10%). Correlation studies revealed that PHS was positively correlated with water imbibition by pod, water imbibition by seeds and fresh seed germination. An indicator of PHS, seed germination in a pod, ranged from 2.75% in the accession IC0485641 (highly tolerant to PHS) to 95.85% in the accession Mash 479 (highly susceptible to PHS). PHS-tolerant accessions also exhibited a slow increase in the α -amylase activity, in contrast to PHS-susceptible accessions, which showed a significant rise in α -amylase activity with high FSG and PHS, particularly at 48 and 72 h after germination. These observations indicated that α -amylase activity could be employed as a biochemical marker to assess the FSD and PHS potential of blackgram accessions. The identified PHS tolerant accessions such as IC485641 and IC485425 (PHS<10%) may be used as donors in the *Vigna* improvement programs to develop PHS tolerant varieties after validating the results over multiple seasons and locations.



Plant Pathology



Poulami Basak

Name of the Student : Poulami Basak
Roll No. : 21694
Chairperson : Dr. Malkhan Singh Gurjar



Dr. Malkhan Singh Gurjar

Title of the Thesis

Characterization of *bipolaris sorokiniana*, transcriptome profiling and assessment of bioagents against spot blotch of barley

Spot blotch disease caused by *Bipolaris sorokiniana* is one of the major constraints in barley production. Forty- five isolates were established from diseased samples collected from different locations of Uttar Pradesh and Bihar, India. Characterization based on morphology revealed highest colony diameter of 80.33 mm in BS 36 (Varanasi, Uttar Pradesh) isolate and lowest colony diameter of 19.33 mm in BS 45 (Sultanpur, Uttar Pradesh) isolate. Conidia length ranged from 74.58 μm - 42.05 μm and conidia width ranged from 22.94 μm - 12.18 μm across isolates. Highest sporulation was observed in BS 32 isolate (Varanasi, Uttar Pradesh) and lowest sporulation was observed in BS 13 (Sultanpur, Uttar Pradesh). Analysis of pathogenicity revealed Pusa, Bihar isolates to be highly pathogenic amongst all other isolates. Cross infectivity assays found barley isolate to be less virulent on wheat and wheat isolate to be less virulent on barley. Out of all evaluated genotypes, 3 (EC0328964, IC0393134, IC0446132) were resistant and 5 were moderately resistant. Transcriptome analysis of resistant (EC0328964) and susceptible genotype (EC0578292) revealed a several defense related genes like resistant gene analogs (RGAs), disease resistance protein RPM1, pathogenesis-related protein PRB1-2-like, pathogenesis-related protein 1, thaumatin-like protein PWIR2 and defensin Tm-AMP-D1.2 to be upregulated and exclusively present in resistant genotype. *In vitro* inhibition studies using strains of *Trichoderma* and biocontrol bacteria against *B. sorokiniana* revealed *Trichoderma asperellum* 8686 and *Trichoderma asperellum* 8687 with highest percent inhibition of 71.73% and 71.37% respectively. *In planta* studies with selected biocontrol agents revealed *Bacillus amyloliquefaciens* to be most effective in seed treatment. Post inoculation with biocontrol agents showed *Bacillus amyloliquefaciens*, to be at par with *Trichoderma asperellum* and *Pseudomonas fluorescens*. In conclusion *Bacillus amyloliquefaciens* showed better and consistent results in all the assays.



Plant Physiology



Chanumolu Hari
Gopala Krishna

Name of the Student : Chanumolu Hari Gopala Krishna
Roll No. : 70016
Chairperson : Dr. Jagadish Rane



Dr. Jagadish Rane

Title of the Thesis

Optimization of phenotyping protocol to assess waterlogging induced roots in cowpea (*vigna unguiculata* (L.) walp.)

Cowpea is a favoured crop for intercropping and crop rotations due to its short growth duration and resilience to drought and high temperatures. However, the absence of waterlogging tolerance traits in improved cultivars, primarily bred for yield, quality, and pest resistance, poses a threat to cowpea production. To address this, efficient non-invasive phenotyping tools are crucial for evaluation of cowpea genotypes for waterlogging tolerance traits. Hence, this study was aimed to optimize an affordable and non-invasive phenotyping protocol for assessing waterlogging-induced roots (WIR). The methods optimised for stress imposition, image acquisition, and image analysis could effectively differentiate waterlogging stress-response of cowpea genotypes. Significant genotype variations in WIR architecture and growth rate were revealed by image derived Total Root Length (TRL), Network Area (NA), Convex Area (CA), Volume (Vol) and Median number of roots (MeN) etc. The efficacy of these traits in distinguishing waterlogging-tolerant and intolerant genotypes was validated with conventional parameters. A strong positive correlation between conventional and WIR image features indicated that WIR, playing a role in waterlogging tolerance, can be reliably measured non-invasively. The phenotyping protocol, along with traditional parameters, could help in identification of promising genotypes viz., CG221 and CG121, showcasing enhanced WIR and superior performance under waterlogging conditions. These genotypes also exhibited remarkable recovery from waterlogging. The affordable phenotyping protocol developed in this study promises to serve as an effective phenotyping tool for assessing waterlogging-induced roots in cowpea and promising genotypes like CG221 and CG121 may serve as donors for waterlogging tolerance.



Post Harvest Management



Vathsala V.

Name of the Student : Vathsala V.
Roll No. : 21706
Chairperson : Dr. Charanjit Kaur



Dr. Charanjit Kaur

Title of the Thesis

Ultrasound-Assisted Extraction (UAE) of pectin from citrus peels: Techno-functional and bioactive characterization

There has been a rising trend in the use of environmentally friendly and green methods for sustainable solutions for the valorization of food waste. In the present study, ultrasonic-assisted extraction (UAE) has been optimized for the extraction of pectin from sweet lime and pummelo peels using Response surface methodology (RSM). The optimum conditions of UAE (sonication time of 9.38 min, power of 44.01%, and L:S ratio 46.79:1 at a constant temperature of 40°C) resulted in maximum pectin yield (26.35%) and high galacturonic acid content (69.11%) from pummelo peels. The pectin extracted via UAE was a food-grade pectin with a low degree of methylation (<50%), and high functional quality in terms of total phenolic content and antioxidant activity. The pectin was characterized through FTIR, TGA, rheology, and biological properties. Pummelo peel pectin had superior rheological and gelling properties than sweet lime pectin. Both the pectin demonstrated high biological activity in inhibiting lipid deposition in HepG2 cells and low cytotoxicity in MTT assay. The findings strongly suggest that a low degree of methylation (LMP) from pummelo peel pectin can be used for formulating low glycaemic foods to manage type 2 diabetes and obesity. Fabrication of low-fat mayonnaise using LMP from pummelo peels has been demonstrated. Overall, UAE merits promising prospects in comparison to traditional extraction methods due to its higher efficiency, shorter processing time, and clean operation.



Seed Science & Technology



Tuhina Ghosh

Name of the Student : Tuhina Ghosh
Roll No. : 21710
Chairperson : Dr. Shiv Kumar Yadav



Dr. Shiv Kumar Yadav

Title of the Thesis

Effect of ZnO nano-particle based priming on seed quality enhancement in tomato (*Solanum lycopersicum* L.) under salt stress

The tomato crop is considered one of the most predominant horticultural crops in the world, but abiotic stress, particularly salt stress result in poor plant stand establishment, leading to yield losses. Recently, use of nano-particles priming in agriculture, has received a lot of attention, due to their role in regulating seed metabolism and signaling pathways, germination and seedling establishment. Thus, zinc oxide (ZnO) nanoparticle (NP) was used as a seed priming agent to enhance seed quality of two tomato genotypes (QA001 and QA002) under salinity stress. The genotype, QA001 performed significantly better than QA002 genotype under both control and salinity stress condition. Among the various concentrations and soaking durations applied, tomato seeds primed with ZnO NP @ 750 ppm for 6 h revealed significantly higher germination (92%), seed vigour index I (1399) and seed vigour index II (1813). Salinity stress (50 mM and 100 mM NaCl) remarkably affected the seed quality parameters as well as biochemical traits of 14 days old seedlings of both tomato genotypes. However, nano-priming with ZnO NP @ 750 ppm was found to notably increase germination percentage, seedling dry weight, total seedling length, seed vigour index I and II, speed of germination, chlorophyll content, phenol content, total soluble sugar (TSS) content, soluble protein content, proline content, superoxide dismutase (SOD), peroxidase (POD), catalase (CAT) activity and remarkably decrease the mean germination time, MDA content over the unprimed seed in both the genotypes under both control (no-stress) as well as salinity stress (50 mM and 100 mM NaCl) conditions. Overall, nano-priming with ZnO NP @ 750 ppm (6 h) significantly boosted the chlorophyll production, antioxidative mechanism and osmotic adjustment, which in turn lower the ROS accumulation and peroxidation of lipid in cell membrane thereby could be used for alleviating the detrimental effect of salinity stress in tomato.



Soil Science



Alapati Nymisha

Name of the Student : Alapati Nymisha
Roll No. : 21712
Chairperson : Mr. Kapil A. Chobhe



Mr. Kapil A. Chobhe

Title of the Thesis

Synthesis and evaluation of bioaugmented zinc oxide coated urea product for its efficacy under wheat crop

Zinc (Zn) is essential for plant, animal, and human development, but Zn deficiency in salt-affected soils harms plant growth and development. Enhancing bioavailable Zn requires solubilizing fixed Zn and reducing fixation of applied Zn fertilizers. Zinc-coated urea improves N and Zn utilization, while cost and availability issues hinder zinc sulfate ($ZnSO_4$) adoption. Insoluble zinc oxide (ZnO) with innovative dissolution techniques and Zn solubilizing bacteria (ZSB) shows potential. In wheat, a key carbohydrate and protein-rich crop, optimal N and Zn management are vital. The study embarks on synthesizing and evaluating bioaugmented Zn oxide-coated urea products, tailored for wheat cultivation. Objectives encompass evaluating Zn solubilizers, synthesizing and characterizing ZnO and Zn solubilizer coated urea, and assessing the impact of these formulations on wheat yield and the uptake of N and Zn. Among 20 bacterial isolates, four strains—*Priestia aryabhatai* WSB119, *Stenotrophomonas pavanii* WSB22, *Bacillus aerius* WSB68, *Klebsiella pneumonia* M35—displayed superior Zn solubilization potential. Characterization studies revealed the uniformity of coating on urea granules through SEM, crystallinity imparted due to ZnO through XRD. Interestingly, FTIR spectra also revealed some unidentified peaks representing low molecular weight carboxylic acids which were believed to be secreted by zinc solubilizing bacteria that was used for coating of urea. Application of bioaugmented zinc oxide coated urea led to enhanced nutrient use efficiency (N and Zn) in wheat. Despite the insolubility of ZnO, effective urea coating can be achieved through binder-enhanced adherence and incorporation of Zn solubilizing organisms. Notably, selected strains for product formulation exhibited a shelf life of two months at 4°C and room temperature. Yield results substantiate the promise of coated urea, demonstrating comparable yields at 75% N application to those achieved through 100% N urea application. In synthesis, this research unearths the potential of bioaugmented ZnO coated urea as an efficacious nutrient supply strategy.



Vegetable Science



Luhana Sohamkumar
Chetandas

Name of the Student : Luhana Sohamkumar Chetandas
Roll No. : 21720
Chairperson : Dr. Shrawan Singh



Dr. Shrawan Singh

Title of the Thesis

Biochemical and molecular studies of curding and flowering behaviour in cauliflower

Cauliflower is a highly thermosensitive vegetable crop consumed for its pre-floral fleshy apical meristem, i.e., curd. Based on the temperature requirement for curd initiation, it is classified into early (20–27 °C), mid-early (16–20 °C), mid-late (12–16 °C), and late (10–16 °C) groups. The regulation of curding and flowering involves complex pathways influenced by internal and environmental factors, with temperature, hormones, and their impact on gene expression playing significant roles. The present investigation aimed to investigate the effects of sowing time on developmental transitions and morphological traits, analyze changes in endogenous gibberellins at different developmental stages, and study the expression patterns of the key curding and flowering genes. A total of twelve genotypes (three per group) were sown five times at monthly intervals and observed for eight morphological traits and seven developmental transitions. Higher temperatures promoted juvenility but delayed curd initiation, while lower temperatures impacted the morphology of tropical cauliflower. Analysis of endogenous gibberellins was performed in one variety per group at six developmental transitions, starting from seedling to bolting stages, and at four time points. A higher endogenous GA₃ concentration at the bolting stage, seedling stage, and curd initiation stage suggested its role in stalk elongation. GA₃ content at the full curd stage was higher in curd tissues than leaf tissues, while at the bolting stage, it was similar in leaf and stalk tissues. Expression analysis of fourteen curding and flowering-related genes was performed at four time points, the same as in the Gibberellins study. Expression of *BoVRN2*, *BoFUL-d*, *BoREM-1*, *BoFT*, *BoCAL*, *CCE1*, *BoTFL1*, and *BoLFY* genes showed significant differences between Indian and snowball (European) cauliflower genotypes. The information generated through the present investigation will help in understanding the role of the investigated determinants of curding and flowering in the cauliflower to widen its growing plasticity.

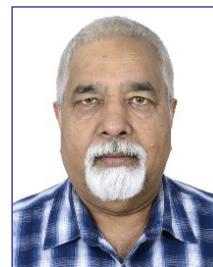


Water Science and Technology



Keerthana Maveril M.

Name of the Student : Keerthana Maveril M.
Roll No. : 21726
Chairperson : Dr. Manoj Khanna



Dr. Manoj Khanna

Title of the Thesis

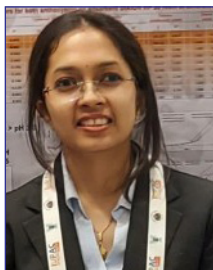
Impact of drip fertigation on GHG emission and crop productivity of tomato

Drip irrigation is crucial for successful crop cultivation, addressing global challenges like water scarcity, food security, and poverty. Acknowledged for efficiency, drip systems minimize losses, enhancing irrigation water application efficiency. The impact of water management on greenhouse gas (GHG) emissions in different crops is significant. Implementing effective irrigation scheduling reduces over-irrigation, while advanced methods like drip irrigation curb water wastage and GHG discharge. Additionally, skillful fertilizer management plays a role in limiting nitrous oxide emissions resulting from excessive use. The present study focuses on understanding crop response, GHG emissions (specifically N_2O), and water productivity in drip-fertigated tomato crops subjected to various irrigation and fertilizer treatments. The field experiment conducted at PFDC, Water Technology Centre research field, ICAR-IARI, New Delhi during the rabi season of 2022-2023, aimed to assess the crop response and N_2O emissions under different fertilizer and irrigation levels. Three irrigation levels-Drip with 100% ETc, Drip with 80% ETc, and surface irrigation flooding along with three fertilizer doses-100% RDF, 80% RDF, and no fertilizer were tested, each replicated three times. CROPWAT 8.0 monitored irrigation scheduling, while nitrous oxide emissions were analyzed using gas chromatography. Results indicated that treatment T_2 -100% ETc x 100% RDF exhibited the highest yield increase (46.42 t/ha), closely followed by T_5 -80% ETc x 100% RDF with a non-significant difference of only 2.5%. T_5 also demonstrated 21% higher irrigation water productivity and 22% better economic water productivity compared to T_2 , despite using less water. Surface irrigation resulted in higher nitrous oxide emissions compared to drip irrigation, emphasizing the environmental benefits of efficient water and fertilizer management. Notably, the study suggests that maintaining yields in 80% ETc is achievable with reduced GHG emissions, offering a sustainable approach to crop cultivation.

Ph.D.
Thesis Abstracts



Agricultural Chemicals



Anindita Paul

Name of the Student : Anindita Paul
Roll No. : 10726
Chairperson : Dr. Supradip Saha



Dr. Supradip Saha

Title of the Thesis

Appraisal of resin assisted purification mechanism of anthocyanins

Anthocyanin, a vibrant food colorant, has wide variety of health benefits. Anthocyanins present both in acylated (AA) and non-acylated (NA) form although the frequency of NA is more in nature. Its purification poses a major challenge. In quest-of cost-effective anthocyanin purification technology, adsorption mechanism of adsorbent and ion exchange resin was explored and evaluated. Six macroporous resins were screened for preferential adsorption of AA (black carrot, purple cabbage) and NA (rose, black rice). Chemo-profiling of anthocyanin extracts through UPLC-TOF-HRMS revealed the molecular identities of the anthocyanins. OPTIPORE-L-493 is the best resin in adsorbing AA (4.01 mg C₃G eq g⁻¹) not phenolics and is equally suitable in adsorbing NA and phenolics. SEM, FT-IR spectroscopy and confocal microscopy-based characterizations confirmed the adsorption process occurred at pore spaces of resins. Pseudo-2nd-order kinetic model explains better sorption kinetics and Freundlich isotherm model explains competitive adsorption ($R^2 > 0.901$, least χ^2 , AIC_c) is the predominant for adsorptions of both anthocyanin, phenolics except sugars. Sugar was the weakest adsorbed on resin. Molecular-simulation study predicted that the thermodynamic stability is the highest for AA (-760.432 kcal mol⁻¹) and least for phenolics (-467.677 kcal mol⁻¹). Adsorption of both type of anthocyanins on both the resins was maximum at pH6.0-7.0 and temperature variation didn't affect the adsorption behavior. Thermodynamic study affirmed the adsorption process is endothermic, spontaneous and random in nature at resin surface. Ultrasonication-assisted anthocyanin adsorption, achieved 90.2% with faster rate than conventional one, was optimized through RSM and genetic-algorithm approach. Real-time study revalidated that the pure anthocyanin gets preferably adsorbed (C₃G-81.3%) with phenolics (Q₃G-91.4%). Column-assisted dynamic method of purification yielded highest purity improvement in black carrot (243.6%). With the standardized investigated parameters and resin, significant improvement in anthocyanin purity can be achieved for its commercial exploitation and it is predicted to be more for acylated-anthocyanin than non-acylated one.



Agricultural Economics



Jaiprakash Bisen

Name of the Student : Jaiprakash Bisen
Roll No. : 10562
Chairperson : Dr. Shiv Kumar



Dr. Shiv Kumar

Title of the Thesis

A Multi-market and multi-regional analysis of important cereals in India: A partial equilibrium approach

The global food system is at the precipice of dire consequences due to climate change, ecological imbalance, increasing food inequality, and other challenges. India, with its rapid population and economic growth, is not exempt from these issues. Understanding the market dynamics and the trajectory of the food situation becomes crucial under the influence of socio-economic, physical, technological, and institutional factors. This study focuses on India's ability to navigate these challenges, particularly in predicting the future trends of food grain supply and demand. Using a cereal outlook model, the study projects market scenarios for rice, wheat, and maize crops up to the year 2040–2041. To forecast the next 23 years, the analysis delves into historical data spanning 37 years, employing a multi-commodity, multi-market, partial equilibrium approach. Two simulations explore the impact of real cost of cultivation and real Minimum Support Price (MSP) growth on various aspects, including area, production, consumption, trade, and stocks.

The study also considers key policies affecting grain trade and, due to data constraints, treats the nation as a single entity for estimating demand, ending stocks, and trade. The market outlook predicts a surplus production and rising demand for rice, wheat, and maize. For instance, rice consumption is expected to reach 117.59 million tons, with production growing from 106.22 million tons in 2017–18 to 139.54 million tons by 2040–41. Similarly, wheat demand is projected to increase by 42.12 million tons, reaching 115 million tons in production. Maize is forecasted to experience a 33.06% rise in demand, equivalent to 6.26 million tons, and a 33% increase in supply, amounting to 9.107 million tons. The study advocates for a Cereal+ farming system, emphasizing diversification for nutritional security, rationalization of excess cereal cultivation area, long-term agricultural infrastructure development, promotion of secondary agriculture, strengthening food value chains, and achieving allocative efficiency in food distribution. This comprehensive approach aims to address the complex challenges posed by the evolving food landscape in India.



Agricultural Engineering



Aseeya Wahid

Name of the Student : Aseeya Wahid
Roll No. : 11398
Chairperson : Dr. S.K. Giri



Dr. S.K. Giri

Title of the Thesis

Development of vacuum impregnation technology for shelf-life enhancement of vegetables

Fresh vegetables are highly susceptible to spoilage, leading to texture loss, diminished nutritional quality, and color deterioration. To address these issues, this study investigated the effects of impregnation process parameters on improving the quality and shelf-life of selected vegetables using a vacuum impregnation (VI) system. A vacuum impregnation system comprising a vacuum chamber, a high- vacuum pump, and an automation setup was developed, with an operating cost of Rs. 12.64/Kg, as per the cost economic analysis. Broccoli florets, coriander leaves, and iceberg lettuce, were impregnated with a solution mixture of ascorbic acid and calcium chloride. To optimize the VI system process variables, response surface methodology (RSM) was applied, utilizing a 4-factor Box-Behnken design. The variables considered included vacuum pressure, vacuum time, solution concentration, and restoration time. The optimization parameters were total phenolic content (TPC), total flavonoid content (TFC), ascorbic acid content (AAC), free radical scavenging activity (FRSA), total chlorophyll content (TCC), and carotenoid content (CC). Additionally, artificial neural network (ANN) modelling was performed, and the predicted values from both RSM and ANN were compared using six standard error functions. The optimized conditions for vacuum impregnation of broccoli florets were 0.2 bar (20Kpa) vacuum Pressure, 11 min of vacuum time, 12 min restoration time and with a concentration of 1.5%. Corresponding to these variables, the values of TPC, TFC, AAC, TCC, FRSA and CC were 297.58 mg/100g, 11.22 mg/100g, 359.92 mg/100g, 1.21 mg/g, 79.77% and 8.58 mg/g, respectively with the overall desirability of 0.896. The optimized conditions for vacuum impregnation of coriander leaves were 0.4 bar (40Kpa) vacuum Pressure, 3 min of vacuum time, 14 min restoration time and a concentration of 0.5%. Corresponding to these variables, the values of TPC, TFC, AAC, TCC, FRSA and CC were 218.48 mg/100g, 9.7 mg/100g, 411.03 mg/100g, 21.52 mg/g, 89.98% and 3.57 mg/g, respectively with the overall desirability was 0.80. The optimized conditions for vacuum impregnation of iceberg lettuce were 0.5 bar (50Kpa) vacuum Pressure, 3 min of vacuum time, 15 min restoration time and a concentration of 1.5%. Corresponding to these variables, the values of TPC, TFC, AAC, TCC, FRSA and CC were 126.5 mg/100g, 2.33 mg/100g, 203.5 mg/100g, 4.83 mg/g, 83.37% and 2.94 mg/g, respectively with the overall desirability of 0.787. The vegetables impregnated under the optimized conditions were subjected to storage studies at two different temperatures (5°C and 25°C) and with various packaging materials, including PET punnets, LDPE pouches, and shrink wrap. A comparative analysis was conducted with fresh untreated samples stored under identical conditions.



Agricultural Extension Education



Aiswarya S.

Name of the Student : Aiswarya S.
Roll No. : 11195
Chairperson : Dr. R.N. Padaria



Dr. R.N. Padaria

Title of the Thesis

An analytical study on livelihood and climate change adaptations among the communities of biosphere reserves and heritage zones

A study was conducted with exploratory and ex post facto research designs to examine the climatic vulnerability, socio-economic and ecological concerns, and effectiveness of indigenous communities' management of Nilgiri Biosphere Reserve (NBR) and Agasthyamalai Biosphere Reserve (ABR) in the Western Ghats. The study also investigated the livelihood strategies, adaptation and conservation behavior, and community participation within the indigenous communities of NBR and ABR. Eleven districts from Kerala, Karnataka, and Tamil Nadu were chosen proportionately, considering the coverage of BRs within these areas, with a total sample size of 1656 households. Vulnerability Index developed by the Shannon's Entropy Method, showed households of NBR (VI=0.563) to be more vulnerable to climate change as compared to ABR(VI=0.481). Analytical Hierarchy Process based prioritization of enlisted 20 adaptation strategies of the indigenous communities ranked 'Adjustment in Crop Calendar' (Overall Priority=0.11) first in NBR(Consistency Ratio=0.017), while 'Crop Diversification'(Overall Priority=0.10) in ABR (Consistency Ratio=0.002. The indigenous communities depending on the forest-based livelihood strategy were found to be food insecure (Herfindahl–Hirschman Index =1.42), in contrast to the business-based (Herfindahl–Hirschman Index =2.31) and crop-based (Herfindahl–Hirschman Index =1.91) livelihood strategies. Thematic analysis mapped 25 socio-economic and ecological concerns and further human-wildlife conflict was identified as the major concern of NBR and ABR with TOPSIS score of 87.89% and 84.67%, respectively. Protected Motivation Theory-Trans Theoretical Model was employed to assess the conservation behavior of indigenous communities. The results of Structural Equation Modelling and Generalized Linear Model revealed that perceived severity ($\lambda_{NBR}=0.868$, $\lambda_{ABR}=0.712$) response efficacy ($\lambda_{NBR}=0.710$, $\lambda_{ABR}=0.889$), perceived vulnerability ($\lambda_{NBR}=0.759$, $\lambda_{ABR}=0.667$) and self-efficacy ($\lambda_{NBR}=0.429$, $\lambda_{ABR}=0.821$) affected positively and significantly the conservation behavior, whereas the response cost ($\lambda_{NBR}= -0.558$, $\lambda_{ABR}=-0.767$) affected conservation behaviour negatively. Application of Management Effectiveness Tracking Tool showed that the indigenous communities' management effectiveness of NBR(Management Effectiveness Score=8) to be higher as compared to ABR (Management Effectiveness Score=6). The major success factors governing the effective management of biosphere reserve were found using the Fuzzy Cognitive Mapping as equity, efficiency, ecological sustainability, decentralization, interests and incentives. Finally, an e-learning module was developed and validated using Dick and Carey Model for the capacity building of stakeholders in effective biosphere reserve management.



Agricultural Physics



Ram Narayan Singh

Name of the Student : Ram Narayan Singh
Roll No. : 10968
Chairperson : Dr. P. Krishnan



Dr. P. Krishnan

Title of the Thesis

Assessment of wheat stripe rust and chickpea wilt through thermal and optical remote sensing

Reliable and quick assessment of plant disease is essential for minimizing losses and for ensuring food security. Field experiments on wheat yellow rust and chickpea wilt were conducted for 2 and 3 years, respectively, for disease assessment using thermal and optical remote sensing. Biophysical parameters were also measured at regular intervals along with Normalize Difference Vegetation Index (NDVI) and visual scorings of disease severity in both crops. Supervised image classification was performed to estimate yellow rust severity. Artificial Intelligence (AI) based Machine learning (ML) models were employed to predict disease severity and predict crop yield based on biophysical parameters and image derived indices at different growth stages in both crops. Results revealed that the LAI, RWC, MSI, photosynthesis, stomatal conductance, transpiration, NDVI, and crop yield in both crops showed a consistent and similar trend of decreasing values with increasing levels of disease severity at all growth stages. The thermal image derived canopy temperature of both crop increased with crop diseases severity. Our results demonstrated the potential of thermal and visible imaging techniques to estimate stripe rust severity with good accuracy. For both visible and thermal images used in this study, support vector machine gave the best estimates of the rust severity with R^2 above 0.85 and accuracies above 98% for both thermal and visible images. Cubist was the best model to predict wheat yellow rust severity. Our results indicated that the model combination techniques improved the prediction accuracy of wilt severity over individual ML models. Least Absolute Deviation combination technique was the best predictor of wilt severity. ML models used in our study were also able to make good predictions of yield under diseased conditions. The present study will be useful to farmers and policy planners for guidance on effective resource allocation. For researchers, it offers valuable insights into using thermal and optical imaging for plant disease assessment.



Agricultural Statistics



Sandip Garai

Name of the Student : Sandip Garai
Roll No. : 11710
Chairperson : Dr. Ranjit Kumar Paul



Dr. Ranjit Kumar Paul

Title of the Thesis

A study on wavelet-based nonlinear time series models for capturing volatility in agriculture

This study explores the use of wavelet-based models for capturing volatility in the agricultural domain. It develops and evaluates wavelet-based artificial neural network (ANN) and support vector regression (SVR) models to improve the accuracy of capturing volatility in agriculture. The research discusses traditional statistical methods and newer approaches utilizing wavelet-based and complete ensemble empirical mode decomposition with adaptive noise (CEEMDAN) methods. It also explores the potential of artificial intelligence and machine learning algorithms, including ANN and SVR. The study prepares the data by ensuring its suitability for modeling through tests for stationarity, normality, non-linearity, and autoregressive conditional heteroscedasticity-Lagrange multiplier (ARCH-LM). It employs feature selection using multivariate adaptive regression splines (MARS) before fitting the wavelet and CEEMDAN decomposed subseries into ANN and SVR models. To optimize the combination of predicted subseries and improve the final prediction of the original series, optimization technique such as particle swarm optimization (PSO) is employed. The proposed wavelet-based models are evaluated using different error functions and model confidence set (MCS)-based tests to assess their accuracy in capturing volatility. The simulation study, utilizing Monte Carlo technique, provides insights into the relationship between degree of volatility and the optimal filter-level combination. To facilitate practical implementation and enhance reproducibility, three R packages have been developed: 'WaveletML', 'CEEMDANML', and 'WaveletMLbestFL'. The developed models demonstrated the effectiveness in capturing underlying patterns, nonlinear relationships and precisely representing volatility. Feature selection technique like MARS and optimization technique like PSO further enhance the accuracy of volatility capture. The findings also emphasize the importance of selecting appropriate wavelet filters and levels of decomposition based on dataset characteristics and provide a more objective and generalized approach to use the technique. The availability of the developed R packages facilitates wavelet and CEEMDAN-based analysis in various domains, supporting decision-making in the agriculture sector and promoting sustainable practices.



Agronomy



Kamlesh Kumar

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Dr. C.M. Parihar

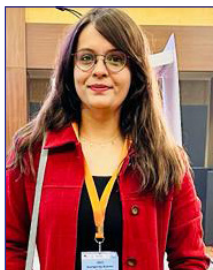
Title of the Thesis

Modelling the impact of tillage and nitrogen management on yield and nitrogen dynamics in a long-term conservation agriculture-based maize-wheat system

A field experiment was conducted at the research farm of ICAR-IARI, New Delhi, during the *kharif* and *rabi* seasons of 2020-21 and 2021-22. Results showed that both tillage and nitrogen management options had a significant impact on growth, yield, nitrogen and radiation use efficiency of maize and wheat. Conservation agriculture (CA)-based plots recorded the highest leaf area index-LAI, grain, and biomass yield for both crops. Among nitrogen management options, N150 and Urea Super Granules-USG recorded the highest crop productivity and profitability. The Decision-Support System for Agro-technology Transfer-DSSAT-crop simulation model-CSM (DSSAT v 4.8) accurately simulated crop phenology, LAI, crop growth, grain and biological yield. The simulated maize grain yields were in accordance with measured values (with prediction error ranging from 0 to 3%), except for nitrogen control-N0 treatments in conventional tillage-CT and zero tillage-ZT. Also in succeeding wheat crop, the DSSAT-CSM model exhibited good accuracy in simulating the crop phenology (with less than 2 days variation in 50% flowering), grain and biomass yield (RMSE 336 kg/ha and 649 kg/ha, respectively), and LAI (RMSE 0.28 & normalized-RMSE; nRMSE 6.69%). Further, the simulation results were aligned with the observed soil nitrate concentration across treatments of both crops. The model accurately captured the differences in nitrate concentration among CT and ZT under different nitrogen management options, demonstrating its ability to predict the dynamics of nitrate in soil. Both the crops showed a substantial increase in nitrogen uptake during the initial days, with a sharp increase observed after the application of fertilizer. The model's predictions were consistent with this trend. The model precisely simulated different appendages of nitrogen dynamics which indicated the robustness and reliability of the model. This study highlights the importance of adopting CA practices along with N150 and USG as nitrogen management options for improving maize and wheat yield and profitability.



Biochemistry



Simardeep Kaur

Name of the Student : Simardeep Kaur
Roll No. : 11464
Chairperson : Dr. Suresh Kumar



Dr. Suresh Kumar

Title of the Thesis

Deciphering miRNome modulation at reproductive stage drought in rice genotypes

Drought tolerance is a complex/multigenic trait controlled by a network of genes, which is fine-tuned by subtle coding/non-coding regulatory mechanisms to mitigate the deleterious effects of drought stress. Reproductive stage drought stress occurs at panicle initiation stage which results in reduced seed-set/grain filling, deteriorated grain quality, and lower yield. MicroRNAs (miRNAs) are one of the non-coding regulators that control gene expression at post-transcriptional level by suppressing the translation process or cleaving the mRNA. Thus, to identify the reproductive stage drought-responsive novel as well as known miRNAs in contrasting rice genotypes, comparative miRNome and transcriptome analyses were performed. SmallRNA libraries for panicle and root tissues of drought-tolerant [Nagina 22 (N-22)] and -sensitive (IR-64) rice genotypes grown under control and reproductive stage drought stress were sequenced using Illumina SE50 bp chemistry. A total of 128 known and 121 novel miRNAs expressed in panicle, while 270 known and 91 novel miRNAs expressed in root of contrasting rice genotypes were identified as differentially expressed miRNAs. Significant alterations in expression level as well as the number of known and novel miRNAs were observed in drought-tolerant (N-22) genotype compared to that in the drought-sensitive (IR-64) genotype. The target of novel miRNA included 409 and 237 genes in panicle and root tissues, respectively, with majority of them belonging to drought-responsive transcription factors involved in metabolic/developmental processes, photosynthesis, panicle and grain development, phytohormonal-crosstalk, root system development via auxin signaling. Validation of the differentially expressed miRNAs as well as their target genes, performed using an independent set of samples, confirmed their expression pattern. Based on the gathered information, the functions of miRNAs in controlling gene expression at reproductive stage drought in rice has been proposed, which might be useful in the genetic manipulation of rice towards the development of climate-smart crops for sustainable food production.



Bioinformatics



Sharanbasappa

Name of the Student : Sharanbasappa
Roll No. : 11739
Chairperson : Dr. Dwijesh Chandra Mishra



Dr. Dwijesh Chandra Mishra

Title of the Thesis

Computational intelligence in the discovery of natural products from agriculturally important metagenomics data

Metagenomics faces a formidable challenge in reconstructing individual genomes from complex DNA mixtures. Binning, a pivotal process in this field, involves organizing sequences from diverse microorganisms and forms the basis for Natural Product (NP) identification, extracting valuable insights from metagenomic data. This study uniquely addresses metagenomics binning and NP discovery problems, and emphasizes their practical implications in agriculturally significant datasets. Introducing innovative binning approaches, Deep Embedded Clustering (DEC) and Variational Autoencoders (VAE), this research showcases their superior performance compared to existing methods. Moving beyond binning, the study delves into NP identification from identified bins of metagenomics data, exploring five NP classes—PKS, NRPS, Terpenes, RiPP, and PKS-NRPS hybrids—utilizing data from the MiBIG database. Protein sequences from each file were extracted, and sequences under the same BGC ID were combined. Physicochemical properties were calculated, and sequence embeddings were generated using NLP techniques like CountVec, TFIDF, and Word2Vec specific to each NP class. An integrated feature matrix was created by merging physicochemical properties and generated embeddings. Then this matrix was used for training and testing nine ML models including Logistic Regression (LR), Naïve Bayes (NB), Decision Tree (DT), RF, KNN, XGBoost, SVM, ANN, and CatBoost. The study explored data balancing techniques, with SMOTE and without SMOTE, and employed Grid Search for parameter optimization. This led to six datasets and 54 models. The LR model, using TFIDF with SMOTE, emerged as the most effective, achieving an accuracy of 0.96, AUC of 0.9912, and other strong metrics. With the proposed approach, we developed an AI-based tool called NaturePred (<http://login1.cabgrid.res.in:5101/>), for NP class prediction and protein physicochemical property calculation. Applied to a genuine Agriculturally Important Metagenomics dataset which is collected from Mustard soil Rhizosphere in the Mau district of UP, the study reveals a rich presence of more than 40% RiPPs signalling robust plant-microbiome interactions and soil health.



Entomology



K. Chandrakumara

Name of the Student : K. Chandrakumara
Roll No. : 11759
Chairperson : Dr. Mukesh K Dhillon



Dr. Mukesh K Dhillon

Title of the Thesis

Elucidating biological and biochemical interaction between popular cultivars of *Brassica juncea* (L.) Czern & Cross. and *Lipaphis erysimi* (Kaltenbach)

The current investigation revealed significant differences for host selection, population build-up, developmental and reproductive biology, bionomics of *Lipaphis erysimi*, constitutive and induced nutritional, anti-nutritional, photosynthetic pigments and the defense enzymes in buds and siliquae of the test *Brassica juncea* cultivars. The aphid preference, resistance index, developmental periods, mean generation time and doubling time were significantly longer, while fecundity, survival, intrinsic and finite rates of increase, and net and gross reproductive rates were significantly lower on RH 0406, RLC 3, DRMR 150-35, RH 749, RH 725, DRMR 150-35, Pusa Mustard 25, NRCHB 101, Pusa Mustard 26, Pusa Mustard 27, Pusa Mustard 30 and Pusa Tarak, except in a few cases. Further, the constitutive and induced levels of different phytochemicals were significantly greater in NRCHB 101, RLC 3, RH 749, DRMR 150-35, Pusa Mustard 26, Pusa Mustard 27, DRMR 1165-40, Pusa Mustard 30 and RH 725. The aphid-induced levels of total sugars, tannins, total chlorophyll, total glucosinolates, FRAP, AP, APX, PAL and TAL levels in *B. juncea* cultivars showed significant association with host preference and bionomics of *L. erysimi*. However, the regression analysis revealed that the total sugars, phenols, antioxidants, FRAP, chlorophyll B, total chlorophyll, catalase, TAL and myrosinase content in buds and siliquae of test *B. juncea* cultivars contributed to 40.11 to 85.30% variability for host preference, multiplication rate and developmental biology, indicating their defensive role against *L. erysimi*, thus could be used as biochemical markers for identifying aphid-resistant mustard genotypes. Overall, DRMR 150-35, RLC 3, NRCHB 101, Pusa Mustard 27, RH 749, Pusa Mustard 28, Pusa Mustard 25 and RH 0406 have shown adverse effects on host preference, population build-up, development, survival and reproductive potential of *L. erysimi*, have greater levels of induced plant biochemicals and defense enzymes, thus could be used in *Brassica* improvement program for sustainable crop production.

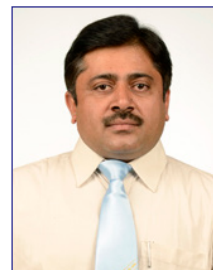


Environmental Sciences



Gayathri J.

Name of the Student : Gayathri J.
Roll No. : 11494
Chairperson : Dr. D. K. Sharma



Dr. D. K. Sharma

Title of the Thesis

Impact of elevated ozone, carbon dioxide and their interaction on pollination ecosystem services in Indian mustard

Tropospheric ozone (O_3) is a phytotoxic air pollutant and CO_2 , a potent GHG escalating due to human activities. Thus, the study aimed to quantify the impacts of elevated O_3 (65 ± 10 ppb) and CO_2 (550 ± 10 ppm) with interaction ($O_3 * CO_2$) on pollination ecosystem services of Indian mustard under free air ozone and carbon dioxide enrichment. Sucrose, sulfur and amino acids content declined in eO_3 and eCO_2 resulting in reduced pollinators' attraction in the pistil metabolomics study. Stigma was receptive for 4 days in eO_3 , 5 days in $eO_3 * CO_2$, 6 days in eCO_2 and 7 days in ambient. Under eO_3 , pollen was viable till 3 days with fewer numbers and in eCO_2 and $eO_3 * eCO_2$ viable pollens thrived till 4 days. The total antioxidant capacity of pollen and pistil was high in $eO_3 > eO_3 * eCO_2 > eCO_2$. Photosynthetic activity, stomatal conductance and seed yield declined by 17%, 32% and 28% under eO_3 . CO_2 enrichment nullified the O_3 effects on yield by a maximum of 11% and increased the photosynthetic rate in eCO_2 (12%). The eO_3 effects were offset by eCO_2 which acts as a defensive mechanism to avoid the entry of O_3 into leaf tissues and restrict the production of reactive oxygen species. Seed quality (protein, sulfur, glucosinolates and fatty acids) declined in eO_3 followed by interaction and eCO_2 whereas the seed yield and oil quantity declined in eO_3 and increased in eCO_2 . The provisioning ecosystem services revealed that monetary loss was high in eO_3 (₹-31,269/ha) followed by the interaction (₹-18,939/ha) and gain was obtained in eCO_2 (₹17,849/ha). Pollination ecosystem services loss was high in eO_3 (₹-32,088/ha) followed by $eO_3 * eCO_2$ (₹-16,397/ha) and elevated CO_2 (₹-3,907/ha). Pollination service is a unique ecosystem service and valuation provides the primary idea to help policymakers evaluate the monetary loss resulting from future climatic conditions of tropospheric ozone and CO_2 enrichment levels.



Floriculture and Landscaping



Uzma Mehraj

Name of the Student : Uzma Mehraj
Roll No. : 11254
Chairperson : Dr. Kanwar Pal Singh



Dr. Kanwar Pal Singh

Title of the Thesis

Induction of doubled haploids through androgenesis and characterization of doubled haploid based hybrids for qualitative and quantitative traits in marigold (*Tagetes erecta* L.)

Under the present study, anthers of marigold (*Tagetes erecta* L.) genotype Af/R/L-1(local) were used for induction of doubled haploids. Excised anthers were given a pre-treatment, to increase the regeneration percentage. Among pre-treatments, best response was recorded from chilling of anthers at 4°C for 9 days. In case of anther starvation with mannitol, best response was recorded when anthers were starved in 0.3 M mannitol solution for 4 days. Afterwards, the basal MS media was modified by adding copper sulphate and best regeneration response was recorded when copper sulphate was added in the concentration of 20 µM. Anther derived regenerants were subjected for ploidy determination using direct and indirect methods and 6 haploids were obtained in total which were treated with chromosome doubling agents. Maximum diploidization was obtained when colchicine was used in the concentration of 100 mg/L for 38 hours while oryzalin gave maximum diploidization at the concentration of 50 mg/L for 38 hours.

Anther derived doubled haploids (DHs) were multiplied *in vitro* and transferred *in vivo* after hardening. Afterwards, these doubled haploids were characterized for various qualitative and quantitative traits and used as pollen parents and crossed with three male sterile lines (MS-5, MS-7 and MS-8) of *Tagetes erecta* L. to develop doubled haploid based inter-varietal F₁ hybrids in marigold which were evaluated for various qualitative and quantitative traits. Doubled haploids (DHs) based 18 promising inter-varietal hybrids were subjected for hybridity testing using SSR markers. All hybrids exhibited markers present in both male and female parents, confirming their hybridity. The protocol developed through this study can be further used to produce doubled haploids in marigold which will be useful to strengthen its breeding programme. Further, knowledge of various qualitative and quantitative traits gained under this study will also help in strengthening breeding programmes in marigold involving doubled haploids.



Fruit Science



Theivanai M.

Name of the Student : Theivanai M.
Roll No. : 11038
Chairperson : Dr. O. P. Awasthi



Dr. O. P. Awasthi

Title of the Thesis

***In vitro* mutagenesis and validation of mutants using molecular markers in Kinnow mandarin**

The investigation was conducted at Division of Fruits and Horticultural Technology, ICAR-IARI, New Delhi. The salient findings of the study are the standardization of *in ovulo* nucellus culture based direct somatic embryogenesis system that includes the collection of >4 mm ovules from stage III (>21 to ≤25 mm diameter) fruits followed by *in ovulo* explant preparation and induction of somatic embryos on DKW + Kinetin 5.0 mg L⁻¹ + malt extract 1000 mg L⁻¹ medium. Germination of cotyledonary embryos on MT + GA₃ 2.0 mg L⁻¹ + NAA 0.5 mg L⁻¹ + spermidine 100 mg L⁻¹ + CW 10% medium followed by preconditioning of germinated seedlings in the liquid medium and plantlet establishment on a potting medium (cocopeat: vermiculite: perlite, 2:1:1). The intact outer integument calli derived suspension culture based indirect somatic embryogenesis system that includes habituation and suspension culture of calli in PBR free medium for somatic embryogenesis followed by maturation of obtained embryos on solid medium (MT + NAA 0.5 mg L⁻¹ + coconut water 10%) and regeneration using DSE system protocol. Histological examinations aided the DSE system on optimization of ovule size and validation of single cell regeneration ability of both DSE and ISE system regenerants. Genetic fidelity testing confirmed the genetic stability of regenerants obtained from both DSE and ISE system. The findings of the *in vitro* mutagenesis protocol includes identification of the optimum gamma irradiation dose [80 Gy (DSE) and 100 Gy (ISE)] and EMS dose [0.5% EMS for 5 hr (DSE) and 0.1% EMS for 3 hr (ISE)]. Further the morphological and molecular validation could differentiate both DSE and ISE system derived M₁ mutants from mother plant. From the detailed investigation it can be concluded that DSE system is highly beneficial for both gamma irradiation and EMS induced *in vitro* mutagenesis.



Genetics and Plant Breeding



Ashvinkumar Katral

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Chairperson : Dr. Vignesh Muthusamy



Dr. Vignesh Muthusamy

Title of the Thesis

Analysis of genetic variability, molecular characterization and marker-assisted enrichment of kernel oil in maize (*Zea mays* L.)

High oil maize (>6%) genotypes enhance the bioavailability of fat-soluble vitamins and higher calorific value of the grain. Allele screening by exploiting functional genomic regions of *dgat1-2* and *fatb* genes in 292 diverse collections revealed the lower frequency of *dgat1-2* (0.15) and *fatb* (0.12) mutant alleles and identified 10 germplasm with both the mutant alleles. Sequence characterization of *dgat1-2* and *fatb* revealed wide variation within the genes. Gene-based InDel-markers developed here would facilitate the characterization of unknown germplasm. Multi-location evaluation of 48 diverse maize genotypes exhibited wide genetic variation for kernel oil content and fatty acid profile. Genetic dissection of embryo size and weight-related traits through generation mean analysis revealed the predominance of dominant and dominant \times dominant epistasis. Marker-assisted introgression of *dgat1-2* and *fatb* genes from IHO-donors into parental lines of four popular multi-nutrient-rich maize hybrids enhanced kernel oil content (>6.5%), a reduction (35%) in palmitic acid and an increment (50%) in oleic acid. Performance for other quality parameters (lysine, tryptophan, proA, and proE) and agronomic traits in introgressed inbreds and improved hybrids were similar to their original parents and hybrids. GWAS identified 64 significant marker-trait associations (MTAs) for tocochromanols and 20 MTAs for phenolic compounds with medium to high prediction accuracies across traits. These are first-of-its-kind genotypes developed with high oil content, better oil quality, and rich in lysine, tryptophan, proA, and proE contents due to the favorable alleles of six target genes (*o2*, *crtrB1*, *lcyE*, *vte4*, *dgat1-2* & *fatb*) in a single genetic background.



Microbiology



Aswini K.

Name of the Student : Aswini K.
Roll No. : 11542
Chairperson : Dr. Archana Suman



Dr. Archana Suman

Title of the Thesis

Microbiome mediated management of heat stress in wheat (*Triticum aestivum* L.)

India's wheat (*Triticum aestivum* L.) production has been declining due to increase in temperature, where every 1°C rise above average causes a yield reduction of 4.1% to 6.4%. Nowadays, studies on plant microbiome have gained increased attention and their role in managing stress by modulating enzymatic actions or producing plant growth hormones has been explored. Accordingly, we hypothesized that the construction of small microbial communities (SMCs), based on a combination of culturable and metagenomics approaches would induce tolerance to heat stress in wheat. In this study, the abundance and diversity of wheat seed endophytic bacteria (WSEB) and wheat associated bacteria (WAB) were investigated from heat^S (heat susceptible, GW322) and heat^T (heat tolerant, HD3298 and HD3271) varieties by culturable and unculturable approaches. The metagenomic analysis of seed microbiota unveiled the predominance of Proteobacteria. Whereas, culturable analysis results evidenced that the diversity was more in heat^S variety than the heat^T. Further morphotyping and environment adaptive functions were evaluated based on their tolerance to temperature, salt, drought and pH, from which the heat^T isolates were selected. Several plant growth promoting (PGP) functions of the selected isolates were analysed qualitatively and the results were combined together based on bonitur scale for the quantification of IAA, GA and cytokinin production, N, P and K solubilisation and siderophore production. Those efficient PGP isolates were identified by 16S rDNA sequencing and found 42 different species in 18 genera. *Bacillus* was found as the most abundant genus of class *Bacilli*, followed by *Gammaproteobacteria*, *Actinomycetia*, *Alphaproteobacteria* and *Betaproteobacteria*. Then, four different small microbial communities (SMCs) were designed based on function, dominance, function+dominance and phytohormone production by combining the results of culturable and unculturable taxonomic and functional annotation. The SMCs formulated were found to have increased PGP effects over the individual isolates in both the susceptible and tolerant wheat varieties. This was also confirmed from the physiological, biochemical, molecular, biometric and yield parameters evaluated under controlled (phytotron) conditions with induced heat stress. Also, the SMCs were validated under field conditions by staggered sowing and the results displayed the promising role of SMCs treatments in assisting the plants to tolerate heat stress. Hence, this study has comprehensively concluded that the SMCs formulated in this study was highly effective under heat stress conditions for promoting the plant growth as well as in sustaining the production.



Molecular Biology & Biotechnology



Sheel Yadav

Name of the Student : Sheel Yadav
Roll No. : 11291
Chairperson : Dr. P. K. Jain



Dr. P. K. Jain

Title of the Thesis

Understanding epigenetic regulatory mechanisms influencing drought tolerance pathways for identification of key genes in chickpea

Modifications within the epigenome of an organism in response to external environmental conditions allows it to withstand the hostile stress factors. Drought in chickpea is a severely limiting abiotic stress factor which is known to cause huge yield loss. The methylomes of two chickpea varieties, ICC 4958 and ICC 1882, which contrast for drought tolerance, were analysed in response to drought stress conditions. It was observed that the mCHH was most variable under drought stress, and the drought tolerant (DT) genotype exhibited substantial genome-wide hypomethylation as compared to the drought sensitive (DS) genotype. Important genes were identified as potential targets of epigenetic regulation in response to drought stress. This included the genes encoding the ribosomal proteins (RPs) and the SPL (Squamosa Promoter Binding Protein-Like) transcription factor (TF) genes. Specifically, the gene *RPS6* (ribosomal protein small subunit) was found to be downregulated in the DS genotype which leads to reduced ribosome biogenesis. An important class of drought-responsive transcription factors, the GRAS (gibberellic acid insensitive, repressor of GAI and scarecrow) TFs was identified. Proteins belonging to the RNA helicase gene family were identified which are involved in the *de novo* methylation in chickpea. Based on homology, it was inferred that the protein encoded by the *CaDExD/H66* gene shares a high degree of homology with one of the CLSY (CLASSY) proteins of *A. thaliana*. The CLASSY proteins are involved in regulation of tissue-specific methylation pattern, both at the genome-wide level as well as in a locus-specific manner. This gene therefore could possibly be involved in regulation of DNA methylation levels in chickpea by regulating siRNA production, in conjunction with other proteins.



Plant Genetic Resources



Siddhant Ranjan Padhi

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Dr. Rakesh Bhardwaj

Title of the Thesis

Genome wide association mapping of cowpea (*Vigna unguiculata* (L.) Walp.) germplasm for key quality traits

Cowpea being a legume is a viable option for enhancing food diversity and eliminating malnutrition because of its rich nutritional composition. In the present study 202 diverse germplasm of cowpea both indigenous and exotic germplasm were taken up for assessment for 11 biochemical parameters i.e., protein, starch, amylose, TDF sugar, phenol, phytic acid, iron, copper, zinc & calcium using standard protocols. The results have exhibited a substantial variability in protein (20.2-29.7 g/100g), carbohydrates [starch (30-47.5), amylose (11.5-14.8), sugar (4.10-6.59) expressed as g/100g], TDF (15.6-24.5 g/100g), anti-nutritional factors [phenol (0.112-0.405 GAE g/100g), phytic acid (1.19-1.80 g/100g)] and in micronutrients [iron (51.1-124.8 ppm), copper (3.48-14.9 ppm), zinc (29.6-76.2 ppm) and calcium (215.6-738 ppm)]. Modified partial least squares (MPLS) regression-based NIRS prediction models were developed for the above given parameters to assess the above parameters rapidly and non-destructively. All of the traits have exhibited high RPD values >2.5 except phenols (1.78). High RSQ values and low SEP(C) values for all the traits indicates excellent prediction capacity for all the worked traits. To identify new sources of genes for nutritional quality in cowpea accessions GWAS (Genome-Wide Association Studies) have been performed. GBS (Genotyping by Sequencing) was done for SNP genotyping A multi-locus GWAS (ML-GWAS) approach was employed utilizing six different models, namely mrMLM, FASTmrMLM, FASTmrEMMA, pLARmEB, ISIS EM-BLASSO, and pKWmEB ($LOD \geq 3$). 42 significant QTNs along with four pleiotropic QTNs was found across 9 traits. Furthermore, gene annotations were exclusively conducted for the QTNs that exhibited a high level of significance and consistency. This decision was based on the notion that these QTNs were more dependable and likely to demonstrate strong performance across various environmental conditions. The findings of this study can be utilized variously in crop improvement programs viz., development of nutritionally rich varieties, MAB, and value addition to national and international gene bank.



Plant Pathology



Pankhuri Singhal

Name of the Student : Pankhuri Singhal
Roll No. : 11567
Chairperson : Dr. V. K. Baranwal



Dr. V. K. Baranwal

Title of the Thesis

Virome analysis for identification and characterization of virus(es) associated with mosaic disease of mustard

Mustard is the 2nd most important commercial oilseed crop of India. Mustard mosaic disease, caused primarily by Turnip Mosaic Virus (TuMV) and occasionally in association with Cucumber Mosaic Virus (CMV), poses a substantial threat to global mustard cultivation, leading to severe economic losses. Despite its prevalence, there remains a dearth of comprehensive studies focusing on virus prevalence, genomic characterization, and transmission modes in Indian mustard crops. Our investigation employed electron microscopy and high-throughput RNA-sequencing techniques to analyze symptomatic mustard samples. Results unveiled mixed infections of CMV and TuMV during the 2020-21 season, and TuMV singular infection during the subsequent 2021-22 season, confirmed through Reverse Transcription-Polymerase Chain Reaction (RT-PCR). Notably, TuMV incidence reached 100% in mustard fields, with genomic analysis revealing the emergence of the world-B3 sub-pathotype in South Asia. Additionally, novel recombinant CMV isolates infecting previously unreported hosts were discovered in India. Our findings shed light on the seed transmission mode of TuMV dissemination, with aphids acting as carriers. We present compelling evidence suggesting true seed-borne transmission of TuMV, emphasizing its presence in immature seeds and subsequent association with TuMV in seedlings grown under aphid-free conditions. Furthermore, our research underscores the significant impact of mixed CMV and TuMV infections on mustard crop health including reduced yield by more than 50%, resulting in severe mosaic and puckering symptoms compared to the milder effects of TuMV single infections. This study marks the first natural observation of TuMV in black mustard and characterizes New Delhi TuMV strains as world-B3. Additionally, it identifies recombinant CMV subgroup IB isolates affecting diverse mustard seed varieties in India.



Plant Physiology



Sandeep Adavi B.

Name of the Student : Sandeep Adavi B.
Roll No. : 11095
Chairperson : Dr. Lekshmy S.



Dr. Lekshmy S.

Title of the Thesis

Genome-wide analysis of calcium signalling network genes and their role in nitrogen response of bread wheat (*Triticum aestivum*)

The current in-practice semi-dwarf wheat genotypes (*Rht-1*) exhibit low nitrogen use efficiency (NUE) contributing to fertiliser N loss, environmental pollution and global climate change. Recent evidence suggests calcium (Ca^{2+}) as crucial mediator of nitrate (NO_3^-) signaling and metabolism. Using the near-complete genome of *Triticum aestivum* and its three progenitor species, we identified different Ca^{2+} signalling genes; 7 CBLs, 24 CIPKs, 17 CPKs, and 6 NLPs exhibiting distinctive expression patterns across tissue, genotype, and NO_3^- treatment. Sequence characterisation of CBL6 supports the possibility of NO_3^- responsive post-translational modification. We discern that optimum cytosolic Ca^{2+} levels ($[\text{Ca}^{2+}]_{\text{cyt}}$) up-regulate the NO_3^- -responsive genes potentially by emulating NO_3^- signal. While high/low $[\text{Ca}^{2+}]_{\text{cyt}}$ hinder nitrate starvation response (NSR). Time-course analysis revealed peak expression of Primary nitrate responsive (PNR) sentinel genes at 30 min post NO_3^- treatment. EGTA, a Ca^{2+} chelator, validated Ca^{2+} 's involvement in PNR gene regulation and NO_3^- uptake. We unveiled tissue-specific, NO_3^- -dose-dependent regulation of nitrate reductase, with Ca^{2+} as a crucial mediator. Elevated NO_3^- levels, with exogenous auxin and Ca^{2+} , inhibit root growth, possibly mediated by ethylene downstream of $[\text{Ca}^{2+}]_{\text{cyt}}$. We uncovered a synergistic interaction between nitric oxide (NO) and native auxin in lateral roots (LRs), with auxin elevating $[\text{Ca}^{2+}]_{\text{cyt}}$, while NO acting downstream, affecting NO_3^- -responsive LR hair growth. High NO_3^- levels hinder root hair development by importing shoot-derived auxin, validated by polar auxin transport inhibitor. Wheat leaf protoplast experiments confirmed NO_3^- -induced $[\text{Ca}^{2+}]_{\text{cyt}}$ changes rely on extracellular Ca^{2+} influx and intracellular Ca^{2+} release. Further field experiment has shown that external calcium supplement will improve the NUE which is mainly due to improved N remobilisation and post anthesis N uptake. This comprehensive evidence underscores Ca^{2+} 's vital role in wheat's NO_3^- responses, simplifying NO_3^- signalling comprehension and offering potential solutions to enhance plant growth, yield and NUE through Ca^{2+} supplementation.



Seed Science and Technology



Archana H. R.

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Dr. D. Vijay

Title of the Thesis

Studies on thermotolerance and its induction during seed germination and seedling growth in rice

Rice is the staple food for about half of the world's population and is known to be susceptible to heat stress. In the present research, we have developed a range of phenotypic assays that can be used to characterize thermotolerance diversity i.e., basal thermotolerance (BT), short (SAT) and long term acquired thermotolerance (LAT) in rice during seed, radicle and early seedling stages and induction of heat tolerance by thermo priming and seed priming and its biochemical basis. Initially, BT was identified in seed (57°C, 30 min), radicle (48°C, 30 min) and early seedling stages (48°C, 30 min). Later, SAT technique was identified to mitigate heat stress in seed (45°C, 75 min), radicle (38°C, 75 min) and early seedling stages (42°C, 60 min). Also, LAT technique was developed in seed (45°C, 75 min), radicle (38°C, 75 min) and early seedling stage (42°C, 75 min) and the methodologies were validated in known heat susceptible/tolerant genotypes. Better tolerance in thermotolerant variety was attributed to higher antioxidants, lower ROS and lower MDA compared to susceptible variety. Recovery during SAT/LAT was due to increased peroxidase activity and reduced membrane degradation. For developing the chemical based seed priming technique to mitigate heat stress, seed priming technique was standardized for different factors. Phase II of imbibition curve with dry back temperature (26°C) was identified as most suitable, followed by selecting imbibition durations among different imbibition methods (direct soaking/blotter/PEG method) and effective concentration of spermidine (0.5/1/1.5 mM). Results indicated PEG (-1 MPa, 56 h) based method with 1 mM spermidine effectively reduce heat stress compared to other methods. This can be attributed to higher antioxidants, available sugars, amylases and lower MDA. Overall, the study emphasizes the significance of thermopriming and spermidine priming in rice which offers valuable insights into effective mitigation strategies against heat stress.



Soil Science



Avijit Ghosh

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Dr. D.R. Biswas

Title of the Thesis

Solubilization of soil phosphorus using rice residues and phosphorus solubilizing microorganisms

Disposal of significant tonnages of rice straw (RS) is expensive, but using it to mobilize phosphorus (P) from inorganically fixed pools in the soil may add value in the Indo-Gangetic Plains. This study was carried out to determine whether the use of RS mixed with phosphorus solubilizing microorganisms (PSM) could solubilize a sizable portion of fixed soil P and affect P transformation, silicon (Si) concentration, organic acid concentrations, and enzyme activity to increase plant growth. For this, soils from semi-arid and humid tropical agro-ecosystems were treated with PSMs, *i.e.* *Pseudomonas striata* ($\sim 10^8$ CFU mL⁻¹) and *Aspergillus niger* ($\sim 10^8$ spores mL⁻¹) and graded doses of RS (at 8, 10, 12, and 14 Mg ha⁻¹) under varying hydrothermal scenarios (temperature and soil moisture suctions), namely, S1 (25°C and 0.033 MPa), S2 (35°C and 0.033 MPa), S3 (25°C and 0.1 MPa) and S4 (35°C and 0.1 MPa). Rice straw application at 12 Mg ha⁻¹ with phosphate solubilising microorganisms (PSMs) in soil significantly boosted the Si content, enzyme activity as well as organic acid production during incubation. In pot experiment the performance of rice straw application with PSM and 75% of recommended dose of P application was tested to justify the practical feasibility of RS and PSM application in wheat-rice cropping sequence. According to path analysis, P solubilisation by Si and organic acids considerably increased P availability (18-32%) in the wheat and rice rhizosphere. Rice straw at 12 Mg ha⁻¹ with PSM and 75% mineral P fertilizer application could solubilize ~ 11 to 15% (*i.e.* 86 to 90 mg P kg⁻¹) inorganic P depending on the soil and environmental conditions. Therefore, cultivators could be advised to use RS at 12 Mg ha⁻¹ with PSM with 75% P of mineral P-fertilizer to save 25% P-fertilizer without reducing yield. This can significantly contribute to reducing P-fertilizer import and promoting P circular bio-economy.



Vegetable Science



Dhananjay A. Hongal

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Dr. Shyam Sundar Dey

Title of the Thesis

Understanding the physio-biochemical and molecular basis for high-temperature tolerance in cucumber

Cucumber is an important fruit vegetable crop with significant yield loss because of sub-optimal temperatures during the growing season. It is necessary to identify the key traits and genotypes with the contrasting response from a large set of germplasm associated with heat stress response for understanding the physio-molecular network associated with heat tolerance. A set of 123 germplasm was evaluated in a growth chamber with temperature stress treatment (40°C/35°C) for two subsequent seasons. Heat tolerance index was developed for 123 genotypes for 7 physiological traits recorded in the present study. A set of genotypes (5 highly tolerant and 5 highly susceptible) with contrasting response were selected for detailed study. Experiment conducted under two different temperature stress (35/30°C and 40/35°C) were evaluated for important physiological and biochemical traits. It was established that tolerant genotypes were able to maintain high chlorophyll retention, stable membrane stability index, higher retention of water content, stability in net photosynthesis, high stomatal conductance and transpiration in combination with less canopy temperatures under high temperature stress conditions compared to susceptible genotypes. Accumulation of biochemicals like proline, protein and antioxidants like SOD, catalase and peroxidase was the underlying biochemical mechanisms for high temperature tolerance. Upregulation of photosynthesis related genes, signal transduction genes and heat responsive genes (HSPs) in tolerant genotype indicate the molecular network associated with heat tolerance in cucumber. Among the HSPs, higher accumulation of HSP70 and HSP90 were recorded in the tolerant genotype, WBC-13 under heat stress condition indicating their critical role. Besides, Rubisco S, Rubisco L and CsTIP1b were upregulated in the tolerant genotypes under heat stress condition. Therefore, the HSPs in combination with photosynthetic and aquaporin genes were the underlying important molecular network associated with heat stress tolerance in cucumber. GWAS analysis was done to identify significant marker-trait associations for different physiological traits in cucumber under optimum and heat stress conditions in two seasons. We found significant QTLs for chlorophyll, membrane stability index, dry weight and canopy temperature for heat stress conditions. The annotation of candidate genes associated with the significant SNPs indicated that most of these QTLs are linked with important functional genes, which control solute transport through the cell membrane and other plant biochemical activities related to heat stress tolerance in cucumber. This comprehensive study provides foundation to design climate smart genotypes in cucumber through integration of favourable physio-biochemical traits and understanding the detailed molecular network associated with heat stress tolerance in cucumber.



Water Science and Technology



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Dr. Susama Sudhishri

Title of the Thesis

Development of filter for drip nutrification with biogas digestate

India's abundant indigenous bioenergy resources viz. biomass and biogas, produce valuable by-products like nutrient-rich biogas slurry (1.5% N, 1.1% P, 1% K). Conventional land-spreading methods pose environmental concerns, but nutrification through drip irrigation emerges as a solution for precise nutrient application, minimizing nitrogen losses and environmental impact. To address these issues the present study was focused on development of filter for drip nutrification with biogas digestate with the objectives (i) characterization of biogas slurry and development of its protocol for its use in drip nutrification (ii) designing the filter for biogas digestate fed drip system to reduce clogging and (iii) Techno-economic evaluation of filtration system in a drip nutrified vegetable crop. The study characterized biogas slurry, noting spatial and temporal variations in macro-nutrients, with nitrogen levels varying by over 3-6% pre- and post-monsoon. Positive correlations existed between nitrogen content and phosphorous, organic carbon, pH, and electrical conductivity. A settling behaviour protocol indicated that higher solid concentrations slowed particle settling (average size: 2.07 mm). In filter design, a lab study determined optimal filtration layers (3:1:1.5 P:G:S) with a dilution ratio of 1:2. The cascade filter showed superior performance with 61.8% slurry storage, 5.1 L m² h⁻¹ filtration rate, 79.4% effluent efficiency, and reductions in turbidity (198 NTU) and total solids (51.2 g/L). Incorporating biogas slurry into drip irrigation enhanced spinach growth, reducing synthetic nitrogen needs. Combining biogas slurry nutrification (BSN) with 80% RDF yielded 5.52 tons/ha, comparable to 100% RDF. BSN promoted balanced enzymatic soil profiles, contributing to improved agricultural outcomes. The filter system's clogging ratio ranged from 6.91% to 29.11%, with acceptable CV for all parameters, making it economically viable with a payback period of 1.33 years and a benefit-cost ratio of 2.29. Biogas slurry nutrification holds promise for sustainable agriculture, aligning with closed-loop economy principles and sustainable development goals.



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