National Virtual Conference on Current Trends and Challenges in Plant Biochemistry and Biotechnology

CTCPBB 2020

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BOOK OF ABSTRACTS

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Message

Dr. S. L. Mehta, President, SPBB

At the outset I would like to offer a very warm welcome to all the distinguished participants to this year's National Conference on "Current Trends and Challenges in Plant Biochemistry and Biotechnology" which is being organized in collaboration with Birla Institute of Technology and Science, Pilani, K. K. Birla Goa Campus. We had planned to mix business with pleasure of visiting one of the finest tourist destinations the Goa. Dr. Kundan Kumar along with his colleagues under the patronage of Prof. G. Raghurama, Director BITS Pilani, Goa and Prof. Souvik Bhattacharya the Vice Chancellor, BITS Pilani had planned for welcoming you to their beautiful Goa Campus. However due to corona pandemic we had to regrettably change it to virtual mode and missing meeting you personally. I, on behalf of the Society offer gratitude to Prof. Souvik Bhattacharya, VC, BITS, Pilani, Prof. G. Raghurama, Director, Dr Kundan Kumar the Organising Secretary and their colleagues for organizing this conference.

The Society for Plant Biochemistry and Biotechnology (SPBB) established in 1991 has provided a unique platform to the research professionals working in the field of plant science and technology to exchange their knowledge and create a scientifically healthy environment and temper. Since its establishment, SPBB has played a major role in bridging the technology and knowledge gap among plant biochemists and biotechnologist for strengthening research and promoting it at international level. For this purpose, the society ventured in bringing out the Journal of Plant Biochemistry and Biotechnology right from the beginning. It is a matter of pride that our journal was then the first one to be included in Current Contents from India. We had given major focus on keeping the quality both in content and production and make it truely an International Journal. It is gratifying that all Chief Editors (Dr. R. P. Sharma, Dr. M. L. Lodha, Dr. T. R. Sharma and now Dr. Srinivasan) along with the Editorial Board kept this vision upfront and it is because of their sincere and dedicated efforts that the journal has international recognition as manuscripts are received from overseas in large numbers and Journal has good international ranking. I would like to express gratitude to them. The Society was fortunate in having outstanding leadership. Dr. S. Ramachandran, Dr. R. S. Paroda and Prof. V. L. Chopra who steared the Society as Presidents until this responsibility was given to me by the Hon'ble members of the Society. It was pleasure for me to be the Secretary of the Society for fifteen years from inception. I was followed by Dr. K. R. Koundal, Dr. P. Ananda Kumar, Dr. N. K. Singh and now Dr. Shelly Praveen as the Secretary of the Society. They all along with the executive members worked with dedication and sincerity for strengthening the Society and furthering the objectives. They all deserve our grateful thanks.

During this period, we all worked hard for strengthening financial health of the Society, achieving international recognition and presence and in organising both national and international events in various themes of scientific interest. I am extremely happy to inform you that in this task we have succeeded in large measure because of the cooperation from all members of the Society. Since its inception, the Society has organized 17 National conferences/Symposia/Seminars including one

International Conference to bring together students, research, young scientist, professional etc. on a common platform to make a roadmap to meet the challenges in agriculture.

The themes chosen for this conference are;
1. Plant Biochemistry and Crop Improvement
2. Plant metabolites and nutraceuticals
3. Plant stress management
4. Genome Editing, Translational Genomics and Plant Breeding
5. Conservation of Genetic Resources, IPR and Biosafety issue

These themes are very important in strengthening and promoting technology development for food and nutritional security. If we look at the development of plant biotechnology from 1986 when the first transgenic flavor savor tomato was developed, only a couple of traits where synthetic pathways were elucidated have been modified for increasing either productivity or nutritional quality through genetic engineering. Now the agriculture faces far too many challenges specially as a result of climate change and awareness about nutritional quality. Fortunately, there have been tremendous technological advances which have given scientists quite a good understanding of the regulatory pathways but the knowledge gained is still a fraction of what is needed to address many challenges. There is need to understand molecular signalling mechanisms, metabolic networking, structure and functions of enzymes, hormones, and intermediary metabolism and its regulation. Elucidation of various pathways and their regulation by metabolites will help in development of transgenics for desired agronomic traits. Plant Biochemistry research has contributed a great deal in initially understanding biosynthetic pathways and their regulation in plants and that permitted designing transgenics with desirable traits. With technological advancements, biochemical research is helping unravel intricate and complex pathways especially metabolic and signaling pathways that now practically cover almost all the fields in life sciences.

Plants are frequently exposed to abiotic and biotic stressful environments and it led to lower productivity. The capacity to endure or adjust and overcome by viably countering these stresses is a multifaceted marvel. Both biotic and abiotic stresses happen at different phases of plant improvement and every now and then more than one stress condition simultaneously influences the yield. Stresses bring about both widespread and unequivocal impacts on plant development and advancement. One of the impressive errands for the plant scientists all around the world is to recognize and to decrease impacts of these factors on the yield of plants. Developments on genomics, transcriptomics, proteomics and metabolomics provide opportunity in understanding regulatory pathways involved in stress mechanism and elucidation of these is going to help development of varieties with inbuilt resistance to withstand stress.

Gene editing in plants make use of several tools to modify the genomic DNA of the cultured cells. Recently, few experimental approaches involved generation of gene edited shoots through the manipulation in the stems of the soil grown plants to avoid undesirable editing. Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR) is a bacterial immune system which works against viral attack. Discovered in 1987, CRISPR took 20 years to get fully understood and has now become a promising ‘gene editing’ tool in the field of biomedical research for myriad applications in healthcare, food, agriculture and all industries relating to biological sciences. Because of its ease, low cost, comparatively less complicated operations along with the accuracy and specificity, it has now been preferred over other gene editing tools such as ZFN (Zinc Finger Nucleases) and TALENS (Transcription Activator-like Effector Nucleases).

Fortunately, the liberal support from ICAR and DBT excellent state of the art infrastructure has been developed which has played an important role in generating skilled human resources in plant biotechnology. Development of DNA sequencing facility by DBT and ICAR has played a key role in

establishing Indian plant research internationally and the achievements of our scientists are admirable. Our record in bringing benefits to the farming community has also been impressive. Introduction of Bt cotton has revolutionized its production and farmers have adapted the technology without reservation and got immense economic benefits. The development of GM crops by Indian scientists is commendable however, their use and introduction into the market is still restricted due to the governmental policies and regulations. As a result, the advantages of GM traits have been restricted to a small number of cultivated crops. Spread of awareness through the public education on the potentials of GM crops on transparent and scientifically proven risk/benefit analysis is today's need. With the coming in of WTO and IPR regulations, we need to build up capacity to manage intellectual properties. IPs generated by the public sector can be considered assets that can be exchanged for private sector-owned IPs or used as bargaining chips in technology transfer negotiations, partnership between the private and public sectors in technology development through sharing of knowhow and IP can hasten technology development, transfer and acquisition and it would be win win situation for both.

With the support from ICAR, DBT, DST, CSIR etc. now many scientists are working in collaboration for providing solutions to the challenges of new agriculture. We are extremely happy that under competitive grant mode new innovative ways are being tried. Developments in technology are taking place at an unprecedented scale. Genomes of many crop plants have been sequenced. As genotyping becomes increasingly cheaper and easier, our future challenges will be precision and high-throughput phenotyping under controlled environments. The consideration of the physiological traits in the breeding programmes would help break the yield barriers. Scientists must discuss molecular breeding strategies, platforms, and tools, including genome-wide selection, SNP genotyping to facilitate enhancing yield, quality, and abiotic and biotic stress tolerance and develop networks. Molecular linkage genetic maps and QTL mapping technologies are helpful for estimating the number and position of the loci governing genetic variation using different types of segregating and fixed populations. Mapping loci to positions in the genome, as well as their phenotypic effects and epistatic interactions with other QTL and loci has enabled identification of the genetic loci associated with complex traits such as drought, salinity, disease and insect resistance in crop plants. The rapid advancement in genome sequencing technologies and marker-aided breeding approaches have resulted in a change in breeding methods, providing new opportunities.

Promoting basic and strategic research holds key for faster development of technology for meeting newer unforeseen challenges. However, for deriving this benefit it is important to have strong centers of basic research in universities. During early phase of Agricultural University development all universities had strong colleges of Basic Sciences. With passage of time and dwindling support the casualty has been the basic science colleges and departments. We need to resurrect the basic science departments in all universities. The new Education Policy approved by the Government has rightly emphasized creation of strong centers of Basic Sciences. ICAR being the regulatory body for higher agricultural education has this responsibility. We from the Society have taken decision for capacity development in Biochemistry and Biotechnology by organizing training and practical workshops in new and emerging areas for the faculty, students and research workers. Another new programme started is awareness programme for students and school teachers in new biology.

In the end let me say that this conference provides a unique opportunity to the researchers and students to discuss ways and means to enhance productivity and nutritional quality of crops through breeding and modern biotechnological approaches by integrating the research efforts of plant biochemistry and biotechnology. I am confident that distinguished delegates participating will deliberate on various issues and come out with recommendations for future research thrusts for meeting new challenges for productivity enhancement.

Dr. S. L. Mehta
President, SPBB

TECHNICAL PROGRAMME

Registration: 08:45AM to 09:15 AM

20th November 2020 (Friday)		
Inaugural Session: 09:30 AM – 11:05 AM		
09:15am–09:30am	Joining for the Conference (through virtual platform)	
09:30am–09:40am	Welcome Address	Prof. G. Raghurama Director, BITS Pilani, K. K. Birla Goa Campus
09:40am–09:50am	Presidential Address	Dr. S. L. Mehta President SPBB, New Delhi
09:50am-10:00am	SPBB-Springer awards/honours	
10:00am-11:00am	***Plenary Session:*** **Chairperson**: **Prof. Samit Chattopadhyay**, Sr. Professor, BITS Pilani, Goa Campus **Convenor: Dr. Malabika Biswas** **Topic: 'Himalayan Plants and their Nutraceutical Potential'** **Speaker: Dr. Sanjay Kumar** Director, CSIR-IHBT, Palampur	
11:00am-11:05am	Vote of Thanks	Dr. Rajesh Mehrotra BITS Pilani, K. K. Birla Goa Campus
11:05am-11:15am	**Break**	

Technical Session 1 (11:15am-01:35pm) **Theme: Plant Metabolites and Nutraceuticals** **Chairperson: Prof. S. R. Bhat** **Convenor: Dr. Vinutha T**; **Rapporteur: Prof. Utpal Roy**		
11:15am-11:45am	Keynote talk: Metabolic Engineering of Oilseed Crops for Enhanced Oil Production and Increasing Tolerance to Abiotic Stresses	Prof. Om Prakash Dhankher (UMASS Amherst, USA)
11:45am-12:05pm	Lead talk: Biotechnological Approaches for Nutritional Improvement in Banana Fruit	Dr. Siddharth Tiwari (NABI, Mohali)
12:05pm-12:25pm	Lead talk: Understanding Plant Triterpene Biosynthesis: Key Enzymes and Pathway Reconstruction	Dr. Sumit Ghosh (CIMAP, Lucknow)
12:25pm-12:45pm	Lead talk: Conservation and *in vitro* Immunomodulatory Potential of *Gymnema sylvestre*	Prof. Padmanabh Dwivedi (BHU, Varanasi)
12:45pm-12:55pm	Oral talk: 'Nutraceutical starch' - An interplay of Food Matrix Components	Dr. Veda Krishnan
12:55pm-01:05pm	Oral talk: Untapped Nutraceutical Potential of *Cocos nucifera* L.- the Kalpavriksha on Earth	Dr. S.V. Ramesh
01:05pm-01:15pm	Oral talk: Phytochemical Analysis of Rhizome of *Zingiber officinale* in Different Solvents	Dr. Renu Mishra
01:15pm-01:25pm	Oral talk: Nutraceutical Characterisation of Anthocyanin-Rich Flower Bracts of Banana cv. Grand Naine (*Musa* spp., AAA)	Dr. M. Mayil Vaganan
01:25pm-01:35pm	Oral talk: Beta Amylase as a Selection Criteria for Improving Diastatic Power in Malt Barley	Dr. Dinesh Kumar
01:35pm-2:00pm	**Break**	

Technical Session 2 (2:00pm-3:50pm) **Theme: Plant Stress Management**		
Chairperson: Dr. Rakesh Tuli **Convenor: Dr. S. K. Mangrauthia; Rapporteur: Dr. Tushar T. Saha**		
2:00pm-2:30pm	***Keynote talk***: Battle Against the Viruses: smallRNAs as Defender	Dr. Manoj Prasad (NIPGR, New Delhi)
2:30pm-2:50pm	***Lead talk***: Induced Plant Mutations in the Genomics Era	Dr. P. Suprasanna (BARC, Mumbai)
2:50pm-3:10pm	***Lead talk:*** Bio-prospection of Plant Diversity for Novel Insecticidal Proteins/genes for Next Generation Insect Tolerant GM Crops	Dr. P. K. Singh (NBRI, Lucknow)
3:10pm-3:30pm	***Lead talk:*** Regulating the ABA-dependent and -independent Signalling for Enhancing Abiotic Stress Tolerance in Plants	Dr. Pradeep K. Agarwal (CSMCRI, Bhavnagar)
3:30pm-3:40pm	***Oral talk:*** Unfolding the Story of RuBisCo Activase in Wheat under Terminal Heat Through Omics Approaches	Dr. R. R. Kumar
3:40pm-3:50pm	***Oral talk***: Conditional Pathogenesis: Understanding Why Potentially Beneficial Rhizobacteria turn Pathogenic under certain Environmental Conditions	Dr. Sridev Mohapatra
3:50pm-4:00pm	Break	
Technical Session 3 (4:00pm-6:00pm) **Theme: Plant Biochemistry and Crop Improvement**		
Chairperson: Dr. S. L. Mehta **Convenor: Dr. Sridev Mohapatra ; Rapporteur: Dr. Sukanta Mondal**		
4:00pm-4:30pm	***Keynote talk***: A Crosstalk between ABA Signalling, miRNA Biogenesis factor and Mitogen Activated Protein Kinase	Dr. Alok K. Sinha (NIPGR, New Delhi)
4:30pm-4:50pm	***Lead talk:*** A story of Mitochondrial Gate-keeper: What we know about VDAC and its Function in Plants?	Prof. Girdhar K. Pandey (University of Delhi, New Delhi)
4:50pm-5:10pm	***Lead talk***: dsRNA to Determine the Role of MYB Family Genes in Orchid Flower Shape and Colour	Prof. Jennifer Ann Harikrishna (University of Malaya, Malaysia)
5:10pm-5:30pm	***Lead talk***: Structure and Function of Plant Mediator Complex	Dr. Jitendra Thakur (NIPGR, New Delhi)
5:30pm-5:40pm	***Oral talk***: A Novel Processing Technique to Reduce Rancidity in Stored Pearl Millet Flour: It's effect on Nutritional Quality and Functionality	Dr. Vinutha Thimmegowda
5:40pm-5:50pm	***Oral talk:*** Plant Signalling- a mode of Communication in Plants	Dr. Siddhi Jalmi
5:50pm-6:00pm	***Oral talk***: Glutathione S tranasferase: A versatile protein family	Prof. Mahesh Basantani
6:00pm-6:30pm	**SPBB Annual General Body Meeting**	

21st November 2020 (Saturday)		
Dr. N. B. Das Memorial Lecture Session (09:45AM-12:05PM)		
09:45am-10:00am	Joining for the Conference (through virtual platform)	
10.00am-10.05am	Opening of the session: Lightening of lamp and floral tribute to late Dr. N.B. Das	
10:05am-10:15am	Welcome Address	Prof. Souvik Bhattacharyya Vice Chancellor, BITS, Pilani
10:15am-10:25am	Opening Remarks	Dr. A. K. Singh Director, ICAR-IARI, New Delhi
10:25am- 10:35am	Current and Prospective Plans of the Society for Plant Biochemistry and Biotechnology (SPBB)	Dr. Shelly Praveen Secretary, SPBB
10:35am-10:50am	Address by the President	Dr. S. L. Mehta President, SPBB
10.50am- 10.55am	Brief account of Dr. N.B. Das Memorial lecture. Introduction of the Chair	
10:55am-11:40am	Dr. N.B. Das Memorial Lecture	Dr. T. Mohapatra Secretary (DARE) & Director General (ICAR)
11:40am-11:50am	Address by the Chair	Dr. Chandrima Shaha President, INSA
11:50am-12:00pm	Felicitation	
12.00pm-12.05pm	Vote of Thanks	Dr. Kundan Kumar BITS, Pilani, Goa
12:05pm-01:00pm	e-Poster Session	
01:00pm-02:00pm	Break	

Concurrent Technical Session 4

Theme: Genome Editing, Translational Genomics and Plant Breeding			**Theme: Conservation of Genetic Resources**		
2:00pm-4:00pm	**Chairperson: Dr. P. K. Gupta** **Convenor: Dr. Sandhya Mehrotra** **Rapporteur: Dr. Gireesha Mohannath**		**02:00pm-03:30pm**	**Chairperson: Prof. S. Krishnan** **Convenor: Dr. Sumit Biswas** **Rapporteur: Dr. Manohara K. K.**	
2:00pm-2:30pm	***Keynote talk:*** Epigenetic Control of Resistance Against Leaf Rust in Common Wheat	Prof. P. K. Gupta (Ch. Charan Singh University, Meerut)	02:00pm-02:30pm	***Keynote talk:*** Role of Educational Institutes in Documentation, Bio-prospecting, Sustainable use and Conservation of Plant diversity of Western Ghats	Prof. S.R. Yadav (Shivaji University, Kolhapur)
2:30pm-2:50pm	***Lead talk***: Genetic Engineering and Genome Editing for Abiotic Stress Tolerance in Rice	Dr. C. Viswanathan (ICAR-IARI)	2:30pm-2:50pm	***Lead talk:*** An Integrated Approach to the Conservation of Plants	Prof. M. K. Janarthanam (Goa University, Goa)
2:50pm-3:10pm	***Lead talk***: Integrating Precision Phenotyping and Genomics in Wheat Improvement amidst Widening Challenges	Dr. A. K. Joshi (CIMMYT-India, New Delhi)	2:50pm-3:10pm	***Lead talk:*** Vegetable Amaranths of Goa for Food Colorant and Nematode Pest Management	Dr. V. Arunachalam (ICAR-CCARI, Goa)

3:10pm-3:30pm	***Lead talk***: A Novel Male Sterility-Fertility Restoration System for the Hybrid Seed Production in Cotton	Dr. Samir Sawant (NBRI, Lucknow)	3:10pm-3:20pm	***Oral talk:*** Utilization of Potential Salt Tolerant Landrace 'Korgut' from Goa Coast for Genetic Improvement in Rice	Dr. Manohara K. K.
3:30pm-3:40pm	***Oral talk***: RNAi Mediated Resistance Development against Rice Diseases: Exploiting Pathogen Genes and Host Non-coding RNAs	Dr. S. K. Mangrauthia	3:20pm-3:30pm	***Oral talk:*** Generation of New Variability for Yield and Novel Traits in Finger Millet through Induced Gamma Mutagenesis	Dr. Ganpathy K. N.
3:40pm-3:50pm	***Oral talk***: Epigenomic Manipulation of Crop Plants for Trait Improvement	Dr. Gireesha Mohannath			
3:50pm-4:00pm	***Oral talk***: Genome-Wide and Candidate Gene Association Studies for Flowering Time Trait in Linseed (*Linum usitatissimum*)	Dr. Dhammaprakash Wankhede			
Concurrent Technical Session 5 **Presentation under Young Scientist Session**					
Theme: Plant Metabolites and Nutraceuticals and Plant Stress Management			**Theme: Plant Biochemistry and Crop Improvement, Genome Editing, Translational Genomics and Plant breeding and Conservation of Genetic Resources, IPR and Biosafety issue**		
04:00pm-06:00pm	**Chairperson: Dr. K. C. Bansal** **Convenor: Dr. R. R. Kumar** **Rapporteur: Dr. Siddhi Jalmi**		**04:00pm-06:00pm**	**Chairperson: Dr. Archana Sachdev** **Convenor: Dr. Kundan Kumar** **Rapporteur: Dr. Malbika Biswas**	
4:00pm-4:07pm	Biochemical Analysis and Mass Profiling of Traditional Medicinal Plants	Dr. D. R Gangapur	4:00pm-4:07pm	Exploring natural variation for investigating thiourea-mediated enhanced growth and stress tolerance in soybean	Dr. Rakesh Manuka
4:07pm-4:14pm	Allelopathic Effects and Characterization of Some Medicinal Plant Extracts in *Vigna radiat*a L. Wilczek and their Efficacy in the Control of Charcoal Rot Disease	Dr. Priyanka Gupta	4:07pm-4:14pm	5N-influx and homeolog expression of nitrate transporter genes under nitrate-limited conditions in contrasting bread wheat genotypes	Amresh Kumar
4:14pm-4:21pm	Evaluation of dehydrated *Celosia argentia* leaves as a potent source of Quercetin-A dietary antioxidant	Dr. D. Amirtham	4:14pm-4:21pm	Identification, cloning and homeolog expression bias in AtNRT1.5 orthologs under different external nitrate concentrations in bread	Muhammed Shamnas V

				wheat (*Triticum aestivum* L)	
4:21pm-4:28pm	Enhancing the functionality and nutraceutical potential of soymilk through fermentation by probiotic Lactic Acid Bacteria (LAB)	Minnu Sasi	4:21pm-4:28pm	In planta transformation technique for crop improvement	Samrity Sharma
4:28pm-4:35pm	Determination of Polyphenols, in vitro Antimicrobial and Antioxidant Activity of Selected Mangrove Species	N. L. Dahibhate	4:28pm-4:35pm	Production and characterization of antifungal metabolites from tomato rhizobacteria for a *Fusarium* wilt-free tomato cultivations	Vijay Karuppiah
4:35pm-4:42pm	Biochemical and histochemical characterization of floral cuticular wax in tuberose	Raktim Bhattacharya	4:35pm-4:42pm	Understanding the genetic basis of rice leaf development and growth	Vikram Jathar
4:42pm-4:49pm	Artificial miRNA mediated resistance in tobacco against geminivirus infecting Jatropha by maintaining photosynthesis and metabolic pathways	Dr. Prashant More	4:42pm-4:49pm	*In-vitro* biotechnological strategies to improve Niger (*Guizotia abyssinica* L.F. Cass) for enhancing edible oil production in India	Dr. Shrinkhla Maurya
4:49pm-4:56pm	Protective Role of Spermidine in Salt Stress Tolerance Mechanism of tomato plant	Dr. Riti T. Kapoor	4:49pm-4:56pm	Chromatin Assembly Factor-1 (CAF-1) plays a role in ribosomal RNA gene regulation and in maintaininggenomic stability in Arabidopsis thaliana	Aveepsha Bera
4:56pm-5:03pm	Overexpression of JcWRKY2 enhances salinity and *Macrophomina phaseolina* tolerance in transgenic tobacco	Dr. Mitali Dabi	4:56pm-5:03pm	Insights into population structure and genetic divergence revealed genetic differentiation among different adaptable and diverse colored sub-populations of Indian carrot (*Daucus carota* L.) accessions	Chaitra Kulkarni
5:03pm-5:10pm	Metagenomic analysis of microbial diversity in control and high arsenic field of West Bengal (Nadia district) under the	Anurakti Shukla	5:03pm-5:10pm	Different mutant alleles of Histone Deacetylase 6 (hda6) have different effects on rRNA genome instability in *Arabidopsis thaliana*	Gargi Prasad S

	thiourea supplementation				
5:10pm-5:17pm	Exploring endophytes isolated from medicinal plants against *Colletotrichum gloeosporioides* (Penz.) Sacc. causing anthracnose in greater yam (*Dioscorea alata* L.)	P. R. Amrutha	5:10pm-5:17pm	A Unary-Offset Integrated OctaFilial Generations Homozygosity values Computational Model, in addition to accommodating "DUS" ThreeBIT Switchkey Schema of EIGHT Staple Indian Millet varieties, based upon Binary/ 2state Elementary Cellular Automata	Praharshit Sharma
5:17pm-5:24pm	Salicylic acid enhances the growth of rice (Oryza sativa L.) plants under drought stress conditions	Korgoankar Shravani	5:17pm-5:24pm	Exploring the genetic resources for functional genomics and marker-assisted breeding of carrot (*Daucus carota* L.)	Sarvamangala S Cholin
5:24pm-5:31pm	Identification and characterization of MAPKKKs from *Cicer arietinum* and their involvement in plant defense against *Helicoverpa armigera*	Radhika Keshan	5:24pm-5:31pm	A Study of AGPase Genes for Thermotolerance in Wheat using Comparative Genomics and Bioinformatics	Dr. Ritu Batra
5:31pm-5:38pm	Green Nanofungicide and their application in biotic stress management	Ranjani S.	5:31pm-5:38pm	Bioprospecting native wild nutmegs from Andaman and Nicobar Islands, India for their sustainable utilization	Dr. Ajit Arun Waman
5:38pm-5:45pm	Cloning, in silico characterization and expression analysis of TIP Members of Rice (*Oryza sativa* L.)	Suhas Karle	5:38pm-5:45pm	*Garcinia andamanica* King: an endemic horticultural genetic resource from Andaman Islands	Dr. Pooja Bohra
5:45pm-5:52pm	Co-expression Network Analysis of Protein Phosphatase 2A (PP2A) Genes with Stress-Responsive Genes in *Arabidopsis thaliana* Reveals 13 Key Regulators	Zaiba Hasan Khan	5:45pm-5:52pm	Study of novel molecular based studies for Indian medicinal plants to create genomic database	Lolla J. Lakshman
			5:52pm-6:00pm	A critical analysis of regulatory framework for biotechnology in India	Rishi Singh Solanki
6:00pm-6:10pm	**Award announcement and Closing remark**				

Contents

Dr. N. B. Das
(1908-1971)

Dr. N. B. Das (Nalin Bandhu Das) was born on June 1, 1908 in a family of jurists, educationists and physicians of Chittagong (now in Bangladesh). He graduated in Honours in Chemistry from the Calcutta University. He then joined Bose Institute as researcher and later on served the Bengal Chemical and Pharmaceutical Works for a short term. In 1930s, on being awarded 'The Lady Tata Memorial Scholarship', he proceeded to Germany for higher studies. He was awarded the Doctorate degree for his fundamental research on the biochemistry of enzymes. His Ph.D. research has been quite frequently cited in the text books on enzymology.

He had the privilege of working with two Nobel Laureates. Initially he was with Prof. Hans von Euler at the Biochemical Institute, University of Stockholm, Sweden. Here he worked extensively on the purification and characterisation of enzymes involved in amino acid metabolism in animal system, especially with respect to cofactors/coenzymes, and on the role of ATP in the conversion of DPN to TPN. Later on, as 'The Lady Tata Memorial Scholar', he moved to the Institute of Medical Chemistry, University of Szeged, Hungary to work with Nobel Laureate Prof. Albert Szent-Gyorgyi, to whom he considered his Guru. He carried out extensive studies on the inhibition of the succinic and lactic-malic dehydrogenases. His research work is widely cited in research papers and books.

After working for nearly 12 years in renowned laboratories abroad, Dr. Das returned back to India on the call given by Prof. P. C. Mahalanobis, the father of modern statistics in India. Patriotic feeling brought Dr Das home to use science and technology for the welfare of people. On his return, he joined the mother campus of Indian Veterinary Research Institute (then Imperial Institute of Veterinary Research) at Mukteswar to work on cattle vaccines and sera. Subsequently, in the year 1949, he joined the Division of Soil Science and Agricultural Chemistry at IARI as the first Biochemist where he established a Biochemistry Laboratory. This was the beginning of introducing and emphasizing the role of biochemistry in agriculture, especially with respect to the quality of food crops. Dr. Das was the first to study the nutritive quality of crops as influenced by variety, manures and fertilizers. From these studies, the first major recommendation that foliar application of urea and micro-nutrient elements enhances crop yield, was made in early 1950s.

Recognising the importance of Agricultural Biochemistry in improving agriculture, a small Biochemistry Section in the Division of Soil Science and Agricultural Chemistry was transformed into the full-fledged Division of Biochemistry in November 1966, and its founding father Dr. N.B. Das was made the first Head of the Division. Biochemical research and education were tailored to meet the new challenges of Indian agriculture. New Post-Graduate courses were designed to impart

skills in new technology that aimed at studying intermediary metabolism, molecular biology, enzymology and nutrition. The first batch of M.Sc. and Ph.D. students was admitted in the academic year 1967-68.

In the formative years, the major emphasis was given on the biochemical and biological evaluation of nutritional value of newly developed strains and varieties of food grains, effect of plant nutrients on nutritional value as well as yield of food grains, biochemical studies in nitrogen fixing bacteria, and utilisation of agro-industrial wastes for the production of lysine as well as enzymes like cellulose and amylase. Under his leadership one of the finest facilities for doing outstanding research in plant biochemistry was built. The technique of PAGE was introduced for the characterisation of soluble proteins and iso-enzymes. Dr. Das guided a number of M.Sc. and Ph.D. students from India and neighboring countries, who later went on to hold various responsible positions within and outside India.

After his superannuation in the year 1970, in recognition of his valuable contributions in the field of biochemistry and his distinct position as a biochemist in the country, he was made Emeritus Scientist by the ICAR.

Dr. N.B. Das was not only a renowned and most respected biochemist, but also an unassuming, quiet and noble gentleman, and his smiling face was characteristic of him. He personified what is best in Indian culture. His commitment to excellence in science was total. This great scientist left for his heavenly abode on 17th November, 1971. The Society for Plant Biochemistry and Biotechnology decided to organise Dr N.B. Das Memorial Lecture' to perpetuate his memory.

DR. N. B. DAS MEMORIAL LECTURE

SPEAKER: Dr. Trilochan Mohapatra

Secretary (DARE) & Director General (ICAR)

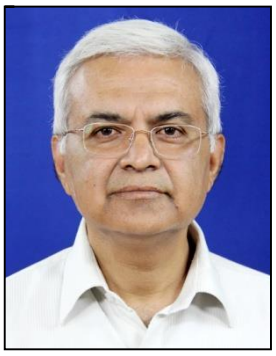
Dr. Trilochan Mohapatra born on 20th April, 1962 at village Kharibil, Dist. Cuttack, Odisha, India. He obtained MSc and PhD in Genetics from Indian Agricultural Research Institute (IARI), New Delhi. Dr. Mohapatra is presently holding the position of Secretary, Department of Agricultural Research and Education, and is also the Director General of the Indian Council of Agricultural Research (ICAR). Prior to this, he served as the Director of the Indian Agricultural Research Institute (IARI), New Delhi, and the National Rice Research Institute (formerly CRRI), Cuttack, Odisha.

Dr. Mohapatra contributed to the development of 12 varieties of rice and mustard including the long grain Basmati variety, Pusa Basmati 1121, and the first high-protein rice variety, CR Dhan 310. Dr. Mohapatra has been recipient of several honors and awards recognizing his academic and research contributions, including the INSA Young Scientist Award, Prof LSS Kumar Memorial Award, NAAS-Tata Award, IARI-BP Pal Award, DBT Bio-science Award, NASI-Reliance Industries Platinum Jubilee Award, Shri Om Prakash Bhasin Award 2016, IMS Diamond Jubilee Memorial Award 2016, Dr. D. Sundaresan Memorial Oration Award 2017, NASI Lecture Award 2017 and Prof NG Ranga Memorial Award by the Andhra Pradesh Science Congress 2017. He also received the Recognition Award of the National Academy of Agricultural Sciences for the biennium 2013-14 for significant contributions in Plant Improvement and the Lifetime Achievement Awards of the Indian Genetics Congress and the Indian Society of Agricultural Biochemists.

Dr. Mohapatra is an esteemed Fellow of the Indian National Science Academy, New Delhi, National Academy of Sciences-India, Allahabad and the National Academy of Agricultural Sciences, New Delhi. He has been conferred doctoral degree (Honoris Causa) by Amity University, Noida, Uttar Pradesh, Odisha University of Agriculture & Technology, Bhubaneswar, YS Parmar University of Horticulture & Forestry, Solan, Himachal Pradesh, Siksha `O' Anusandhan University, Bhubaneswar, Odisha and Pandit Deen Dayal Upadhyaya Verterinary and Animal Sciences University, Mathura, Uttar Pradesh.

Plenary Session

Theme: **Plant Metabolites and Nutraceuticals**
Keynote speaker: **Dr. Sanjay Kumar, CSIR-IHBT, Palampur**



Himalayan Plants and their Nutraceutical Potential

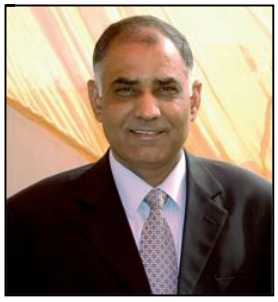
Vikram Patial, Yogendra Padwad, Shashi Bhushan and Sanjay Kumar
IHBT, Palampur
Email: director@ihbt.res.in

Abstract:
Medicinal and aromatic plants are used in traditional system of medicine for centuries. The medicinal properties of such plants are attributed to a range of metabolites like phenolics, terpenoids and alkaloids. Our group deciphered the molecular basis of biosynthesis for series of such compounds. This include picrosides, shikonins, catechins, podophyllotoxin and steviol glycosides in *Picrorhiza kurrooa*, *Arnebia euchroma*, *Camellia sinensis*, *Sinopodopyllum hexandrum* and *Stevia rebaudiana*, respectively. Some of these species have been used to develop a range of nutraceuticals as well. The preclinical trials of *P. kurroa* extracts showed promising results in diabetes through pancreatic β -cell regeneration and increased insulin secretion in diabetic rats. Iridoid glycosides-rich fraction of *P. kurroa* prevented cyclophosphamide-induced renal toxicity and peripheral neuropathy by interacting with PPAR-γ linked apoptosis and inflammatory pathways. The extract was also investigated against non-alcoholic fatty liver disease in zebra fish model, and was effective in lowering fat deposition and expression of related genes in the liver. The green tea catechins and epigallocatechin gallate proved to be a potential modulator of cellular senescence and can be used for development of novel anti-aging nutraceutical. Epigallocatechin gallatein combination with probiotic *Lactobacillus fermentum* was identified as a second generation symbiotic due to enhanced systemic immune responses and antioxidant capacity in aged mice.

KEYNOTE TALKS

Session I

Theme: **Plant Metabolites and Nutraceuticals**
Keynote speaker: **Dr. Om Prakash Dhankher, University of Massachusetts, USA**



Metabolic Engineering of Oilseed Crops for Enhanced Oil Production and Increasing Tolerance to Abiotic Stresses

Om Parkash Dhankher[1], Hesham Abdullah[1,2], Sudesh Chhikara[1], Kenny Ablordeppey[1], Parisa Akbari[1], and Danny Schnell[2]
[1]Stockbridge School of Agriculture, University of Massachusetts, Amherst, MA 01003;
[2]Department of Plant Biology, Michigan State University, East Lansing, MI 48824-1312
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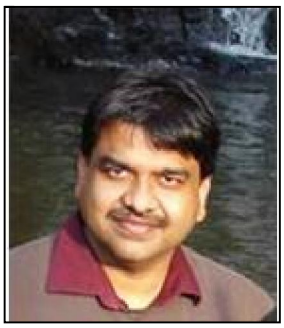
Abstract
Renewable transportation fuels (biodiesel and green diesel) from plant seed oils are considered as environmentally and economically feasible alternatives to petroleum-derived fuels. *Camelina sativa*, due to its unique seed and oil attributes, has attracted much interest as an emerging crop dedicated for biodiesel and jet fuel production. To increase oil yield, we engineered Camelina by co-expressing *Arabidopsis DGAT1*and yeast *GPD1* genes under the control of seed-specific promoters. Transgenic lines exhibited up to 13% higher seed oil content and 52% increase in seed mass compared to wild-type plants. Further, DGAT1- and GDP1 co-expressing lines produced almost double seed and oil yields per plantbasis compared to wild-type or plants expressing DGAT1 and GPD1 alone. To identify the bottlenecks for further improving the seed and oil yield in Camelina, we utilized metabolomic and transcriptomic profiling approaches in developing seeds in Camelina overexpressing TAG related genes. Our approach revealed several key genes/gene networks associated with significant changes especially in the TCA cycle and storage/retention of lipids in seeds. Overexpression of candidate genes showed further increase in oil and seed yield. We are now translating this strategy in edible oilseed crops such as Indian mustard and soybean for increasing edible oil contents and seed yields. Further, to enhance plants productivity under the adverse conditions, we overexpressed novel stress related genes including wax synthase gene (WS) for increasing the tolerance to multiple abiotic stresses. WS transgenic plants, when exposed to drought, salinity and heavy metals stresses, exhibited strong tolerance phenotype and had reduced water loss and cuticle permeability due to increased deposition of epicuticular leaf and stem wax loading. Ultimately, our aim is to stack the genes/gene networks responsible for increasing seed and oil yields as well as abiotic stress tolerance to enable these cultivars to growth on marginal lands and under extreme environmental conditions.

Session II

Theme: Plant Stress Management
Keynote speaker: Dr. Manoj Prasad, NIPGR, New Delhi



Battle against the viruses: small RNAs as defender

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Abstract:
Tomato leaf curl disease (ToLCD), caused by strains of Tomato leaf curl virus (ToLCV), is a major constraint to tomato production. To understand the molecular mechanism of virus tolerance, we studied the abundance of viral genomic replicative intermediate molecules by host plant in a naturally tolerant (H-88-78-1) and susceptible (Punjab Chhuhara) cultivars at different days-post-infection. We showed that less abundance of viral replicative intermediate in tolerant cultivar may have a correlation with a relatively higher accumulation of smallRNAs. MicroRNAs are speculated to be involved in defense against geminivirus infection; however, the studies are limited to determining the abundance of miRNA as well as the corresponding targets in response to infection. With a view to providing mechanistic insight into the miRNA-mediated defense mechanism, we examined the miRNAome of tomato in response to *Tomato leaf curl New Delhi virus* (ToLCNDV) infection. The relatively higher abundance of microRNA159 (miR159) during infection in the tolerant cultivar and the inverse correlation of miR159 abundance with its target, *MYB33* suggested their putative involvement in the defense response. Molecular characterization of the sly-miR159 and *SlMYB33* demonstrated their role in regulating the expression of a Resistance (*R*) gene, *Sw5*. Functional characterization and knock-down analysis showed that *SlSw5* interacts with AC4 gene (viral suppressor of RNA silencing) of the virus to trigger hypersensitive response (HR) at infection sites to limit the virus spread. Altogether, the study delineates the interaction between miR159-MYB33 module and Sw5 to activate HR for promoting the tolerance in tomato.

Session III

Theme: Plant Biochemistry and Crop Improvement
Keynote speaker: Dr. Alok K. Sinha, NIPGR, New Delhi

A crosstalk between ABA signalling, miRNA biogenesis factor and Mitogen Activated Protein Kinase

Alok Krishna Sinha
National Institute of Plant Genome Research, New Delhi 110067
Email: alok@nipgr.ac.in

Abstract:
Recruitment of HYPONASTIC LEAVES 1 (HYL1), a double-stranded RNA binding protein also termed as DRB1, to the microprocessor complex is crucial for accurate primary-miRNA (pri-miRNA) processing and accumulation of mature miRNA in plants. Mitogen activated protein kinase (MAPK) cascades are known to transduce variety of signals for the appropriate cellular readjustment. We report here regulation of miRNA biogenesis factor, HYL1/DRB1 by a MAPK. HYL1/DRB1 not only get phosphorylated by MAPK but also exhibit molecular protein-protein interaction. Abscisic acid (ABA) is known to activate MAPK and also regulate miRNA biogenesis and/or accumulation. We found that a ABA responsive transcription factor regulates HYL1 expression in a MAPK dependent manner. Finally we show that the crosstalk among ABA signalling, miRNA biogenesis factor and MAPK play important role in seed germination and post-germination growth in *Arabidopsis thaliana*.

Session IV

Theme: Genome Editing, Translational Genomics and Plant Breeding
Keynote speaker: Dr. P. K. Gupta, Charan Singh University, Meerut

Epigenetic Regulation of Gene Expression During Resistance to Leaf Rust in Wheat

P. K. Gupta
Department of Genetics and Plant Breeding
Charan Singh University, Meerut
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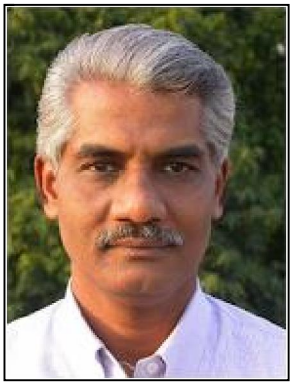
Abstract:
Our studies on epigenetic regulation of differential gene expression during resistance to leaf rust in common wheat involved both seedling resistance or all-stage resistance (ASR) due to the gene *Lr28* and adult plant resistance (APR) due to the gene *Lr48*. The studies were based on collaborative work undertaken by the following three institutes: (i) CCSU, Meerut, (ii) ICAR-IARI, New Delhi and ICAR-IIWBR, Shimla Centre. The work was facilitated by the availability of the following material (along with phytotron facilities) made available by ICAR-IARI; (i) a pair of near-isogenic lines (NILs) for ASR gene *Lr28* in the background of wheat cv HD2329, and (ii) a wheat cv CSP44, which carried an APR gene *Lr48*. In both cases, we examined differential expression of genes between compatible (susceptible) and incompatible (resistance) interactions, and the extent to which this differential expression was controlled by epigenetic modifications including the following: (i) genome-wide DNA methylation (involving cytosine methylation); (ii) acetyaltion of H3K4 and H3K9 and tri-methylation of H3K4 and H3K27; (iii) ncRNAs and lncRNAs. DNA methylation (including cytosine methylation in CG, CHG and CHH contexts) involved use of MSAP, MeDIP and BiSeq in case of *Lr28* and only MeDIP in case of *Lr48*. Histone acetylation (H3K4ac/K9ac) was examined for six differentially expressed genes using ChIP-qPCR, and histone methylation (H3K4me3/K27me3) was studied at genome-wide scale using ChIP-Seq. ncRNAs including miRNAs and lncRNAs were examined using RNA sequencing for *Lr28* only. The results in each case were compared with RNA-seq data to identify the fraction of differentially expressed genome that was due to epigenetic modifications. This collaborative work was undertaken during a periof of almost 10 years and led to publication of a series of research papers. Some of the results of these studies will be discussed during the presentation.

Session IV

Theme: Conservation of Genetic Resources IPR and Biosafety issue
Keynote Speaker: Dr. S. R. Yadav, Shivaji University, Kolhapur



Role of Educational Institutes in Documentation, Bio-prospecting, Sustainable use and Conservationof Plant diversity of Western Ghats

S. R. Yadav
INSA Senior Scientist, Department of Botany,
Shivaji University, Kolhapur-416 004 (Maharashtra) India
Email: srysuk@rediffmail.com

Abstract:
Plants are universally recognized as a vital part of the World's biological diversity and most essential resource for the planet. Many thousands of wild plants have great economic and cultural importance, potential to provide food, medicine, fuel, clothing and shelter for the people of the world. Plants play a key role in ecosystem stability and constitute an important component of the habitat for the world's animal life. Total number of flowering plants described is approximately 295,383 species; many of them are in danger of extinction because of habitat transformation, agriculture, over exploitation, alien invasive species, pollution and climate change. The disappearance of such vital and large amount of biodiversityis an important issue for the world community to halt the destruction of the plants diversity that is so essential to meet the present and future needs of Human kind. India is one of the 12 megacenters of biodiversity and has unique biogeographical composition. The three megacenters of biodiversity of India are Eastern Himalayas, Western Himalayas and Western Ghats. Western Ghats is a major center of endemism which alone provides a niche for about2253 endemic species of flowering plants. The present lecture is the synthesis of importance of plant diversity, role of educational institutes in plant diversity conservation, bio-prospecting plant sources and protection of Western Ghats.

LEAD TALKS

Theme: Plant Metabolites and Nutraceuticals

Lead Talk I: Dr. Siddharth Tiwari, NABI, Mohali

Biotechnological approaches for nutritional improvement in banana fruit

Dr. Siddharth Tiwari, Scientist E
National Agri-Food Biotechnology Institute (NABI), Department of Biotechnology, Government of India, Knowledge City, Sector-81, Mohali 140306, Punjab.
Email: siddharth@nabi.res.in

Abstract:
The application of conventional breeding for genetic improvement in a cultivated banana is difficult due to the triploid genome and the nature of parthenocarpic fruit development. Therefore, we have used modern biotechnological approaches as a promising tool for banana improvement programs. Vitamin A micronutrient deficiency (VAD) is the leading cause of preventable blindness, growth retardation and decreased immunity. It is a major health issue, especially in South-East Asian and African countries. The β-carotene is known as a main precursor for vitamin A biosynthesis in vegetarian diets of human beings. In plants, this precursor is synthesised by the carotenoid biosynthesis pathway. We aimed at enhancing β-carotenein banana by using gain-of-function (over-expression) and loss-of-function (genome editing by CRISPR/Cas9) biotechnological approaches. Two necessary enzymatic steps regulated by 1-deoxyxylulose-5-phosphate synthase (DXS) and lycopene epsilon-cyclase (LCY-ε) were identified by us for genetic engineering in the banana carotenoid biosynthesis pathway. DXS provides the substrate flux in the carotenoid biosynthesis pathway, whereas LCY-ε acts at branching point and diverts lycopene towards α-carotene. Our study revealed *DXS2*asa promising candidate for over-expression study, and the best overexpressing line showed nearly 20-fold higher content of β-carotene compared to control in banana fruits. Besides, targeted gene editing was established in banana by editing of *phytoene desaturase* (*PDS*) gene through CRISPR/Cas9 approach, and subsequently, implemented for mutation of *LCY-ε* gene in the banana genome. Our results establish that the loss-of-function (genome editing) and gain-of-function (overexpression) can be useful modes for nutritional improvement of banana.

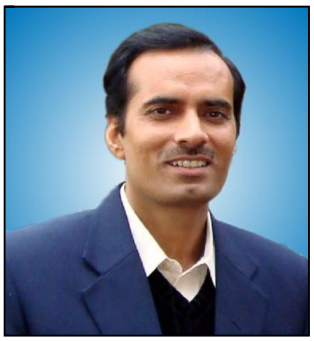
Lead Talk II: Dr. Sumit Ghosh, CIMAP, Lucknow

Understanding plant triterpene biosynthesis: key enzymes and pathway reconstruction

Dr. Sumit Ghosh, Principal Scientist,
Council of Scientific and Industrial Research-Central Institute of Medicinal and Aromatic Plants (CSIR-CIMAP), Lucknow 226015, India
Email: sumitghosh@cimap.res.in

Abstract:
Triterpenes (C-30 isoprene compounds) represent a large and structurally diverse class of natural products with various pharmaceutical and industrial applications. However, understanding triterpene biosynthetic pathway and the enzymes remain largely incomplete. Our research group at CSIR-CIMAP employed interdisciplinary approach to functionally characterize a suite of oxidosqualenecyclase (OSC) and cytochrome P450 monooxygenase (P450) enzymes that catalyze key cyclization and oxidation reactions towards triterpene scaffold diversification in medicinal plants. The co-expression of OSCs and P450s in heterologous hosts resulted in triterpene biosynthetic pathway reconstruction, indicating the utility of plant enzymes for medicinal triterpene biosynthesis in alternate hosts. Overall, my presentation will cover recent work of our group towards the identification of triterpene biosynthetic pathway enzymes and triterpene pathway reconstruction in alternate hosts.

Lead Talk III: Prof. Padmanabh Dwivedi, BHU, Varanasi



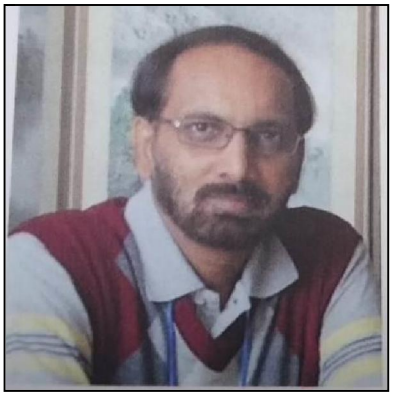
Conservation and *in vitro* immunomodulatory potential of *Gymnema sylvestre*

Vineet Kumar Singh and Padmanabh Dwivedi
Department of Plant Physiology, Institute of Agricultural Sciences
Banaras Hindu University, Varanasi, India
Email: pdwivedi25@rediffmail.com

Abstract:
Gymnema sylvestre R. Br (Family, Asclepiadaceae) is a highly valuable medicinal plant used in folk medicine to treat diabetes, obesity, asthma, etc., in India for antiquity andhas emerged as a potential panacea for the management of diabetes. Indiscriminate collection, over-utilization of this plant for commercial purposes by pharmaceutical companies, poor seed viability, low rate of germination and poor rooting ability of vegetative cuttings caused *G. sylvestre* as threatened to extinction and fast disappearing plant. Tissue culture offers an alternative propagation method which accelerates large scale multiplication, improvement and conservation of plant. *Gymnema sylvestre* showed better multiple shooting and regeneration of explants in full strength MS medium with 3% sucrose in comparison to ½ MS media. 0.5 mg/l BAP, 0.5 mg/l Kinetin and 3.0 mg/l IBA produced maximum number of shoots (7.00±0.70) and maximum length of shoots (6.57±0.75 cm). After hardening, they were established in the polyhouse and later transferred in the field where they showed 70% survival rate after two months. Diabetes mellitusis a syndrome characterized immunologically by lymphocyte apoptosis and reduced cell mediated and humoral immunity. Modulation of immune responses to alleviate diseases has been of interest, and traditional herbal medicines may play an important role in this regard. *In vitro* immunomodulatory effects leaf extract of *Gymnema sylvestre* (GS) was evaluated by gauging its effects on NBT reduction and NO production by peritoneal macrophages and on mitogen (ConA, PHA and LPS) induced splenic lymphocyte proliferation, in rat model.EC50 value was 3.10, 3.75 and 2.68µg/ml forNBT reduction, nitrite release and lympho proliferation, respectively. Potential effect was observed at 100 µg/ml in NO and ROS generation in macrophages and 20 µg/ml in lymphocyte proliferation. These findings suggest gymnemic acid and methanolic extract of *G. sylvestre* leaf that stimulates both myeloid and lymphoid components of immune system, and therefore, can restore the innate immune function. Through this study, the traditional knowledge of anti-diabetic property of *G. sylvestre* is scientifically supplemented with its immunemodulatory properties.

Theme: Plant Stress Management

Lead Talk I: Dr. P. Suprasanna, BARC, Mumbai



Induced Plant Mutations in the Genomics Era

Dr. Suprasanna Penna
Nuclear Agriculture and Biotechnology Division,
Bhabha Atomic Research Centre, Trombay, Mumbai – 400 085, India
Email: penna888@yahoo.com

Abstract:
Food security has become the prime concern because of the continued pressure of world population increase, dwindling eco-resources and climate change. There is a need to develop sustainable solutions to enable plant breeders to develop highly productive crops. Plant mutation breeding has become relevant and over the past several decades has played an influential role in the basic and applied aspects of agriculture. Mutant genes have played a vital role since their successful introduction into commercial crop varieties has significantly enhanced the quality and agronomic attributes of crop plants. To date, 3362 mutant varieties have been released for commercial cultivation and some of these have significantly contributed to economy. Large numbers of mutant varieties have been developed in Asia with China Japan and India in the top three positions in the world. Indian contribution has been important in the development of new mutant varieties with desirable traits such as higher yield, improved quality traits, disease and pest resistance, improved plant type and abiotic stress resistance. Induced mutations have played a major role in the discovery of genes that control important traits, understanding their functions and mechanisms of functional traits. Molecular tools have provided new screening avenues of mutation detection, and advances in genomics and crop genomes have added a new dimension into analyzing mutational events and mutant traits. New mutagenic resources of mutation induction combined with high throughput screening techniques and novel mutants applied to good agricultural purpose will foster the potential applications to improve plant breeding towards sustainable agriculture.

Lead Talk II: Dr. P. K. Singh, NBRI, Lucknow

Bio-prospection of plant diversity for novel insecticidal proteins/genes for next generation insect tolerant GM crops

P. K. Singh, Anoop Kumar Shukla, Santosh K. Upadhyay, Mithlesh K. Singh, Sunil K. Yadav, Jyoti Singh, Sharad Saurabh, and Manisha Mishra,
CSIR-National Botanical Research Institute, Lucknow.
Email: pksingh@nbri.res.in

Abstract:
White fly (*Bemisiatabaci* species complex) is one of the highly invasive insect pests of several field crops of agricultural, horticultural, and ornamental importance all over the world. High temperature, humidity, dense cropping, and nitrogen content in soil promote multiplication of this insect. Crops grown in polyhouses are also severely affected by this pest. The insect damages plants by sucking phloem sap, promoting growth of sooty mold and spreading plant viral diseases. Known insecticidal proteins viz; Cry toxins, enzyme inhibitors, lectins, chitinases, ribosome inactivating proteins etc. are either not efficacious or cause low toxicity to whitefly, thus transgenic crops for defence against white fly is not yet available. Moreover, researchers have not explored alternative strategies for identifying new insecticidal proteins in last two decades.
Plant biodiversity is a vast resource of biologically active molecules and functions. It has been seldom explored for new proteins (genes) with a targeted function. We screened untapped plant resources for insecticidal activity and identified a few potential plants. Our endeavour led to the isolation of 5 new insecticidal proteins; three proteins are efficacious to whitefly and other two possess to cotton aphids. All proteins are unique in their sequences. One of the insecticidal proteins (named as Tma12, 21.6 kDa) that kills whitefly (LC_{50} 1.9 µg/ml) is purified from a fern *Tectaria macrodonta*. The insecticidal protein was initially characterized as a chitin binding protein with minor chitinolytic activity, but subsequent studies established it as a Lytic Polysaccharide Monooxygenase (LPMO). It is notable that LPMO is found in microorganisms only and they use this enzyme in the digestion of complex carbohydrates. Tma12 is the first LPMO from a terrestrial plant. However, its role in source plant is yet to be elucidated. Tma12 is expressed in transgenic cotton under regulation of constitutive and phloem specific promoter. The optimally expressing transgenic cotton lines show excellent protection against whitefly. These lines control whitefly population by inhibiting egg laying and nymphal development and thus hampering colonization. Selected GM cotton line (Event 403) was tested at Faridkot, Punjab which is a hot spot for whitefly. The GM cotton requires one spray of pesticides to curb early attack of whitefly whereas Bt cotton requires 4-6 sprays. Absence of viral diseases and its DNA in transgenic and presence in non-transgenic cotton leaves in 4-month-plants shows that the transgenic strategy offers significant control over viral diseases.
T. macrodonta, the source of insecticidal protein, is an edible fern. It is consumed as vegetable in Nepal and used in concoction for gastric diseases in Central India. In a limited study, purified Tma12 in sub-chronic doses did not produce any symptomatic change in model animals. On other hand Tma12 cotton also did not show any toxic effect in other cotton pests and beneficial insects. This suggests that deployment of Tma12 in crop for protection against whitefly and viral diseases might be safe. Nevertheless, detail safety study with purified proteins and transgenic plant are required to meet the requirement of regulatory guidelines. Presently, we are stacking Tma12GM Cotton with Bt-cotton for broad insect resistance in Indian cotton varieties.
This is for the first time a new insecticidal protein is discovered from lower plant biodiversity. Whitefly and virus resistant transgenic crops have been an unmet need of agriculture biotechnology worldwide; our research has fulfilled the gap. This gene can be deployed in other crops as well to protect the yield from whitefly and associated viral diseases without application of hazardous pesticides.

Lead Talk III: Dr. Pradeep K. Agarwal CSMCRI, Bhavnagar

Regulating the ABA-dependent and -independent signalling for enhancing abiotic stress tolerance in plants

Pradeep K. Agarwal
Plant Omics Division
CSIR-Central Salt & Marine Chemicals Research Institute, Council of Scientific & Industrial Research (CSIR), Gijubhai Badheka Marg, Bhavnagar-364 002. Gujarat. India
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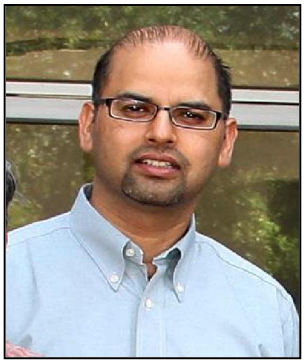
Abstract:
The climate resilient crops are required to overcome the huge crop loss caused by abiotic stresses worldwide. In the last two decades, several attempts had been made to substantiate the role of ‘‘single-function’’ gene(s) as well as transcription factor(s) towards abiotic stress tolerance. Since, the abiotic stress tolerance is multigenic in nature, therefore, the genetic transformation with transcription factors (TF) can provide better stress adaptation as they regulate the expression of an array of downstream genes. Transcription factors like MYB, MYC, bZIP, follow ABA- dependent and CBF/DREB follow ABA-independent signal transduction pathways. However, some TFs like NAC, WRKY, HDZipI/II, ERF and HSF follow both the pathway shows highly intrinsic role to manoeuvre stress tolerance. Recently several of these TFs are characterized from the glycophytic plants, however very limited research has been carried out from the halophytes. We have characterized both ABA-dependent and –independent type of TFs from the halophytes such as *Salicornia brachiata* and *Aeluropus lagopoides*. Salicornia is a succulent halophyte and accumulates 20-25% salt in its pith and is a good source for preparation of herbal salt. Aeluropus on the other hand is recretohalophyte with adaptive features like epicuticle wax production, salt secreting structures for salt secretion, small waxy leaves and strong root network. In our laboratory we had cloned MYB, DREB and NAC TFs which are involved in abiotic stress tolerance. Two different MYB TFs, SbMYB15 and SbMYB44 have been isolated from *S. brachiata.* Expression analysis revealed that SbMYB44 gets regulated with ABA, however SBMYB15 appear to follow an ABA-independent signalling. Both of these genes showed regulation by defence signalling molecules like SA and MeJa. Salinity, dehydration, high and low temperature also strongly regulate the transcript regulation of SbMYB15 and SbMYB44. The SbMYB44 recombinant protein showed binding to abiotic and anthocyanin responsive *cis* elements like $MRE_{CHS,}$ $MBS_{BZ-1,}$ rd22, MBS. The SbMYB44 conferred both salinity and drought stress tolerance in tobacco.The SbDREB2A showed higher expression in response to NaCl, drought and heat stress. The recombinant protein showed binding to both DREs (dehydration-responsive element), ACCGAC and GCCGAC. The SbDREB2A overexpressing lines showed both hyperionic and hyperosmotic stress tolerance by overexpression large number of abiotic stress tolerant genes.
Different NAC TFs are isolated from *A. lagopoides.* The AlNAC4 TF regulated by the dehydration and H_2O_2 treatments, showing its role in osmotic and oxidative stress, respectively. The ectopic expression of AlNAC4 gene in tobacco showed significant tolerance to H_2O_2 by maneuvering biochemical and molecular pathways. Another TF, AlNAC1 showed very strong tolerance towards drought tolerance and active photosynthesis rate during stress condition. These results indicate that DREB2A/MYB/NAC TFs can be used for engineering stress tolerance in crop plants.

Theme: Plant Biochemistry and Crop Improvement

Lead Talk I: Prof. Giridhar Pandey, South Campus, Delhi University



A story of mitochondrial gate-keeper: What we know about VDAC and its function in plants?

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Abstract

Adverse environmental conditions, such as salinity, drought, and extreme fluctuation in temperature, cause enormous losses to agricultural productivity globally. Moreover, degrading environmental conditions are the major cause for a steep decline in average yields for many key crop plants. Several of these abiotic stresses lead to generate reactive oxygen species (ROS), which causes the oxidative stress and hamper the overall growth and development of plants.

Voltage-dependent anion channels (VDACs) are highly conserved β-barrel proteins in eukaryotes and regulate metabolite transport between mitochondria and cytoplasm. VDACs are known to play an important role in regulating mitochondrial Ca^{2+} homoeostasis. However, in plants, the relationship of VDACs with Ca^{2+} is not elucidated in detail. VDACs can also transport reactive oxygen species (ROS) such as superoxide radical ($O_2^{\bullet-}$) from mitochondria to the cytosol. Both Ca^{2+} and ROS can also, in turn, modulate permeability and conductance of VDACs and effect VDACs functioning. So, we have characterized the Arabidopsis VDAC proteins using *Δpor1* to test their role in response to ROS and salt stress inducing agents. Using this system, we have demonstrated the role of Arabidopsis VDAC proteins in respiration, maintaining mitochondrial membrane potential (MMP), reactive oxygen species (ROS) homeostasis and (oxidative and salt) stress. Furthermore, we hypothesized that oxidative stress leads to generation of Ca^{2+} signature, which is transduced downstream in the pathway by calcineurin B-like protein (CBL) -interacting protein kinase, CIPK9 and this in turn, phosphorylates VDAC3 at the mitochondria. The phosphorylated VDAC3 probably serves as a gateway for passage of ROS from mitochondria to cytosol and regulate the cellular physiology. In conclusion, we report a CIPK's involvement with outer membrane mitochondrial channel "VDAC" in potentially regulating the oxidative stress responses in the plant.

Lead Talk II: Prof. Jennifer Ann Harikrishna, University of Malaya, Malaysia

dsRNA to determine the role of MYB family genes in orchid flower shape and colour

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Abstract:
Application of double-stranded RNA (dsRNA) has emerged as a useful and rapid reverse genetics tool to study gene functions. Genes regulating cell shape and pigment biosynthesis have immense importance in generating plants with novel flower colour and shape. R2R3-MYB transcription factors were reported to play important roles in regulating cell shape and pigment biosynthesis in several plant species. However, little is known about the function of the *R2R3-MYB* genes and the association with pigment formation and flower cell shape in the popular orchid genus *Dendrobium*. This study identified 82 full-length *DhMYB* transcription factor gene coding sequences within a *Dendrobium* genome. Phylogenetic analysis has identified three *R2R3-MYB* genes (*DhMYB1, DhMYB2* and *DhMYB3)*, clustered with MYB sequences that are known to be involved in flower colour and cell shape. These three *DhMYBs* showed differential expression during six different stages of flower development. Exogenous application of*DhMYB1*, *DhMYB2* and *DhMYB3*dsRNA on *Dendrobium* hybrid (*Dendrobium* Burmese ruby × *Dendrobium* Mae-klong River) flower buds showed reduced expression of RNA compared with untreated control but no apparent difference in flower pigmentation. Analysis of adaxial epidermal cells of labellum of flower treated with dsRNA of *DhMYB1* using scanning electron microscopy showed flattened epidermal cells while those of control flowers were conical shaped. In contrast, flowers treated with dsRNA of *DhMYB3* and *DhMYB4* showed decreased pigmentation in flowers and lower anthocyanin content (*DhMYB3*; 1.38-2.28-fold and *DhMYB4;* 1.3-4.09-fold) compared to control flowers.

Lead Talk III: Dr. Jitendra Thakur, NIPGR, New Delhi

Structure and Function of Plant Mediator Complex

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Abstract:
Mediator is an important component for the regulation of class II gene transcription. It serves as a connecting link between transcription factor and transcriptional machinery. Mediator is a huge complex in which subunits are arranged in four different modules; head, middle, tail and kinase. These modules establish contacts with plethora of other proteins to regulate the process of transcription. Our study suggests that presence of intrinsically disorder regions in several subunits makes the Mediator complex very flexible. There is not much study on the holistic view of plant Mediator complex. So, we generated an interaction map of Arabidopsis Mediator subunits to understand the arrangement of the subunits followed by mapping the domains involved in these interactions. Structures of interacting regions were predicted by using bioinformatics tools and then placed together to expound the overall structure. One subunit, MED15, in the tail module contains KIX domain at its amino terminus. The KIX domain, important for protein-protein interaction, was first discovered as a part of the large multidomain transcriptional activator histone acetyltransferase p300/CBP. Later on, this domain was identified in Mediator subunit MED15. We found that in CBP, the disorder region following the KIX domain, has evolved from the Med15 KIX domain. In both of these proteins, the KIX domain has been shown to be a target of activation domains of diverse transcription activators and found to be essential in several gene-activation pathways in fungi and metazoans. However, not much is known about KIX domain proteins in plants. We made an attempt to characterize all the KIX domain proteins coded by *Arabidopsis* and rice genomes. Interestingly, KIX domain was found not only in p300/CBP- and MED15-like plant proteins as known earlier, but also in F-box containing proteins in rice and DNA helicase in *Arabidopsis*. In rice, expression analysis revealed overlapping expression of *OsKIX*_3 (OsMed15a), *OsKIX*_5 and *OsKIX*_7 in seeds of different stages of development, suggesting their individual or combined role during rice seed development. In my talk, I will focus on OsMed15a. Association analysis using the genotyping data of *in silico* mined SNP loci in 539 rice genotypes identified one non-synonymous SNP locus in the KIX domain of OsMed15a showing significant correlation with the grain size/weight. Though several grain size/weight-associated transcription factors (TFs) and their target genes are known, the molecular landscape regulating this trait is unclear. I will present data to establish OsMed15a, a Mediator subunit, as a connecting link between rice grain size/weight-regulating TFs and their target genes.

Theme: Genome Editing, Translational Genomics and Plant Breeding

Lead Talk I: Dr. C. Viswanathan, ICAR-IARI, Delhi.

Genetic engineering and genome editing for abiotic stress tolerance of rice

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Abstract:
Rice is the major staple food crop of India. Rice productivity is adversely affected abiotic stresses such as drought, salinity, heat and cold stresses. Tolerance to these abiotic stresses is regulated by ABA-dependent and –independent pathways in plants. Hence genes for ABA-dependent pathways and ABA-independent pathway were analysed in rice for their ability to confer tolerance to various stresses. In ABA-dependent pathway, rice ABA receptor genes were analysed by using transgenic approach in rice. Transgenic rice cv. Pusa Sugandh 2 overexpressing ABA receptor *OsPYL6* either from constitutive and stress inducible promoter conferred enhanced drought tolerance at both vegetative and reproductive stress through enhanced expression of various stress responsive genes. $P_{AtRD29A:}PYL6$ transgenics also exhibited about 25% lesser whole plant transpiration as compared with WT plants under drought stress. However, *PYL6* overexpression significantly reduced grain yield under non-stress conditions. Stress-inducible overexpression ABA receptor *OsPYL10* significantly enhanced higher survival rate of transgenic rice cv. MTU1010 under cold stress and tolerance to drought stress (-80 kPa SMP). In ABA-independent pathway, *AtICE1* overexpression conferred enhanced tolerance to cold, salt and drought stresses to the rice transgenic MTU1010. *ICE1* transgenic rice plants produced significantly higher grain yield as compared with WT plants under control conditions as well as stress conditions. CRISPR-Cas technology helps development of elite cultivars with desirable alleles by precision gene editing. Hence, a study was carried out to create mutant alleles of *DROUGHT AND SALT TOLERANCE* (*DST*) gene by using CRISPR-Cas9 gene editing in *indica* rice cv. MTU1010. A transgene-free homozygous *dst* mutant with 366 bp deletion ($dst^{\Delta 184–305}$) was identified which has a deletion of amino acid residues from 184 to 305 in frame. The $dst^{\Delta 184–305}$ mutant enhanced leaf water retention under dehydration stress, reduced stomatal density and enhanced tolerance to salt stress. Thus, appropriate regulation of ABA-dependent and –independent genes by using genetic engineering and genome editing offers solution to development of stress tolerant rice varieties.

Lead Talk II: Dr. A. K. Joshi, CIMMYT-India, New Delhi

Integrating precision phenotyping and genomics in wheat improvement amidst widening challenges

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Abstract:

The importance of wheat as a staple food crop continues to grow. In fact, it appears much more important in the post-Covid world. The demand for wheat grain is increasing with population growth and also due to increased preference for diet based on wheat-based commodities. Wheat productivity can increase at significantly higher rate through various interventions. Significant progress continues to be made to understand the genetic basis and diversity of key traits and in developing adapted germplasm combining multiple traits needed for their successful adoption by the farmers. Genetic diversity present in improved germplasm for various targeted traits including nutritional quality, combined with upscaling of breeding and phenotyping and utilization of new tools and approaches offer great potential to enhance genetic yield gains in combination with other necessary traits. One of the promising tools to increase genetic gain is genomic selection. In order to identify the best lines for grain yield and other economically important traits in wheat cultivars, there is need to complement phenotypic selection with genomic selection based on the genomic estimated breeding values. This will require a combination of precision phenotyping with high level of genotyping. The successful wheat breeding program rely on quick adoption of strong partnership with the national and international institutions. Following this approach, it is believed that it will be possible to achieve breedin targets for genetic gain in wheat for 2050.

Lead Talk III: Dr. Samir Sawant, NBRI, Lucknow

A novel male sterility-fertility restoration system for the hybrid seed production in cotton

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Abstract:
The developments of new technologies are needed to meet the demands of global food security by increasing the gross crop productivity without increasing water and fertilizer use in the definite arable land. The hybrid crop offers 20 to over 50% yield increase and presently contributes to more than half of the major crop production. Inductions of male-sterility in the female parent followed by fertility restoration in F1-hybrid are the prerequisite for the hybrid seed production at the commercial scale. We developed a novel male sterility-fertility restoration system for hybrid seed production by engineering the innermost nutritive anther wall layer tapetum. We also report novel use Arabidopsis *BECLIN1* when over-expressed in the tapetum using a expression system confers male sterility in transgenic plants.
Further, we developed a novel transcriptionally regulated reversible expression system (ES) that drives high-level and stringent expression of the desired gene in the post-meiotic tapetal cells and this expression was completely abolished in F1-progeny when regulated by another system. The ES works on functional complementation of TATA-box mutant (TGTA) and TATA-binding protein-mutant-3 (TBPm3) whereas the fertility of F1-hybrid was restored by limiting TBPm3 availability through Constitutive-photo-morphogenesis-1 (COP1)-mediated degradation of Long Hypocotyle-in-Far-Red1 (HFR1) tagged TBPm3 protein ($HFR1^{NT131}$-TBPm3). *Nicotiana tabacum* has been used initially for the proof of principle using the reporter gene (*gusA*). Furthermore, the ES was deployed to generate a complete male-sterile female parent in tobacco by expressing the Arabidopsis *BECLIN1* gene and complete restoration of male-fertility was achieved in F1-progeny by abolishing its expression. The BECLIN1-triggered autophagy at the point of developmentally programmed tapetal-PCD that reprogram cell death pathway by altering gross cellular homeostasis, resulting in pollen abortion. This proven system (ES) was then deployed in cotton by developing male sterility-fertility restoration transgenic lines using somatic embryogenesis methods on the cocker-312 background. We further aim to establish this system from transgenic cocker-312 to elite parental lines of commercial hybrid through marker-assisted backcrossing (MABC) to exploit its economic benefits.

Theme: Conservation of Genetic Resources, IPR and Biosafety issue

Lead Talk I: Dr. M. K. Janarthanam, Goa University, Goa

An integrated approach to the conservation of plants

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Abstract:
At the global level, several conservation programmes on plant species are going on. Diverse literature, both from the immediate past and the current, is providing testament to these efforts. Most of them are successful, at least in the short term and have contributed to the knowledge base of conservation science. However, the major drivers that lead to the rarity of the species, viz. (1) Habitat degradation/destruction, (2) Over harvesting from the wild, (3) Spread of exotic weeds, (4) Climate change, (5) Ecological disruptions, (6) Economic considerations for abandoning the traditional cultivars, (7) Factors that are intrinsic to a given species, and many more, continue to operate. More importantly, the increasing disconnect between human and nature is making conservation efforts much tougher. In our country, concerted actions of Department of Biotechnology (DBT) have given positive results. However, the objective of this presentation is to show how a narrow approach towards conservation is pointless in the long run at the same time advocating for an integrated method for better results. Our experiences and efforts towards the conservation of few RET species of the Western Ghats such as *Dipcadi* spp., *Impatiens* spp., *Phyllanthus talbotii* and *Pseudoglochidion anamalayanum* are shared. Based on our as well as experience of contemporary botanists, we emphasize here that for successful conservation programme, it is necessary to (i) conduct thorough integrated ecological, taxonomical and phytogeographical study on the species concerned, (ii) take into confidence the multiple stakeholders and (iii) minimize if not eliminate the factors that pushed them to the threatened category. In the case of medicinal plants, we suggest having a mechanism similar to 'Aroma mission'. However, when it comes to the traditional cultivars, the issue is much trickier, which could be solved only through an integrated national mission.

Lead Talk II: Dr. V. Arunachalam, ICAR-CCARI, Goa

Vegetable amaranths of Goa for food colorant and nematode pest management

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Abstract:
Plant genetic resources form a very valuable asset in crop improvement. The objective is to collect, conserve amaranth germplasm and characterise for betacynanin content and pest susceptibility. Betacyanins exhibit antioxidant activity and are used as food colorant in beverages and confectionery. Amaranth with high degree of susceptility to nematode and show potential as trap crop in integrated pest management strategies. The exploration visits across Goa state were conducted from 2011 to survey collect, and conserve the germplasm. The collected germplasm accessions were regenerated and characterized with two released varieties Arka Arunima and Co-2. The study led to 25 conserved accessions of three species with national identity numbers (*A. tricolor* L. IC 0598179 to IC 0598193; IC 0611600 to IC 0611606; *A. cruentus* IC 0598178, and *A dubius* IC 0611598 to IC 0611599). A single incomplete dominant gene controlled the leaf colour of amaranth with green (rr), intermediate (Rr) and red (RR) genotypes. Betacyanin content in leaves ranged from 35 ±0.3 in IC-0598193 to 416 ±19 µg per gram fresh weight in IC-598190. The color grab smart phone app, fourier transform infrared spectroscopy, spectroradiometer, and hunterlab colorimeter were also employed to assess the color. Three highly susceptible genotypes and one tolerant genotype to root knot nematode were screened with inoculums of two populations (Old Goa and Varanasi) of *Meloidogyne incognita* Kofoid and White. The study led to identification of two potential conserved amaranth germplasm accessions one with high foliar betacyanin content (IC 0598190) and a highly nematode susceptible accession (IC 0598184).

ORAL PRESENTATIONS (OP)

Theme: Plant Metabolites and Nutraceuticals

OP1.1: 'Nutraceutical starch' - An interplay of food matrix components

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Abstract:
Nutraceuticals and starch have been well known as dietary components owing immense health promoting effects but the term 'nutraceutical starch (NS)' has recently used. Starch is the major dietary source of energy, but in excess through carbaholic diets it leads to chronic hyperglycemia leading to type II diabetes mellitus (TIIDM) and its sequalae. As there is no effective cure for TIIDM, the existing management strategies have majorly focused on identifying low glycemic index (GI) foods which controls the post prandial glucose spike. Recently, in the quest for a better substitute to refined carbohydrates which can significantly suppress quick glucose release, two types of starch namely slowly digestible starch (SDS) and resistant starch (RS) got unprecedented attention. Studies have highlighted the fact that carbohydrate source rich in both SDS and RS, in combination known as NS can play role in prevention and in therapeutic regimes to manage DM. Such tailored bioavailability of starch was majorly fine-tuned by the matrix composition and inherent microstructure. Initial studies in this direction, we optimized to isolate and quantify NS, profiled in various cereal model crops and correlated with their inherent microstructure. A possible correlation has been deduced among the molecular structure and NS content, where the inherent hierarchy, starch granule morphology as well as compactness in packing leading to complex crystallinity, was highlighted. Further the role of inherent food matrix components like polyphenols and lipids, their physical interactions among themselvestowards NS formation were also evaluated. Possibility of exogenous lipid addition towards altering starch structure, bioavailability and NS formation, shared novel insights on the formation of stable crystalline amylose-lipid binary complexes. Many more understanding further complex ternary and quaternary complexes led to propose novel model for NS formation. NS starch being of low glycaemic amplitude, has immense applications for developing newer food prototypes and for enriching the menu of diabetics.

OP1.2: Untapped nutraceutical potential of *Cocos nucifera* L.- the Kalpavriksha on earth

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Abstract:
Coconut (*Cocosnucifera* L.) belongs to family Arecaceae is an important crop of tropics and sub-tropics. Almost all the parts of coconut are either used as the food, oil, fibre, coir, etc. The coconut tree has given number of secondary products (eg. virgin coconut oil, inflorescence sap-derived sugar etc) of immense nutritional value to humans. Biochemical analysis of coconut and its products have revealed their composition, functional bioactives and nutritive importance. Coconut testa is a brown coloured skin covering the endosperm which remains underutilized in the coconut processing industries. Biochemical analysis of testa-derived biocolourant and oil from diverse genotypes of coconut suggest the products have rich anti-oxidant potential since it comprises polyphenols including flavonoids and anthocyanins. Fatty acid profiling of coconut testa oils revealed lauric acid as the most predominant fatty acid. Poly and mono unsaturated fatty acids contents of the testa oils are relatively high underscoring their nutritional benefits. Also the emerging biochemical evidences of coconut oil in conferring neuroprotective effects (in the treatment of diseases like Alzheimer's) will be discussed.

OP1.3: Phytochemical Analysis of Rhizome of *Zingiber officinale* in Different Solvents

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Abstract:
The important of medicinal plants in drug development is known to us and human have used them for different diseases from the beginning of human history. Traditional folk treatment from wild plant has always guided researchers to search for novel medication to develop healthy life for human. In addition, some medicinal plants are still obscured within the plant which need to be scientifically evaluated. The present study was performed to study the phytoconstituents in methanolic and aqueous rhizome extract of *Zingiber Officinale*. This plant has been used to treat common ailments such headache nausea, vomiting, indigestion, flu, diarrhea, arthritis, colic, and even painful menstruation. The phytochemical analysis of aqueous crude extract of the *Zingiber officinale* rhizome indicated the presence of carbohydrate as primary metabolites and glycoside as secondary metabolites. The phytochemical analysis of methanol extract of *Zingiber officinale* showed the presence of carbohydrate and protein as primary metabolites and glycoside and tannin as secondary metabolite. HPLC analysis reveal that methanol fraction of *Z. officinale* contains a bioactive component gallic acid, one of the tannin components. It can be concluded that the active compounds tannin and glycosides present in *Zingiber officinale* species should certainly find place in treatment of various bacterial infections and indicate that this spice should be studied more extensively to explore its potential in the treatment of infectious diseases.

OP1.4: Nutraceutical characterisation of anthocyanin-rich flower bracts of banana cv. Grand Naine (*Musa* spp., AAA)

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Abstract:
Banana is an important crop cultivated in the country and the fruit, flower, centre core stem and leaf posses a large array of bioactive compounds chiefly carotenoids, flavonoids including anthocyanins and fructans. Flower bracts are a rich source of anthocyanins with commercial varieties possessing as high as 95 mg/100 g and some genotypes possessing more than 350 mg. Anthocyanins are natural colourants with high health-promoting properties. Here, anthocyanins from flower bracts of Grand Naine, a popular Cavendish subgroup cultivar, were profiled using HPLC, macroencapsulated by spray drying at four temperatures with maltodextrin (20 DE) as wall material at 20% conc. and characterised and antioxidant and anticancer activities of free and encapsulated anthocyanins were studied. The main anthocyanins identified were cyanidin 3-*O*-rutinoside (Cy-3-glu) (72%) and cyanidin 3-*O*-rhamnoside (12%). The best spray dried product was obtained at 140 ^{o}C and retention, solubility and encapsulation efficiency of anthocyanins were 74.43 mg, 95.82% and 75.12%, respectively. Morphological characterisation by SEM of the microcapsules showed spherical in shape with dented surface and mean size distribution of anthocyanins was around 10 µm. Antioxidant activities measured by TEAC and ORAC assays were 166.5 and 624.4 µmol TE/100 g, respectively. *In vitro* assays by MTT and MMP revealed that free and encapsulated anthocyanins more effectively inhibited colon and cervical cancer cells (HT-29 and HeLa). The investigation prove that anthocyanins of flower bracts of bananas could be used as an effective nutraceutical and the predominant anthocyanin in flower bracts of Grand Naine is Cy-3-glu, nutraceutical properties obtained in the study is attributed to this metabolite.

Keywords: Anthocyanins, cyanidin 3-*O*-rutinoside, macroencapsulation, antioxidant activity, nutraceutical

OP1.5: Beta Amylase as a Selection Criteria for Improving Diastatic Power in Malt Barley

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Abstract:
Barley (*Hordeum vulgare* L.) is an ancient and one of the earliest domesticated cereals. Barley is usually considered as a poor man's crop owing to lesser resource requirement and ability to grow in harsh/poor soil conditions as compared to other cereal crops. In India the crop is slowly changing to an important industrial crop due to increased consumption of malt-based products owing to increasing urbanization, changing lifestyles and globalization. Barley is the preferred grain for malting due to certain physical and biochemical characteristics. The major uses of barley malt are in making beer, energy drinks, confectionary and several other products. However, the barley to be used for malt making must have certain minimum quality standards to qualify as malting barley. Besides the higher starch content, the barley grain must have the starch hydrolysing activities for degradation of starch. The collective activity of several starch degrading enzymes that accumulate or are activated during malting (beta-amylase, alpha-amylase, limit dextrinase and beta-glucosidase) is commonly known as diastatic power. Off late the malt industry is demanding higher diastatic power in the malt. Therefore, it is important to identify the biochemical parameters correlated with higher diastatic power for selection of better genotypes for barley improvement and for screening smaller quantity of grains in early generations of breeding. In this study 32 genotypes were evaluated for grain protein content, grain beta amylase, malt diastatic power, malt alpha-amylase and malt beta amylase. A strong positive correlation was obtained between malt diastatic power and grain and malt beta amylase activity in comparison to grain protein content. Therefore, selection for higher beta amylase activity can be one of the better criteria for higher diastatic power in malt.

Theme: Plant Stress Management

OP 1.1: Unfolding the Story of RuBisCo Activase in Wheat under Terminal Heat Through Omics Approaches

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Abstract:
RuBisCo activase (Rca) is a catalytic chaperone modulating the activity of RuBP carboxylase (RuBisCo) - the key enzyme involved in carbon assimilatory pathway in plants. RuBisCo is present in an inactive form inside cells and requires a complimentary protein RuBisCo activase (Rca) in order to become active and execute the carbon fixation process. At the ambient temperatures, RuBisCo is maintained in an active state by the continued action of Rca that converts RuBisCo from an inactive closed conformation to an active open conformation. Rca is heat labile protein having optimum temperature of 32ºC (as reported in other crops). Mechanistic, structural and kinetics of Rca have been hampered by its exceptionally high degree of thermo-lability, size, polydispersity and propensity to subunit aggregation. Very limited information about the wheat *Rca* is available on public domain. Here, we have identified 12 putative transcripts of *Rca* through de novo transcriptomic and gel-free proteomics approaches. Further, we cloned five novel Rca genes from contrasting wheat cvs. We also purified ~46 kDa recombinant Rca protein from *E. coli* cells through heterologous expression. Further, 18 Rca mutants were developed through site-directed mutagenesis and were characterized for their thermal stability. *In vitro* activity assay showed maximum stable activity under differential HS in case of mut138, whereas other mutants showed drastic decrease in the activity with increase in the HS. Rca has the potential to modulate the activity of RuBisCo under HS, and provides the most probable solution for mitigating the terminal HS problem in wheat. Mechanistic role of thermostable Rca will help in developing more efficient carbon assimilatory pathway with ~10% increase in wheat yield under elevated temperature. The approach is aimed at developing a 'climate-smart' wheat crop.

OP1.2: Conditional pathogenesis: understanding why potentially beneficial rhizobacteria turn pathogenic under certain environmental conditions

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Abstract:
Plant growth promoting rhizobacteria (PGPR) are beneficial soil bacteria that colonize the rhizosphere and help plants in myriad ways. Some PGPR that are isolated from extreme environments can with-stand abiotic stresses and help plants in ameliorating the impact of such stresses. Our laboratory focusses on understanding the precise molecular mechanisms underlying such beneficial interactions between plants and PGPR. Here we discuss a unique situation which we call "conditional pathogenesis" in which a certain strain of drought and thermo-tolerant PGPR, namely, *Pseudomonas putida* AKMP7 becomes pathogenic towards *Arabidopsis thaliana* under drought conditions, while being beneficial under well-watered conditions. *Pseudomonas putida* AKMP7 was able to withstand extreme drought-like conditions as evidenced by growth under 25% polyethylene glycol supplementation. It also released high quantities of the auxin conjugates, IA-Asp, IA-Phe, IA-ala and indoleacetamide and the cytokinin, zeatin into the growth medium. The concentrations of some of these phytohormones/conjugates were actually higher under dehydrating (PEG supplemented) conditions than under normal (non-stressed) conditions. We also found that, when inoculated to the roots of *A. thaliana* under drought conditions, AKMP7 caused enhanced growth stunting, faster drying and diminished plant water content as compared to drought treated plants without AKMP7 inoculation. We also found the drought-treated, inoculated plants to have typical root structure architecture associated with enhanced dehydration. Based on our observations, we hypothesize that the bacterial phytohormone conjugates may have a role to play in this accelerated drought mediated injury of inoculated plants, since compounds such as IA-Asp are known contributors to bacterial pathogenicity. The precise molecular mechanisms leading to such a phenomenon of conditional pathogenesis is currently under investigation in our laboratory.

Theme: Plant Biochemistry and Crop Improvement

OP1.1: A novel processing technique to reduce rancidity in stored pearl millet flour: It's effect on nutritional quality and functionality

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Abstract:
Pearl millet is considered as a highly nutritious food crop having unlimited health benefits. Despite being nutrient dense, use of pearl millet is limited due to rancidity and off-odor development in the flour during storage. Higher lipid content (5 to 6%) with highly active rancidity causing enzymes (lipase, lipoxygenase, peroxidase and polyphenol oxidase) causes hydrolysis of lipids to free fatty acids and its peroxide derivatives leading to rancid flour, which hinders the commercialization of pearl millet and its products. Rancidity/off-odour development not only affects the quality of flour but also affects taste, odour and can have an impact on nutritive value. We optimized an efficient processing technology – called *"hydro treatment (HT)-hydro thermal (HTh) and thermal near infrared rays (ThNIR)" successive treatments* (Fig.1) and filed patent (Patent Application No. 202011037363 and Filing Date- August 31, 2020). This method is not only effective in reducing rancidity but is also an economically feasible option due to less energy input. The optimized processing method was applied to pearl millet variety (Dhanshakti) and the treated flour was stored up to 90 days at room temperature (RT). From our results, it was evident that, the optimized processing method is highly efficient in reducing rancidity from 90 to 97.72% at 60 days of storage and 66 to 68% at 90 days' storage of treated flour at RT. Further, the processed pearl millet flour showed positive impact on nutritional quality and functionality. Thus, innovated successive hydrothermal treatment is highly efficient technology to limit the rancidity of flour even after storage up to 90 days at RT. This technology thus can enable to pave the way forward to generate consumer demand for pearl millet through value added processed foods.

OP1.2: Plant signalling- a mode of communication in plants

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Abstract:
Although, plants are non motile, nature has gifted them with best sensory mechanism with which they sense the environment, communicate and act accordingly. The signaling networks help plants to perceive environmental signal and translate it into a response. There are different signaling molecules present inside plant working specifically against specific environmental stress signal. One of such important signaling pathway is "Mitogen Activated Protein Kinase (MAPK) pathway", and intensively studied to be involved in environmental stress and developmental response. MAPK pathway is composed of three tier signaling system which perceives extracellular signals and conveys to the nucleus by phosphorelay mechanism. As rice is the most important crop plant and is staple food in many countries, its yield is adversely affected by rice pathogen *Xanthomonas oryzae*. Researchers all around the world are finding solutions to increase the yield of the rice crop to sustain food security. In my piece of work, I was succeeded in finding a MAPK cascade composed of MKK3-MPK7-WRKY30, which protects rice plant from pathogen *X. oryzae*. In this study, gene expression analysis was carried out to study the MAPK components activated and upregulated in response to *X. oryzae*. Further, different protein-protein interaction techniques were used to study the interactions between upstream and downstream MAPK components. The role of this cascade was studied by generating transgenic in rice overexpressing MKK3-MPK7-WRKY30 cascade wherein it was observed that these plants were protected from *X. oryzae*.

OP1.3: Glutathione S transferase: A versatile protein family

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Abstract:
Glutathione-S transferase (GSTs; EC 2.5.1.18) is a multifunctional protein family in plants. It has evolved primarily from gene duplication of an ancestral GSH binding protein. It has been categorized in 14 classes in photosynthetic organisms on the basis of evolution, corresponding functions, sub cellular location, and active site residues. All plant GSTs have relative molecular masses of around 50 kDa and are homodimer or heterodimer composed of two similarly sized (~25kDa) subunits. GSTs consist of two domains: a conserved N-terminal domain (G-site for binding of GSH) and relatively less conserved C-terminal domain (H-site, with which hydrophobic toxic molecules interact). It is functionally active in cytoplasm, nucleus, mitochondria, chloroplast, and also in plasma membrane. It is involved in diverse plant functions like biotic and abiotic stress management, plant growth and development, phytohormone signaling, cell signaling, regulation of redox homeostasis, biosynthesis and transport of secondary metabolites such as anthocyanin, tetrapyrrole metabolism, and controlled cell death (apoptosis). Considering its versatility, this protein family has attracted attention in various biotechnological applications such as in developing stress resistant crops, in nanotechnology, in developing biosensors, in environmental biotechnology, in plant breeding, etc.

OP1.4: Genome wide and candidate gene association studies for flowering time traits in linseed (*Linum usitatissimum*)

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Abstract:
Assessment of genetic diversity, extent of trait variation among germplasm and deciphering genetic basis of important traits facilitate the effective use of genetic resources. In linseed, early maturity is desirable as it helps avoid several biotic and abiotic stress. In present study, panel of 131 diverse germplasm accessions were evaluated for 25 agro-morphological traits in six different environments comprising three different locations during 2017-18, 2018-19 and 2019-20. Remarkable variability was observed for flowering, maturity and other economically important traits such as thousand seed weight, capsule number, seed, and capsule area. These 131 accessions were used for generating genome wide SNPs using Genotyping by Sequencing approach. For 131 accessions, a total of 68925 high quality SNPs were obtained after standard filtrations. The genetic population structure analysis classified the 131 linseed germplasm accessions into four distinct populations. The genome wide association study was conducted using these SNPs showed that eight SNPs were associated with important traits such as days to 50 % and 95% flowering, capsule size, seed size and plant height with p value (–log10(p)) of more than 5.0. Additionally, allelic variation in a potential candidate gene, a floral homeotic gene encoding APETALA2 transcription factor was studied in two early and two late flowering and maturing accessions by PCR amplification and sequencing. Total 12 SNPs were identified, of which six could distinguish early and late accessions. The genetic and genomic resources identified here are expected to aid in linseed genetic improvement programme targeted to specific traits, especially, early flowering.

Key words: Linseed, flowering and maturity time, genotyping by sequencing, SNPs, association

Theme: Genome Editing, Translational Genomics and Plant Breeding

OP1.1: RNAi mediated resistance development against rice diseases: Exploiting pathogen genes and host non-coding RNAs

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Abstract:
RNA interference (RNAi) is the sequence-specific gene-silencing mechanism which involves small non-coding RNAs to regulate gene expression and genome integrity. MicroRNAs (miRNAs) and small interfering RNAs (siRNAs) are the most studied small endogenous non-coding RNAs ubiquitously found in eukaryotic organisms. MicroRNAs confer adaptive changes in host plant during diseases and can either target resistance genes or directly regulate defense responses to impart plant immunity against pathogens, while siRNAs produced exogenously from key pathogen genes can impart resistance by arresting the replication and growth of the pathogen. We revealed RNAi pathway and candidate target genes for RNAi mediated pathogen-derived resistance in *Rhizoctonia solani* causing sheath blight disease in rice. Resistance was developed against tungro and sheath blight diseases of rice by producing siRNAs against coat protein3 and polygalacturonase genes, respectively. Known and novel miRNAs were identified in six diverse rice cultivars during *R. solani* infection using deep sequencing approach. Fungal infection/immunity associated miRNAs and target genes were analyzed in *Oryza sativa* and six wild relatives of cultivated rice. Further, fungal genome encoded miRNA-like RNAs (milRNAs) of *R. solani* were identified by RNAseq of small RNAs. Some of the notable gene regulons such as Osa-KANADI1:Rhi-milR-124, Osa-vacuolar-sorting receptor precursor: Rhi-milR-13, and Osa-nuclear transcription factor Y:Rhi-milR-131 were identified, revealing a novel dimension of cross talk of gene regulation during host-pathogen interaction. In the absence of host-plant resistance, RNAi based approaches could be alternate strategies for the development of resistance against these invincible pathogens causing huge damage to rice crop.

OP1.2: Epigenomic manipulation of crop plants for trait improvement

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Abstract:
Improvement of crop plants over the decades has been accomplished primarily by utilizing genetic variation that existed among crop plants and their wild-type relatives. Lack of genetic variation for various crop plants has often been the limiting factor in crop improvement, an endeavor we must carry on thanks to perennially increasing human population. In model plant Arabidopsis, generation of epi-Recombinant Inbred Lines (epiRILs) has resulted in the creation of novel sources of heritable epigenetic variation for several traits of agronomic importance. For creating these epiRILs, wild-type Arabidopsis plants were crossed with mutant plants which lacked DDM1 (Decrease in DNA Methylation 1) gene which affects genome-wide DNA methylation in all the three cytosine contexts (CG, CHG, CHH). Using these epiRILs, epi-quantitative trait loci (epiQTLs) imparting enhanced defense responses have been identified. Moreover, such epiRILs have been used to generate superior epiHybrids in Arabidopsis. Epigenetic diversity has also been shown to increase productivity and stability of plant populations in Arabidopsis. Further, such lines display increased meiotic recombination (crossovers) and thus, increased genetic variation. These findings signify that every plant genotype has potential to be improved through manipulation of its epigenomic landscape. Based on our recent work, we have identified few epigenetic mutants showing enhanced homologous recombination, which potentially can be exploited to enhance both genetic and epigenetic variation. As part of the multi-institutional DBT project, we are currently in the process of generating epiRILs in rice and tomato. Genome editing tools are being employed to create required epigenetic mutants which will be used for generating epiRILs.

Theme: Conservation of Genetic Resources IPR and Bio-Safety Issue

OP1.1: Utilization of Potential Salt Tolerant Landrace 'Korgut' from Goa Coast for Genetic Improvement in Rice

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Abstract:
Korgut, a rice landrace from Goa state of India is popular among farmers due to its suitability for cultivation under salt affected coastal saline soils. Initial screening studies carried out under hydroponics ($EC_{iw(1:2.5)}$12 ds/M) confirmed its tolerance to salt stress at seedling stage. The tolerance in Korgut is due to its low ionic ratio of Na^+-K^+ (0.18) in shoot as compared to salt sensitive check IR29 (0.68). The same has been registered with NBPGR as 'genetic stock' (INGR No. 14055 and IC No. IC0599689) for 'tolerance to salinity stress at seedling stage'. Despite its tolerance, wide variation exist for agronomic and grain quality characteristics leading to harvest losses and reduced market price. Two pure lines *viz*., KS 12 and KS 17 were isolated employing pure line selection with improved grain yield and quality parameters, and later released as Goa Dhan 1 and Goa Dhan 2, respectively, for cultivation in coastal saline soils of Goa state. Haplotype analysis using 14 *Saltol* Quantitative Trait Loci linked Simple Sequence Repeat markers revealed that one of the selected line KS 17 (Goa Dhan 2) from Korgut population has completely different haplotype in comparison to salt tolerant check FL478 haplotype suggesting involvement of QTLs other than *Saltol* for governing salt stress tolerance. A mapping population (Recombinant Inbred Lines) from Jyothi X Korgut has been phenotyped for various yield and its attributing characters under coastal salinity condition. Mapping QTL governing salinity tolerance in this landrace would help in widening the genetic base for salt tolerance in rice.

OP1.2: Generation of new variability for grain yield and novel traits in finger millet through induced gamma mutagenesis

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Abstract:
Recombination breeding has not been exploited to the fullest extent in finger millet due to small sized florets and difficulties in hybridization. Induced mutagenesis could serve as an alternate approach in crops where hybridization is difficult especially in small grain cereals like finger millet and other small millets. Three released varieties (GPU28, GPU67 and MR6) were subjected to gamma irradiation (200-100 Gy) with the objective of correcting specific weakness in these varieties. Large M_1 populations (1000 plants) were raised in field during kharif 2015. Individual M1 plants were harvested separately and were raised finger to row progenies in M_2 and M_3 generations. Selections were exercised for grain yield components and selected progenies were generation advanced till M_7 generation. Superior M_7 progenies were evaluated in field trials in randomized block design during kharif, 2017, 2018 and 2019. Stability analysis was performed to identify superior and stable mutants for grain yield. GPU67-8362, GPU67-8368, GPU67-8337, GPU28-8307-1 recorded highest average yield of 2500-2700 kg/ha which is about 10% superiority over the respective parents. GPU67-8362, GPU67-8368 in addition to high grain yield also showed stability in performance over three seasons. These high yielding stable lines could serve as potential and diverse candidates for its use as parents in breeding also for its direct release as variety. Two mutant MR6-310 and MR6-311 recorded partial male sterility and could serve as female lines for its use in recombination breeding for improving the percent recovery of experimental F1 hybrids. Partial male sterile lines are advantageous over the genetic male sterility due to its easy in maintenance in breeding programs.

YOUNG SCIENTIST TALKS (YST)

Theme: Plant Metabolite and Nutraceutical

YST1.0: Biochemical Analysis and Mass Profiling of Traditional Medicinal Plants

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Abstract:
Andrographis paniculata is herbaceous plant. It is mainly found in tropical and subtropical asia, Southeast Asia, India and Srilanka and it has been used as traditional medicine in many countries. *Andrographis paniculata* was evaluated through biochemical and bioactive metabolites mass profiling. From the results, leaves have high concentration of total protein, total amino acids and polyphenols. GC-MS analysis shows that leaves and stem part of the plant contains maximum number of compounds with medicinal value for anti-microbial, antiviral, anti-bacterial, anti-oxidant, anti-cancer, anti-tumor. Result shows that root contains minimum number of compound but some unique compounds such as levoglucosan, tetracosanol, 5-Hydroxy-3',4',6,7-tetramethoxyflavanone have great biological activities that are important for human health. From these observations the *Andrographis paniculata* cultivation might be useful in development of nutraceutical compound for human health.

YST1.1: Allelopathic Effects and Characterization of Some Medicinal Plant Extracts in *Vignaradiat*a L. Wilczek and their Efficacy in the Control of Charcoal Rot Disease

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Abstract:
Macrophomina phaseolina (Tassi goid) is a pathogen that causes Charcoal rot in mungbean varieties resulting into a great economic loss. In this study there is the effect of *Ocimum sanctum* L., *Calotropis procera*(Ait.).Ait.f. and *Astragalous tribuloides* Delile extracts on the survival of *Macrophomina phaseolina* was studied. In study of *Macrophomina phaseolina* alkaline extract of *Ocimum sanctumL*. shows maximum growth of *Macrophomina phaseolina* as comparison to other extracts. All these medicinal plant extracts has detrimental effects and they shows the modulation of several metabolic components in various biochemical parameters like chlorophyll content, phenolics and antioxidant enzymatic responses of superoxide dismutase, peroxidase were observed in all extracts treatments. We concluded that Alcoholic extract of *Ocimum sanctumL*. Shows great efficacy of bioactive compounds on SML-668 Variety of mungbean. We take three mungbean varieties are there; these varieties are IPM-02-03, RMG-492, SML-668. In this study, we evaluate that SML-668 variety is treated with *Ocimum sanctum L*. Alcoholic extract is better than other extracts of *Ocimum sanctum* L. and other plant extracts. The allelopathic effect of medicinal leaf extracts of *Ocimum sanctum* L., *Calotropis procera* (Ait). Ait.f., *Astragalous tribuloides* Delile are also observed and it showed different plumule length of mungbean in vivo conditions. The alcoholic extract of *Calotropis procera* (Ait).Ait.f. Considerably produce the higher length of plumule as comparison to other extracts as well as *Astragalous tribuloides* showed positive effect of alcoholic and alkaline extract as comparison to aqueous acidic extract on the plumule of mungbean in vivo condition. Similarly in vitro condition alcoholic extract of *Ocimum sanctum* L. showed highest radical length as comparison to other extracts in vitro condition.

YST1.2: Enhancing the functionality and nutraceutical potential of soymilk through fermentation by probiotic Lactic Acid Bacteria (LAB)

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Abstract:
A sustainable bioeconomy must prioritize the production of high quality foods. More innovative valorization strategies targets to recover high value ingredients from plant based products, as sources of bio-active compounds for drug and functional food formulation. With this aim, fermentative processes using lactic acid bacteria (LAB) which can be explored in the bioceutical industry owing to their health promoting properties, has been studied. The soybean crop, because of its inherent health promoting compounds like omega-3-fatty acids, lectins, peptides, saponins, phytates, phytosterols, and isoflavones has enormous potential to improve the dietary quality of people either as a vegetable crop or soy-enhanced food products. In our present study, soymilk fermentation using 5 strains of probiotic *Lactobacillus* sp. for 48 hours have been carried out. Investigations on the effect of probiotic fermentation on various physio- biochemical properties indicates that, compared to the control (unfermented soymilk), there was an increase in total antioxidant activity (33.13%- 73.82%), mineral bioavailability (Fe (0.13- 1.67µg/ml)&Zn (0.12- 0.62 µg/ml)), reduction in anti nutritional factor- phytic acid (1.185g/ 100g- 0.190g/ 100g), lowering of pH (5.98- 4.23), increase in Titratable acidity (0.10%- 0.41%) and bioconversion of isoflavone into more bioavailable aglycones, were observed after fermentation. The viable count of bacteria could be maintained up to 7.5 * 10^8 CFU/ ml after 7 days of fermentation when stored at 4°C. Hence, soymilk- fermentation is an ideal strategy to guide the consumer towards appropriate prophylactic and therapeutic uses of probiotics that deliver the desired beneficial health effects.

YST1.3: Determination of Polyphenols, in vitro Antimicrobial and Antioxidant Activity of Selected Mangrove Species

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Abstract:
The objective of this study was to determine total phenolic and flavonoid contents, antioxidant and antimicrobial activities. Additionally, selected phenolic acids and flavonoids were characterized in all mangroves species by UPLC-ESI-MS/MS. The phenolic and flavonoid contents of extracts were determined spectrophotometrically using Folin-Ciocalteau and aluminium chloride methods, respectively whereas antioxidant activity of the extracts was determined using 1,1-diphenyl-2-picrylhydrazyl (DPPH) radical scavenging method. The antimicrobial activity was performed by disc diffusion assay against nine reference bacterial strains including Gram-negative and Gram-positive bacteria and *Candida* species. Antimicrobial screening showed *Staphylococcus aureus, S. epidermidis, Enterococcus faecalis* and *Pseudomonas aeruginosa* were most susceptible to ethyl acetate extract as compared to ethanol and methanol extract. Ethyl acetate extract of *Avicennia marina* and *Bruguiera gymnorhiza* showed strong antibacterial activity, whereas *Candida* species was most susceptible to *Aegiceras corniculatum* and *Acanthus ilicifolius* ethyl acetate extract. Phytochemical analysis revealed the presence of saponins, phenolics, flavonoids, alkaloids, tannins, and terpenoids, which was found to be variable as per the solvent used for extraction. In addition, total phenolics and total flavonoids content with different solvents were found in the range of 11.08-196.76 mg GAE/g and 12.92-110.3 mg QE/g of extract respectively. Moreover, antioxidant capacities expressed in terms of IC_{50} (mg/mL) showed that methanol extract of *Aegiceras corniculatum* exhibited higher antioxidant capacity. Finally, the validated UPLC-ESI-MS/MS method has been successfully applied for mangrove to characterize the polyphenolic pattern. The dominant compound was chlorogenic acid and was present in all examined mangrove plants ranged between 8.13 ng/mg to 5.690 µg/mg. Epigallocatechin gallate showed its exceptional presence in three mangrove species. Phenolic acid such as, (ferulic acid, caffeic acid, *p*-coumaric acid), flavonols (quercetin, rutin, myricetin), flavonones (naringenin), and flavones (apigenin) presence were varied as per the mangroves species.

YST1.4: Evaluation of dehydrated *Celosia argentia* leaves as a potent source of Quercetin-A dietary antioxidant

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Abstract:
There are many underutilized greens available in Tamil Nadu with lots of nutraceutical properties like anti-diabetic, anti-inflammatory, anti-cancer and anti-microbial properties. Dehydrated vegetables are good source of energy, minerals and vitamins. In the process of drying or dehydration, sufficient moisture is removed and thus the product is ensured against spoilage. Dehydration process should be done in such a way that the food value, natural flavor and characteristics, cooking quality of the raw material may be retained after rehydration.The current study has been focused on the evaluation of anti-oxidant status of fresh and dehydrated of under- utilized green leafy vegetable ***Celosia argentea, known as cocks comb*** **(Tamil: Pannai Keerai)**,belongs to family Amaranthaceae, an indigenous plant; traditionally known for its antioxidant, anti-diabetic and anti-cancer properties as mentioned in the literatures. The total phenolic content (TPC), total flavonoid content (TFC) and total antioxidant activities were evaluated in the ethanolic extract of both fresh and dehydrated leaves to assess the *in vitro* antioxidant activities. The results showed that there exist a linear correlation between polyphenol content and antioxidant property. The ethanolic extract of dehydrated *Celosia* leaves showed the highest phenolic content (289.34 ± 0.48mg GAE/g), and total antioxidant activity (643 ± 46µmolTrolox/100 g). HPTLC analysis has revealed the presence of significant quantity of Quercetin (14.81%), an important flavonoid of tremendous antioxidant, antiviral and anticancer property in both the fresh and dehydrated leaves which might be the chief bioactive principle in *Celosia.*

YST1.5: Biochemical and histochemical characterization of floral cuticular wax in tuberose

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Abstract:
Agave amica (Medik.) Theide & Govaerts (syn. *Polianthes tuberosa* L.) or commonly known as tuberose from family Asparagaceae is a widely cultivated horticultural crop and is famous for its pleasant and aromatic fragrance. Several in-depth studies had already been undertaken on the floral scent emission mechanism of tuberose, but no study has been conducted on the nature of the floral cuticle in tuberose. In most plants, the cuticle layer consists of waxy substances which gave the characteristic glossy appearance to the leaves and flower petals. Cuticle layer also acts as a first line of defence and as a transpiration barrier to prevent water loss. Very recently it has been found to play a pivotal role in floral scent emission. In this study, one of the most common commercial cultivar of tuberose, 'Calcutta Single' was chosen. The cuticular wax was characterized thoroughly using GC-MS analysis. A total of 70 compounds were detected in different developmental stages of the flower, consisting of seven different chemical classes dominated by fatty acids, alkanes and fatty alcohols. Crude wax extraction from the flowers was also carried out. Significant variation was found in the wax load between different developmental stages. Histolocalization of wax using cuticle specific stains confirmed the presence of these compounds in the cuticular region. Surface ultrastructural study using SEM confirmed the presence of waxy nanoridges on the petal surface. The results obtained from this study can be used to explain the correlation between scent emission and cuticle formation in flowers.

Theme: Plant Stress Management

YST1.0: Artificial miRNA mediated resistance in tobacco against geminivirus infecting Jatropha by maintaining photosynthesis and metabolic pathways

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Abstract:

Jatropha, a biodiesel crop, suffers economic losses due to leaf curl diseasecaused by geminiviruses. It was observed that the Jatropha plantation at CSIR-CSMCRI fields had more than 70% disease incidence. In the present study, we report a new strain of a *Jatropha leaf curl Gujarat virus* (JLCuGV) infecting Jatropha in the Gujarat region, which encodes six ORFs and each ORF possesses RNA silencing suppressor activity. Therefore, three artificial microRNAs (amiRNAs; C1/C4, C2/C3 and V1/V2) were designed employing overlapping regions, so that each amiRNA can target two ORFs of JLCuGVand transformed in tobacco. The resistance against JLCuGV was obtained in the C1/C4 and C2/C3 amiRNA transgenics, while V1/V2 amiRNA transgenics were tolerant against JLCuGV. The viral load and the relative level of amiRNAwere inversely related to each other,indicating a correlation of amiRNA level with disease resistance.The photosynthesis parameters were found significantly better performing in amiRNA expressing transgenics as compared to wild type (WT) after JLCuGV agroinfiltration. The metabolite profiling showed slight alteration in amiRNA transgenics but showed noticeable changes in sugar metabolism and tricarboxylic acid (TCA) cycle in WT on virus infiltration. This study demonstrates that amiRNAs provide complete resistance against JLCuGV by targeting two overlapping RNA silencing suppressor genes of JLCuGV, with the maintenance of photosynthesis parameters and metabolic pathways in amiRNA transgenics on JLCuGV infiltration.

YST1.1: Protective Role of Spermidine in Salt Stress Tolerance Mechanism of tomato plant

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Abstract:

Plants are exposed to various adverse abiotic or biotic environmental stress conditions. The exposure to the stressful conditions can lead to a significant decline in crop yield. Abiotic stresses such as drought, extreme temperature, salinity and nutrient deficiency are considered as the most prominent causes of crop loss. It has been estimated that 50% reduction in the yield of the major annual and perennial crops globally is due to the abiotic stresses. Polyamines are low molecular weight, ubiquitous, phytohormone like aliphatic amine compounds containing unsaturated hydrocarbons with two or more primary amino groups and organic non-protein polycations, play a significant role in fundamental processes of plant growth and development. Polyamines such as spermidine, spermine and putrescine are also considered as growth enhancers.

In the present investigation, the foliar application of spermidine appeared to protect against salt stress by strengthening the growth and antioxidant defense system which helped in maintenance of biochemical processes in tomato seedlings. Results revealed that foliar application of spermidine enhanced growth parameters of tomato seedlings and induced the biosynthesis of free amino acids, soluble sugars and proline for osmotic adjustment. This may compensate the adverse effects of salt stress on the biomass of tomato seedlings. Hence, spermidine can be used as growth regulator for maintenance of physiological functions in tomato seedlings to overcome the adverse effects of salt stress.

YST1.2: Overexpression of JcWRKY2 enhances salinity and *Macrophomina phaseolina* tolerance in transgenic tobacco

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Abstract:

Plants being sessile are exposed to various abiotic and biotic stresses. They have evolved sophisticated and elaborate signalling network to respond to these stresses. WRKY transcription factors (TFs), constitute one of the largest TF families in higher plants are widely involved in the regulation of various biological processes in plants, including stress responses. Here, we report a group III WRKY gene from *Jatropha curcas*, and functionally validated it against salinity and *Macrophomina phaseolina* fungal stress. Overexpression of JcWRKY2 ameliorates salinity tolerance in transgenic tobacco by regulating physiological growth parameters, elevated chlorophyll content, and improved antioxidative activities and increased endogenous salicylic acid (SA) content. Furthermore, SA and hydrogen peroxide (H_2O_2) pre-treated transgenic seeds showed early germination during salinity stress. During Macrophomina infection, the microscopic studies of the root and leave tissues, linked with cell death and the pattern of hyphae attachment revealed that JcWRKY2 participated in preventing the spread of infection. Quantitative RT-PCR studies reveals that expression level of antioxidative enzymes, calcium/calmodulin, dehydrins, and phospholipase genes were increased under salt stress and transcript expression of SA biosynthetic (*NtICS1*) gene, pathogenesis related (*NtPR-10)* gene and antioxidative enzymes (*NtCAT1* and *NtSOD*) gene on Macrophomina treatment which unveil the role of JcWRKY2 in coordination with SA production and suppressing generation of reactive oxygen species towards enhancing resistance. These results provide useful information regarding the regulatory mechanism of WRKY and SA-H_2O_2 loop towards the adaptation to environmental stresses.

YST1.3: Metagenomic analysis of microbial diversity in control and high arsenic field of West Bengal (Nadia district) under the thiourea supplementation

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Abstract:

Though the planet earth is inhabited by humans, there are many places which are still unoccupied by us. On the contrary, microorganisms are ubiquitous. In the current study; we used thiourea (TU) for ameliorating arsenic (As) stress in rice and to understand the impact on microbiological profile of rhizospheric soil, and plants through metagenomic analysis. For this, two fields from Sarapur village, Nadia district were chosen, one was the control field with As content up to 18 mg kg-1 and other was high As field with 54.4 mg kg-1of As load. Rhizospheric soil and rice plants samples (leaf and root) were collected in triplicates and in two-time points; 3 days before TU spray (500 ppm) and after 3 days of TU spray. Microbial diversity was analysed from kingdom level to species level. The result demonstrated the differences in the microbial communities under different soil conditions and depicted influence of TU supply. Major phyla found in all the samples were Proteobacteria, Actinobacteria, Firmicutes, Planctomycetes, Nitrospirae, Chloroflexi etc. but their percentage abundance varies depending on soil condition and whether the samples were subjected to TU spray. The percentage abundance of Nitrospirae phylum was found to be more in the samples which were subjected TU spray. At the species level, some important species showing differential responses were: *Exiguobacterium*, *Erwiniadispersa*, *Paenibacillus*, *Pantoeaananatis*, *Aurantimonas* sp., *Psuedomonas*sp. etc. The functional analysis for the predicted microbiome was also performed. The important functional categories included were membrane transport, amino acid metabolism, energy metabolism, signal transduction mechanism, transcription, lipid and carbohydrate metabolism etc. based on KEGG pathway database using COG and KOG identifiers.

YST1.4: Exploring endophytes isolated from medicinal plants against *Colletotrichum gloeosporioides (Penz.) Sacc.* causing anthracnose in greater yam *(Dioscorea alata L.)*

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Abstract:
Root and tuber crops are very much important in terms of their contribution to a substantial part of the global food supply. They were defined as the most resilient and resistant crops, because of their ability to survive in utmost climatic conditions. *Dioscorea alata*, a tuber crop commonly called greater yam, a fundamental ingredient in the diets of people all over the world. Anthracnose-a field disease, the major constraint for the production of greater yam, is caused by an ascomycotic fungi *Colletotrichum gloeosporioides*. In this study, endophytes were isolated from medicinal plants and tested for their antagonism against *Colletotrichum gloeosporioides*. Morphologically distinct 90 bacterial and 84 fungal endophytes were screened for antagonism. Two bacterial endophytes viz; PN.RT.1.7 (*Phyllanthus niruri* root isolate) and AV.LF.1.1 (*Aloe vera* leaf isolate) showed significant inhibition (84 ± 4.3 % and 82.9 ± 2.0 %) and were identified as *Bacillus amyloliquefacience* and *Bacillus licheniformis* respectively. Pot trial evaluation was done to test the efficiency of potent endophytes in managing anthracnose disease. Disease incidence was 100% among all the treatments including fungicide control. The lowest disease severity of 10.20 % was in the combination of tuber treatment and spraying of *Bacillus licheniformis* followed by spraying of *Bacilluslicheniformis* and in the fungicide control it was about 13%. Tuber yield was highest in Spraying of *Bacillus licheniformis* about, followed by *Bacillus amyloliquefacience*, spraying + tuber treatment combination. The above-mentioned results depicted that endophytes can be employed for the management of anthracnose disease after validation.

YST1.5: Salicylic acid enhances the growth of rice (*Oryza sativa* L.) plants under drought stress conditions

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Abstract:
The drought stress affects crops at physiological, biochemical and molecular levels, thereby affecting its yield. The present study was conducted to evaluate the role of foliar-applied salicylic acid (SA) in alleviating the detrimental effects of polyethylene glycol (PEG) induced drought in rice (*Oryza sativa* L.). Rice seeds were subjected to two levels of polyethylene glycol (PEG-6000) followed by exogenous application of SA at a concentration of 0.1 mM, 0.25 mM, 0.5 mM to access changes in germination percentage, root and shoot length, RWC, chlorophyll content, lipid peroxidation, osmolyte content and endogenous SA. The stress substantially reduced the growth of rice seedlings in terms of plant height, biomass, RWC and chlorophyll content with higher levels of lipid peroxidation. However, the exogenous application of 0.25 mM salicylic acid remarkably improved the plant height, biomass, and chlorophyll content both under drought and well-watered conditions. The results showed that the SA application ameliorates the drought-induced decrease in growth through the accumulation of osmoprotectant content. Higher proline content resulted in lower oxidative stress in rice. The results of this study indicated the role of salicylic acid in enhancing plant growth under stress condition.

YST1.6: Identification and characterization of MAPKKKs from *Cicer arietinum* and their involvement in plant defense against *Helicoverpa armigera*

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Abstract:

Mitogen-Activated Protein Kinase Kinase Kinases (MAPKKKs) are important components of MAPK cascades, which are universal signal transduction modules and play important role in plant growth, development and biotic and abiotic stress responses. In this study using computational analysis of sequenced *Cicer arietinum* genome we have identified 52 MAPKKKs. Phylogenetic analyses of MAPKKKs from chickpea, *Arabidopsis* and rice, have classified them into three subgroups, which include MEKK, Raf and ZIK. Conserved motifs in the deduced amino acid sequences of Chickpea MAPKKKs strongly supported their identity as members of the three subfamilies. Further, the expression patterns of MAPKKK genes from chickpea was evaluated in response to infestation by a major pest, *Helicoverpa armigera* via quantitative real-time PCR (qPCR), which suggested involvement of 15 upregulated MAPKKKs in plant defense against *H. armigera*. Structure prediction of the H. armigera-inducible MAPKKK proteins were performed in order to understand their participation in the MAPK cascades. This study provides insights into the role of MAPKKKs in plant defense against herbivores.

YST1.7: Green Nanofungicide and their application in biotic stress management

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Abstract:

Phyto-pathogens affect agricultural crops and reduce the yield worldwide. Agrochemicals including fungicides have been widely used to control the plant fungal pathogens. Moreover, these agrochemicals are lethal to the beneficial organisms. Hence, there is a pressing need to develop potent and cost effective antifungal agents. The synthesis of green nano fungicide using green approach and its application in biological fields is a burgeoning field of nanotechnology. *Aspergillus niger* produces the potent mycotoxins called ochratoxins that contaminates food grains. *Fusarium graminearum* causes Fusarium head blight or scab of wheat and barley. *Fusarium graminearum* produces group of vomitoxins which contaminates wheat and barley and cause liver diseases. *Fusarium udum* causes wilt disease in pigeon pea plants. All these pathogens spread through the irrigation and damage growth, development and yield in food crops. The above selected fungal plant pathogens are commercially important and cause various diseases on vegetables, fruits, cereals, and cereal crops. In this study, we have synthesized green nanofungicide as an alternate to the commercial fungicides to control plant fungal pathogens such as *Aspergillus niger, Fusarium graminearum* and *Fusarium udum.* The green nanofungicide showed broad-spectrum antifungal activity against the phyto-pathogens by inhibiting the radial growth. Green nanofungicide could be used as effective antifungal agents against harmful phytopathogenic fungi. Our results suggests that green nanofungicide can be utilized as an alternative for fungicides to prevent diseases in food crops and to eliminate the contamination of food grains to eradicate food poisoning and its associated health effects

YST1.8: Cloning, in silico characterization and expression analysis of TIP Members of Rice (*Oryza sativa* L.)

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Abstract:

Tonoplast Intrinsic Proteins (TIPs) constitute a significant class of the aquaporins. The TIPs control water trade among cytosolic and vacuolar compartments and can also transport glycerol, ammonia, urea, hydrogen peroxide, metals/metalloids, and so forth. Additionally, TIPs are engaged with different abiotic stress responses and developmental processes like leaf expansion, root elongation and seed germination. In this study, ten TIP genes in the rice genome were identified from *Oryza sativa* ssp *indica*. Among these, representative groups of TIP genes were cloned and sequenced whilst some TIP sequences showed stop codons in the coding region. The secondary structure analysis represented six conserved transmembrane helices along with the inter-helical regions having conserved motifs. The representative three-dimensional tetrameric design of protein sequence of TIP1;1 displayed key features like NPA motifs, aromatic/arginine (ar/R) selectivity filters, and Froger's residues. The vacuolar localization, transmembrane topological properties, and conserved motif analysis of the cloned genes altogether supported their identity as TIPs. An unrooted phylogenetic tree delineated the relatedness of TIPs from *Oryza* with different species and bunched them into five clades. The promoter analysis uncovered key regulons associated with administering abiotic stress responses. Gene expression studies showed that TIPs are differentially regulated under salt and drought stress at various time points in shoots and roots of rice. Also, the pattern of expression was found to be significantly variable in five different rice tissues. The heat-map based tissue and stress- specific expression analysis supported the experimental findings. In conclusion, the identification and transcript-level expression studies of TIPs significantly contribute towards the comprehension of their utilitarian significance in the abiotic stress response.

YST1.9: Co-expression Network Analysis of Protein Phosphatase 2A (PP2A) Genes with Stress-Responsive Genes in *Arabidopsis thaliana* Reveals 13 Key Regulators

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Abstract:

Continuous exposure of plants to environmental stresses caused by drought, salt, cold, heat, osmotic stress, and biotic stresses hinders their growth and development and subsequently results in less yield, productivity, and threaten food security worldwide. Exposure to such stress conditions triggers an internal signaling cascade in plants to initiate a unique response to a particular stress or shared responses common to individual stresses. In plants, several studies have been carried out to understand molecular responses to abiotic and biotic stresses. However, the complete circuitry of stress-responsive genes that plants utilise in response to those environmental stresses is still unknown. Protein phosphatases (PPs) are an important group of enzymes, which in combination with their counterpart protein kinases mediate diverse cellular processes in cells by dephosphorylation and phosphorylation respectively to their target proteins. Among them, protein phosphatase 2A (PP2A) gene has been known to have a crucial role in abiotic and biotic stresses; but how it regulates the stress response in plants is still not known completely. In this study, we constructed gene co-expression networks of PP2A genes with stress-responsive gene datasets from cold, drought, heat, osmotic, genotoxic, salt, and wounding stresses to unveil their relationships with the PP2A under different conditions of stress. The graph analysis identified 13 hub genes and several influential genes based on closeness centrality score. Our findings also revealed the count of unique genes present in different settings of stresses and subunits. We also formed clusters of influential genes based on the stress, CCS, and co-expression value. Analysis of *cis*-regulatory elements, recurring in promoters of these genes was also performed. Our study has led to the identification of 16 conserved *cis*-regulatory elements. The data will be presented in the conference.

Theme: Plant Biochemistry and Crop Improvement

YST1.0: Exploring natural variation for investigating thiourea-mediated enhanced growth and stress tolerance in soybean

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Abstract:

Soybean is a staple oil seed legume crop; which productivity is negatively affected by multiple abiotic stresses. One of the earliest effects in response to these stresses includes the enhanced production of reactive oxygen species (ROS), which is essential for the activation of stress-specific defense. However, uncontrolled ROS levels lead to oxidative damage leading to reduction in plant growth. In view of this, we have explored the genetic basis of thiourea (TU; a non-physiological thiol-based ROS scavenger) mediated enhancement in growth and stress tolerance in soybean (var. Maus47). Initially, post-germination phenotyping was performed at seedling stage with variable doses of TU (50-500 µM) which indicated that foliar application of 100 µM TU could improve the seedling biomass, both under control as well as NaCl stress conditions. Further, the results were validated under the realistic field conditions using the local varieties of soybean (JS-20-29 and JS-20-69). A significant enhancement in seed yield (15-40%) was noticed in field trials performed during 2018 and 2019. In order to study the genetic basis of TU mediated effect, a total of 117 SNP-genotyped soybean accessions were procured from USDA, which showed significant variation in terms of growth and agronomic-related traits. Further, a sub-set was phenotyped under NaCl stress with/without TU treatment, resulting in the identification of TU-responsive and non-responsive soybean accessions. Taken together, findings not only support TU supplementation as an effective management strategy for enhancing the soybean productivity; but, also provide the initial framework for doing genome-wide association studies in soybean.

YST1.1: In planta transformation technique for crop improvement

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Abstract:

Agriculture is a way of life, it holds a major importance in human living and economy. One of the most important sector of agriculture is the crop production i.e. growing crops for usage as food and raw materials (fiber). Due to unpredictable changes in the frequency and severity of abiotic and biotic stresses there is a huge need for crop improvement. Biotechnology have been proved to develop successful direct and indirect genetic transformation techniques like Agrobacterium mediated genetic transformation for the production of improved crop plants. Huge efforts have been made in the past years to produce easy, efficient and eco-friendly techniques. Recently, *Agrobacterium* mediated In-planta transformation technique is being employed which is resulting well in terms of not only successful genetic transformations but also skipping long tedious tissue culturing steps in order to produce stable transgenic plants. It is the direct transfer of *Agrobacterium* construct containing desired gene construct in to the plant. Therefore importance of in-planta technique in crop improvement is concluded.

YST1.2: Understanding the genetic basis of rice leaf development and growth

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Abstract:
Leaves are the prime photosynthetic organs of plants and leaf development a features strongly influence overall crop performance. Therefore, understanding the detailed genetic mechanisms regulating leaf development is of utmost importance towards desirable optimization of crop performance. Leaf developmental features have undergone significant changes during the course of evolution and domestication. For example, the leaf morphological and anatomical features of cultivated/domesticated rice varieties are remarkably different from their wild relatives. These differences in wild and cultivated rice allow a systematic comparative study of leaf growth and developmental differences, and underlying genetic basis. We used leaf kinematics approach to quantify leaf growth differences between cultivated and wild rice. In addition, a comprehensive transcriptomic comparisosn is performed for four different leaf developmental stages to identify genetic regulators of rice leaf dvelopment. Kinematics analysis showed that longer division zone and faster cell elongation rate contribute to larger leaves in wild rice species. Giberellic acid (GA) increased the leaf size of cultivated rice by increasing the size of division zone, and associated increase in the expression domain of cell cycle genes. Transcriptomics based gene regulatory network and expression Analyses suggested that GA-mediated increase in division zone, leading to larger leaf, Involve GRF (Growth Regulatory Factor) transcription factors. The GA-GRF-Cell cycle Module could potentially be used to control the rice leaf size. Transcriptomics Comparisons showed that wild rice with larger leaves complete the anatomical differentiation process faster, which is associated with early onset of photosynthesis. Gene regulatory networks promoting faster differentiation and early onset of Photosynthesis could potentially be used to optimize the leaf development and photosynthesis.

YST1.3: Production and characterization of antifungal metabolites from tomato rhizobacteria for a *Fusarium* wilt-free tomato cultivations

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Abstract:
Tomato stands second among the widely consumed horticulture crops worldwide, next to the potatoes. It forms a vital component of daily food intake as both raw and processed vegetables However, the sustainable yield is often threatened by several fungal diseases. Among the most devastating fungal diseases to tomato plants, vascular wilt caused by *Fusarium oxysporum* f. sp. *lycopersici* (Fol) experiences substantial economic losses. The first objective of this study was to identify the antifungal metabolites from tomato rhizosphere bacterial isolatesdirectly inhibiting the melanin biosynthetic pathways in vascular wilt pathogen *Fusarium oxysporum* f. sp. *Lycopersici* (Fol). The second objective was to address the mechanistic action of mycophagous tomato rhizobacteria feeding on the mycelia of virulent test and reference pathogenic strains of Fol using high throughput screening methods like FT-IR, SEM,molecular probing and confocal microscopy. Third objective was to identify rhizobacteria able to produce siderophore molecules for indirect antagonism to Fol and GC-MS analysis of siderophores. *In vitro* screening for plant growth-promoting properties and agar confrontation assays were performed to select the potential antagonists followed by the respective characterization methods and docking studies to decipher the possible interactions. Novel antifungal metabolites of pyrrole pyrazine chemistry, rhizobacteria with three different mycophagous behaviour and novel siderophores from pseudomonads were identified in this study. As an outcome, all the three candidates deserve the potentials to be prepared as separate consortia in suitable forms. However, *in vivo* studies are underway to justify this proposition in near future.

YST1.4: ^{5}N-influx and homeolog expression of nitrate transporter genes under nitrate-limited conditions in contrasting bread wheat genotypes

Amresh Kumar[a], Sarvendra Kumar[b], Karnam Venkatesh[c], Nagendra Kumar Singh[a], Pranab Kumar Mandal[a], Subodh Kumar Sinha[a]*

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Abstract:
Nitrate-uptake is one of the most important traits that can be tapped for improving nitrogen use efficiency of wheat (*Triticum aestivum*L.). In the present investigation, we attempted to understand, how do the two contrasting for N-uptake wheat genotypes (K9107 vs. Chotilerma), regulate their nitrate-uptake and -translocation system under different external nitrate concentrations at seedling stage. We also studied contribution of each homeolog expression of five genes (*TaNRT2.1*, *TaNPF6.1, TaNPF6.2, TaNPF6.3* and *TaNPF6.4*) in root tissue along with their overall transcript expression. We showed that K9107 has more ^{15}N-influx than that of Chotilerma under limited external N-condition, whereas Chotilerma showed improved translocation efficiency. We observed that nitrate starvation invariably increases the total root size in both the genotypes. Dry matter in root and shoot also differs under these growing conditions. K9107 showed significantly higher expression of *TaNRT2.1* at low external nitrate concentrations and *TaNPF6.1* and *TaNPF6.2* at high external nitrate concentrations. Further, we observed genotype-specific and nitrate-starvation dependent homeolog expression bias in all five nitrate transporter genes. The nitrate amount present in it, influence ^{15}N-influx and expression of all five genes. Our data suggest that K9107 has more efficient system for N-uptake than Chotilerma at seedling stage involving nitrate transporters encoded by different sub-genome of major nitrate transporter genes.

YST1.5: Identification, cloning and homeolog expression bias in AtNRT1.5 orthologs under different external nitrate concentrations in bread wheat (*Triticum aestivum* L)

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Abstract:
Partitioning of NO_3^- assimilation in root and shoot depends on plant species, external NO_3^- concentration, temperature, light intensity etc, however, the shoot assimilation is energetically more preferred than that of root,therefore efficient translocation of nitrate from root to shoot will play major role in nitrate uptake efficiency in wheat.ArabidopsisNRT1.5 (NPF7.1) has been demonstrated to be key low affinity nitrate transporter responsible for root to shoot nitrate transport. In the present study, genome wide identification, cloning and quantitative sub-genome specific expression of *AtNRT1.5* orthologue in bread wheat (*Triticum aestivum* L) was studied. Two orthologs, *TaNRT1.5A* and *TaNRT1.5B,* located in chromosome 6 of all three sub-genomes were identified. Phylogenetic analysis indicated two separate groups of the two orthologs in which one is more closure to brachypodium, whereas the other is with rice. The homeolog specific expression of both *TaNRT1.5A* and *TaNRT1.5B* genes in root tissues of 21 days old seedlings of two wheat genotypes (e.g., HD2985 and K9107) at two external nitrate concentrations demonstrated that D sub-genome specific*TaNRT1.5A* expressed maximally compared to that of A and B genomes at both the concentration of N, but expression level was more in K9107 than HD2967.Whereas, A sub-genome specific *TaNRT1.5B* expression was more than the other two sub-genomes again in K9107 compared to HD2985. Cloning of homeolog specific cDNA sequence revealed two spliced variants of *TaNRT1.5A,* termed as *TaNRT1.5A* (L/S). Further functional validation of these spliced variants may unravel functional divergence of these genes in nitrate transport from root to shoot in bread wheat.

Theme: Genome Editing, Translational Genomics and Plant Breeding

YST1.0: *In-vitro* biotechnological strategies to improve Niger (*Guizotia abyssinica* L.F. Cass) for enhancing edible oil production in India

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Abstract:
Despite steady improvement in oilseeds production, there is a yawning gap between demand and supply of edible oil leading to dependence on imports. To reduce the import dependency, a speedy recourse is necessary to boost indigenous edible oil sector. There is a need for increased production of edible oil from minor oilseed crops such as Niger (*Guizotia abyssinica* L.F. Cass) having 32-40% quality oil content and 18-24% protein in seeds, could play a significant role in meeting the edible oil requirements of the country. Since last decade, area under niger cultivation is declining due to low harvest index resulting from self-incompatibility, shattering nature, non-determinant types and cuscuta infestation. Therefore, the objective of niger breeding programme is to develop cultivars with high seed yield and oil content. *In vitro* biotechnological tools could serve as an alternative means for genetic upgrading. Double haploid (DH) technology includes induction and regeneration of haploid embryos from anther culture is a much faster way of developing genetically pure breeding lines in less time compared to conventional breeding. Besides this, DH production can also be integrated with radiation induced mutagenesis to create additional variability resulting to the selection of novel genotype with desirable traits. Somatic embryogenesis (SE) also offers a platform through which value-added traits can be introduced *via* genetic engineering resulting into the production of elite lines. These *in-vitro* techniques can effectively be used for the creation of genetic diversity and a base of new varieties with higher oil content and yield. Authors' would like to elaborate the strategic plans and possibilities for improving Niger using *in-vitro* tools thereby would contribute addressing the increasing demand for edible oil in India.

YST1.1: Chromatin Assembly Factor-1 (CAF-1) plays a role in ribosomal RNA gene regulation and in maintaininggenomic stability in Arabidopsis thaliana

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Abstract:
Chromatin Assembly Factor 1 (CAF-1) is a heterotrimeric H3.1/H4 histone chaperone responsible for DNA replication-dependent nucleosome assembly. It is composed of Chromatin Assembly Complex (CAC) 1-3 in yeast, p150, p60 and p48 in humans and FASCIATA1 (FAS1), FASCIATA2 (FAS2) and MULTICOPY SUPPRESSOR OF IRA1 (MSI) in *Arabidopsis thaliana*. Disruption of CAF-1 function in *A. thaliana* results in various genomic instability events like shortening of telomeres, loss of 45S ribosomal RNA (rRNA) gene repeats and mitotic chromosome abnormalities. In *A. thaliana*, rRNA genes are located on chromosomal locations called Nucleolus Organizer Regions (NORs) on chromosomes 2 (NOR2) and 4 (NOR4). Each NOR consists of ~ 400 rRNA gene repeats. In the *caf-1*mutants of *A. thaliana*, we show that locus conversion of both NOR2 and NOR4 along with the associated telomeres has occurred, indicating possibility of non-homologous recombination between NOR2 and NOR4. We also show that genomic instability of 45S rRNA genes results in altered gene expression pattern. Lastly, our data suggest increased recombination frequency among homologous chromosomes in the *caf-1*mutants, which if confirmed could be highly valuable in crop improvement due to possibility of creating more genetic variation.

YST1.2: Insights into population structure and genetic divergence revealed genetic differentiation among different adaptable and diverse colored sub-populations of Indian carrot (*Daucus carota* L.) accessions

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Abstract:
Carrot (*Daucus carota* L.) is an economically important horticultural crop that has gained importance as a primary vegetable in many countries. It is consumed in various ways by all the age groups across the globe for its nutritionally rich carotenoids, vitamins, minerals with zero cholesterol. Expansion of carrot germplasm collections and systematic evaluation of them will be vital to future breeding success. In this study an Accession panel (AP) consisting of 144 Indian accession belonging to Asiatic and Western gene pools representing temperate and tropical regions were utilized. The gene pool represented five different root colors *viz.*, light orange, dark orange, yellow, red and black/purple. This AP was assessed for population structure and genetic diversity using 80 polymorphic DNA markers *viz.,* carrot specific genic, genomic microsatellites, SCARs, *indels* and EST that are distributed throughout the genome. A total of 305 alleles were extracted, ranging from 2.0 to 9.0 alleles with an average of 3.81± 0.20 alleles per locus. Based on population structure, neighbor-joining tree, principle coordinate analyses, AP was divided into 3sub-population/clusters and showed higher genetic differentiation across the sub-populations (Fst=0.148). A total of 62 private alleles were detected for tropical adapted sub-population. Higher genetic variation by AMOVA among the sub-populations (13.00%) and moderate to high Fst between different sub-populations signifies the clear genetic differentiation within Indian carrot accessions. We also demonstrated the phylogenic relationship of the recent secondary domesticated dark orange carrot with other root colors. The study would help the breeders to explore them in the future tropical carrot variety improvement by MAS.

YST1.3: Different mutant alleles of Histone Deacetylase 6 (hda6) have different effects on rRNA genome instability in *Arabidopsis thaliana*

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Abstract:
Histone deacetylase 6 (HDA6) of Arabidopsis is a broad-specificity histone deacetylase which is involved in silencing transposons and supposedly a subset of rRNA genes by interacting with DNA methyltransferase 1 (MET1). Several *hda6* mutant alleles have been reported. Initial studies on Arabidopsis plants carrying different *hda6* mutant alleles reveal varying patterns of instability of 45S rDNA and the associated telomeres, resulting in loss of one or other variant type and one of the NOR-telomere junctions. In *Arabidopsis thaliana*, ~ 400 copies of 45S rRNA genes are present within nucleolus organizer regions (NORs) on chromosomes 2 (NOR2) and chromosome 4 (NOR4). These genes are transcribed by RNA Polymerase I, yielding primary transcripts that are processed into 18S, 5.8S, and 25S RNAs of ribosomes. The expression of rRNA genes is developmentally regulated where in the mechanism for this selective silencing was thought to be gene specific. However, recentstudies in Arabidopsis showed thatthe NORs act as regulatory units whereby NOR2 undergo silencing while NOR4 remain transcriptionally active. Genetic mapping data revealed that there is exchange of chromosomal segments between NOR2 and NOR4 in these mutant alleles. The observed data provided us an opportunity to analyse the role of HDA6 in rRNA gene regulation and in maintaining the genomic stability.

YST1.4: A Unary-Offset Integrated OctaFilial Generations Homozygosity values Computational Model, in addition to accommodating "DUS" ThreeBITSwitchkey Schema of EIGHT Staple Indian Millet varieties, based upon Binary/ 2state Elementary Cellular Automata

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Abstract:

In the realm of Plant Breeding and Genetics, Filial Generations are classified as F0, F1, F2, F3, F4, F5, F6, F7 and F8. Here, an attempt has been pioneered for Modeling the "Homozygosity" values for these Octa-Filials above based on a Elementary Cellular Automata (ECA) Framework, on the basis of Tripartite Symmetric Allele-encoding (Heterozygous, Homozygous Dominant/ Recessive). For instance, the Two "ECA-rules" namely, 191 and 247 exactly Model F2 and F5 Filial Generations, with Homozygosity values of 75% and 96.875% respectively. Interestingly, in such an ECA-based Octa-Filials Modeling Framework, the successive Filial Homozygosity values are found to be incremented by consecutively-Decreasing powers of 2, so as to say from (2^7=127) to (2^0= 1,unary offset) Additionally, a neat direct correlation is illustrated with the Generic "Breeder's equation" which is well characterized in terms of within, and across, Generational variation. Furthermore, it is very interesting to make a striking Observation here, in this Context, that our Novel "ECA-Octa Filials" Framework can also accommodate for that matter, what can be construed as "Fractional Filials" (i.e,) intermediate Filial Generations as well, inbetween F0-F1, F1-F2, F2-F3, F3-F4, F4-F5, F5-F6, F6-F7 and F7-F8. Filials beyond Eight, such as F9 etc., are beyond scope of present model. Finally, 88 (= 8 X 11) of such "256" ECA are Fundamentally inequivalent, allowing "DUS" schema grouped in 11 X (8*8) for Sorghum, Foxtail/ Finger/ Pearl/ Little/ Proso/ Barnyard/ Kodo – millets, upto 64 per Variety.

YST1.5: A Study of AGPase Genes for Thermotolerancein Wheat using Comparative Genomics and Bioinformatics

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Abstract:

AGPase is a rate-limiting enzyme in starch synthesis pathway and its activity is affected by heat stress. The enzyme is composed of a large sub-unit (AGPase-LS) and a small sub-unit (AGPase-SS). Utilizing the maize AGPase gene sequences as a reference, we identified 11 genes of AGPase family in wheat; six genes for AGPase-LS and five genes for AGPase-SS which were distributed on chromosomes of homoeologous groups 1, 5 and 7. We first compared the genes for AGPase of wheat (having highest sequence identity at protein level with the genes of the reference species) with genes of other monocots and dicots. We then performed detailed analysis of all the 11 wheat AGPase genes. *In silico* expression analysis revealed the expression of all the AGPase-LS and SS genes in grains and spikes except for the AGPase-LS genes on chromosomes of group 5 which showed expression in leaves. The qRT-PCR analysis showed expression of most of the AGPase genes (7/11) in developing wheat grains at 10 to 15 DAA. SNPs for 11 AGPase genes were mined using the available genome sequences of ~65 wheat genotypes. Although sequence polymorphism for 10 of the 11 AGPase genes (except AGPaseLS on 5A) was available, maximum polymorphism (based on SNPs) was recorded for the AGPase-LS gene on chromosome 5B. Using the polymorphic SNPs, we propose to develop gene based functional markers for use in marker assisted selection for developing thermo-tolerance in wheat genotypes.

YST1.6: Exploring the genetic resources for functional genomics and marker-assisted breeding of carrot (*Daucus carota* L.)

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Abstract:

Carrot (*Daucus carota* L.) is a major source of principle nutrient component 'carotenoid' and it has an incredible antioxidant and detoxifying properties. Carrot is a cool season crop and breeding efforts on tropical carrot are meager. Due to its out-crossing nature, high inbreeding depression, biennial nature and suitability to temperate conditions creates challenges in tropical carrot improvement. Proper exploitation of genetic resources and their characterization at phenotypic and genotypic level is necessary for development of improved varieties or hybrids. Uniformity in root morphology, higher carotenoid content and minimum vernalization requirement for flowering are the prime criteria's for development of biennial tropical carrots. Our study began with collection of >150 diverse accessions across India and subjected to their characterization for economic traits by phenotyping and different types of DNA markers by genotyping to understand their suitability to tropical region. The germplasm characterization identified superior genotypes and hence, four founder parents superior for nutritional and productivity traits were selected for development of tropical adaptable varieties through our novel Marker-Assisted Recurrent Selection (MARS) program. The objective was to develop tropical suitable biennial, nutrient rich carrot for commercial production of both higher root and higher seed yield. Gene specific markers based selection resulted in improved genetic gain for the target traits. Simultaneously, two elite genotypes belonging to temperate and tropical climates were subjected to transcriptomic profiling of two economic parts *viz*., root and flower. The objective was to identify the differentially expressed genes for adaptability and flowering for their utilization in future breeding. Root transcriptomic data identified 111 differentially expressed genes (DEG) and further identification of DEG from flower tissue is continued. These genetic variations are being utilized for QTL mapping of the root productivity traits. Our study is exploring the modern plant breeding and molecular biology platforms for basic, translational and applied research in carrot.

Theme: Conservation of Genetic Resources, IPR and Biosafety issue

YST1.0: Bioprospecting native wild nutmegs from Andaman and Nicobar Islands, India for their sustainable utilization

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Abstract:
Nutmeg (*Myristica fragrans*) is a commercially valuable species of Myristicaceae family, which has been used as a spice, medicine and source of fat for industrial uses. Andaman and Nicobar Islands hold good diversity of wild nutmegs; however, mostof these have been poorly studied. In the present study, two endemic species *viz*. *Myristica andamanica* and *Knema andamanica*, and one native species *i.e.Horsfieldia glabra* were compared with the commercial nutmeg on morphological and biochemical basis. Distinct variations were observed for seed morphological parameters among these species and seed dimensions were found to be the maximum in seeds of *M. andamanica*. Fatty acid composition of seeds was done using FAME analysis which revealed saturated fat content between 59.4% (*H. glabra*) and 83.4% (*M. andamanica*). Methyl tetradecanoate was the most dominant compound in all the species with values ranging from 46.87 to 68.84%, while (Z)-9-Octadecenoic acid methyl ester and Methyl hexadecanoate were other dominant compounds. Higher quantities of Methyl dodecanoate (27.02%) and Methyl *cis*-13-docosenoate (16.97%) were obtained from *M. andamanica* and *H. glabra*, respectively, while these compounds were present in minute quantities in other species. Higher total phenolic content was recorded in methanolic extracts than acetone extracts and the methanolic extract of *M. andamanica* had the highest total phenolic content (6.54 mg/g GAE). Considering this, these wild relatives of nutmegs could be utilized for industrial purposes as a supplement to commercial nutmeg. Such alternative uses would play a key role in conservation of these important genetic resources by promoting their sustainable utilization.

YST1.1: *Garcinia andamanica* King: an endemic horticultural genetic resource from Andaman Islands

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Abstract:
Clusiaceae is an important family members of which have been valued for their use as fruits, acidulants, medicine *etc*. *Garcinia andamanica* is an endemic species of this family distributed in Andaman group of islands. It is used for a variety of purposes by aboriginal tribes as well as settler communities of the islands. However, no systematic efforts have been made to explore its horticultural potential. Systematic studies on collection, characterization and utilization resulted in interesting findings. The species was found naturally distributed in areas with soil pH of 6.1 to 6.9, poor to moderate nutrient statusand high water table. Physicochemical analysis suggested acidic nature of the fruit making it suitable for use as acidulant. Fruits were source of carotenoids, phenols and exhibited antioxidant activity. Dehydrated rind flakes were prepared and successfully stored for about a year at ambient conditions of storage. Fatty acid analysis of seeds using GC/MS revealed presence of eight compounds, mainly unsaturated fatty acids. Methyl oleate (44.351%) was the major constituent and hence, seeds have potential to be used as source of oil for edible and industrial uses. Being endemic species, conservation is of utmost importance and hence, seed germination technique was standardized and habitat enrichment activities were undertaken in different parts of the islands. Further, to popularize this species as a backyard crop, planting material was distributed to the farmers. This pioneering attempt in this species could not only help in its conservation but would also support the resource poor farmers in remotely located islands.

YST1.2: Study of novel molecular based studies for Indian medicinal plants to create genomic database

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Abstract:
Medicinal plants form a large group of economically important which provide basic raw materials for medicines, flavors, perfumes and cosmetics. Medicinal plants are rich in secondary metabolites and are potential sources of drugs as well as it includes alkaloids, glycosides, flavonoids, steroids etc. These plants have been increasingly recognized for their role as not only for health care but also for improving the economic status. There comes the need of protecting these plants and storing their genomic data. For protecting these plants, novel biological and environmental methods are introduced. To maintain the environmental biodiversity and plant ecological system of these plants, molecular based research work is necessary.
Most of the research has done work for maintaining the good number of plant individuals; so far genomic data is not available for these critically endangered plants. Not only environmental methods the genomic data also play a key role in molecular based research studies, it is necessary to preserve the genomic data for these critically endangered medicinal plants.

YST1.3: A critical analysis of regulatory framework for biotechnology in India

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Abstract:
The Ministry of Environment and Forests (MoEF) has notified the Rules for the Manufacture, Use, Import, Export and Storage of Hazardous Microorganisms/Genetically Engineered Organisms or Cells 1989 (known as 'Rules, 1989') under the Environment (Protection) Act, 1986. These rules and regulations cover the areas of research as well as large scale applications of Genetically Modified Organism (GMOs) and products made there from throughout India. The rules also cover the application of hazardous microorganisms which may not be genetically modified. Hazardous microorganisms include those which are pathogenic to animals as well as plants.
These rules also define the competent authorities and composition of such authorities for handling of various aspects of the rules. Presently there are five competent authorities that is , Institutional Biosafety Committees (IBSC), Review Committee of Genetic Manipulation (RCGM), Genetic Engineering Approval Committee (GEAC), State Biotechnology Coordination Committee (SBCC) and the District Level Committee (DLC). The RCGM established under the Department of Biotechnology (DBT) supervises research activities including small scale field trials, whereas approvals for large scale releases and commercialization of GMOs are given by the GEAC, established under the MoEF. The SBCCs and DLCs have a major role in monitoring. The Rules also mandate that every institution engaged in GMO research establish an IBSC to oversee such research and to interface with the RCGM in regulating it. The IBSC has a nominee of DBT on its Committee.
The Rules, 1989 are supported by the following bio-safety guidelines: Recombinant DNA Safety Guidelines, 1990 & 1994;Revised Guidelines for Research in Transgenic Plants and Guidelines for Toxicity and Allergeni city Evaluation, 1998;Guidelines and SOPs for the conduct of Confined Field Trials of Transgenic Plant, 2008;Guidelines for the Safety Assessment of GM Foods, 2008,;Protocol for Safety Assessment of Genetically Engineered Plants / crops, 2008; Regulations and Guidelines on Biosafety of Recombinant, DNA Research and Biocontainment, 2017.
In addition, there are other acts, rules and policies which are also applicable to use of biotechnology in India.

POSTER PRESENTATIONS

Theme: Plant Metabolite and Nutraceuticals

P1: Cooking fats and their time of addition tailors the inherent glycaemic potential of differentially pigmented rice varieties: A comprehensive, structural and functional study

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Abstract:
Inherent glycaemic potential of staple grains like rice is majorly governed by their microstructure as well as due to their unique matrix composition or interactions. Among the components, starch-lipid complexation has got sufficient attention being an indigenous cooking practice as well as due to the recent knowledge behind the formation of resistant starch (RS) type V, altering the glycaemic profile. Lipids have known to form amylose–lipid inclusions which get resistant to α-amylase, leads to prolonged enzymatic hydrolysis. The complexation ability has been attributed to the composition (amylose, amylopectin and fatty acids) or their chain length or lipid saturation. Further the unique food matrix composition in pigmented staple grains have shared novel insights on food matrix interactions like binary (starch-lipid), tertiary (starch-lipid-protein) and quaternary (starch-lipid-protein-phenolics) in manipulating the inherent glycaemic potential. In this present study, investigations on *in-vitro* glycaemic response, starch-lipid complexing ability, resistant starch (RS) formation in three rice types [white rice (WR), black rice (BR) and red rice (RR)] cooked with four fats [ghee, coconut oil (CO), virgin coconut oil (VCO) and rice bran oil (RBO)], with three cooking conditions ('before', 'during' and 'after') has been characterized. Considering cooking conditions, fat types and rice varieties it has been found that most significant effect of least glycaemic response was observed with RBO when added 'during' with RR having complexing ability (28.67%), RS (2.26%). Hence, the role of fatty acids chain length and degree of saturation has a great importance as a 'lipid induced resistance towards glycaemic response' model towards modulating the molecular configuration, complexing ability and RS-V formation.

P2: Flavonoid metabolites and their antioxidant activities of fruits of banana cultivars from North Eastern region of India

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Abstract:
Flavonoids are ubiquitous secondary metabolites, which have excellent applications in medicine, foods and diet industries for their nutraceutical potential. In North Eastern areas of the country, some unique bananas belonging to various genotypes are grown. In this study, the flavonoids contents in unripe fruits of 14 banana cultivars and ripe fruits of 21 cultivars collected from North Eastern region were estimated, individual flavonoid metabolites analysed using HPLC and their antioxidant activities measured. Peel of unripe Beejikela (BB), *Musa balbisiana* (BB) and Katchkela (ABB) possessed more than 350 mg of total flavonoids and pulp of unripe fingers of *Musa balbisiana* contained highest quantity of flavonoids with 270 mg. In ripe fruits of 21 cultivars, Beejikela (BB), *Musa balbisiana* (BB) and Katchkela (ABB) contained high quantity with more than 300 mg/100 g DW in peel and *Musa balbisiana*, Chinali (AAB) and NepaliChinia (ABB) contained more than 200 mg flavonoids in pulp. Generally, the 'B' (*Musa balbisiana*) genome cultivars possessed higher quantity of flavonoids than 'A' (*Musa acuminata*) genome bananas; between peel and pulp, the peel contained higher quantity of flavonoids. Three main metabolites detected are epigallocatechin, epicatechin and catechin with predominance of first one, particularly in 'B' genome bananas. Antioxidant activities of methanolic peel and pulp extracts of North Eastern banana cultivars measured by TEAC and ORAC assays showed Attikol (BB), Bhimkol (BB), *M. balbisiana* and Beejikela exhibiting greatest antioxidant potential in the range of 80-120 µmol TE/100 g. Epigallocatechin as individual flavonoid metabolite exhibited similar level of antioxidant activity. The study shows peels of unripe banana fruits of 'B' genome with high epigallocatechin are potential nutraceuticals.

P3: The Broad-spectrum Antifungal Activity of Amphoteric Peptides Purified from Mixtures of Secondary Metabolites

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Abstract:
Lipopeptides are small compounds synthesized by various microorganisms as secondary metabolites. Due to their amphipathic structures, lipopeptides exhibit diverse bioactivities including antimicrobial and antitumor activities, and therefore have potential in chemical, agricultural, pharmaceutical, food and feed industries. These beneficial effects are related to the amphoteric nature of the lipopeptides and the signaling cascades that are induced. Lipopeptides from *Bacillus* of plant and soil origin have broad-spectrum antibiotic properties and exhibit moderate to strong antimicrobial effect to many multidrug-resistant organisms. Application of lipopeptides as antibiotics is promising due to their wide anti-microbial spectrum, rendering it difficult to produce resistance.
In the present investigation, antifungal lipopeptides were isolated from a soil-dwelling wild-type *Bacillus* by acid precipitation, solvent-based and adsorption chromatography purification methods followed by reversed phase high performance liquid chromatography. Purification resulted in 5 co-produced antifungal lipopeptides and their nature was confirmed by thin layer chromatography. Re-chromatography of these fractions at analytical scale was performed for molecular mass determination of purified compounds by LC-MS. Three of these were selected for further investigation due to higher antifungal efficacy against target organisms, and, *in vitro* pharmacodynamic and ultrastructure studies were used to determine killing kinetics and preliminary mode of action respectively. Our results so far suggest that the three heptalipopeptides have similar molecular mass. The lipopeptides have low MIC values against target organisms and their effect on fungal cells has been visualized by scanning electron microscopy. Time-kill curve analysis demonstrated that concentration-dependent activity of each lipopeptide has a significant log reduction within 24 hours.

P4: Starch quality matrix: An analytical model based on primary and secondary index parameters for predicting inherent glycaemic potential in rice

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Abstract:
Rice is a global staple food, feeding half of the world's population. Even though white rice (WR) dominates in consumption and attracting foreign exchange, it is a major contributor to the glycaemic load and associated with increasing type 2 diabetes mellitus (T2DM). Directed research is thus required to understand the existing variations in the inherent glycaemic potential as well as to develop further newer varieties of low glycaemic potency. Even though the starch digestibility is well correlated with the structural milieu, bestowed due to components, molecular order as well as other attributes, few inter-relationship studies have been conducted probing a link among the starch quality parameters. Hence the present study was carried out in twenty rice genotypes analysing their primary and secondary indices of starch digestibility [six traits comprising total starch (TS), total amylose content (TAC), total amylopectin content (TAPC), resistant starch (RS), microstructure, gelatinization temperature (GT)] for developing a predicting matrix model. Pearson's correlation and Cramer's V statistics were used to develop the starch quality matrix (SQM). A regression model was further developed based on most significant variables TSC and TAC. As the predictability indices were the sum of the squares of residuals, coefficient of determination and so on, further to limit outrageous prediction the model was refined and fitted using outlier analysis, Q-Q plots and Crook's distance analysis. Based on this, 4 most promising candidates (Karupanel, Chimbalate Basmati, Basmati 397 and VLT6) were shortlisted and validated further using *in vitro* starch hydrolyzation kinetics simulating human gastro-intestinal conditions. The high slowly digestible starch (SDS), RS and nutraceutical starch (NS) % quantified, exemplified Chimbalate Basmati as the most preferred genotype with low glycaemic amplitude. Thus our study showed a perspective relationship among 6 traits affecting starch digestibility and developed SQM based prediction tool which would assist in trials to breed high quality-low glycaemic rice varieties in future.

P5: Profiling of Amino acids and vitamins in Mangalore melon (*Cucumis melo* var. *acidulous*) using liquid chromatography-Mass spectrometry

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Abstract:

Mangalore melon (*Cucumis melo* var. *acidulous*) is a non-dessert type melon extensively grown in coastal regions of Southern India. Both mature and immature fruits of Mangalore melons are cooked as vegetable. Off-white, turgid and crunchy flesh of Mangalore melon that holds crunchiness even after cooking is a delicious, yummy and low-calorie vegetable. Despite its high nutritional and medicinal values, nutritional profiling of Mangalore melon has not been reported. Profiling of amino acids and vitamins in skin, flesh and seeds of three Mangalore melon accessions (MS4: Golden yellow fruits, MS21: Striped fruits and MS78: green fruits) and muskmelon variety Arka Jeet was carried out using liquid chromatography-mass spectrometry. Ten amino acids and seven vitamins or their precursors were identified in all the three tissues of Mangalore melons and one muskmelon variety. Mangalore melon accessions were found be higher in threonine, glutamine and arginine. Glutamine was found to be 19.64 and 9.79 times higher in the skin of MS78 and MS4 respectively than the muskmelon. Arginine accumulation was highest in the seeds of MS4 (45.53x) and MS78 (17.12x). Among the vitamins, skin of MS 4 is rich in vitamin B3 (6.73 times) and riboflavin (9.09 times) higher than the muskmelon. Seeds of Mangalore melon are rich vitamin B5. Nutritional supplementation with amino acids and vitamins has been shown to affect immune variables. Glutamine and arginine are thought to be good candidates for immune system support. Consumption of Mangalore fruits may be a good source of vitamins and amino acids to boost the immunity.

Theme: Plant Stress Management

P1: *Aeluropus lagopoides* HKT2; 1 promoter: regulation with ABA and ionic stresses

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Abstract:
High affinity K^+ transporters are integral membrane proteins found exclusively in plants and play a crucial role in salinity tolerance via ion homeostasis. In this study, we isolated HKT promoter from halophyte *Aleuropus lagopoides*. The full-length promoter region (765 bp) was cloned sequenced and analysed for the presence of putative *cis*-regulatory elements (CREs') using bioinformatics tool PlantCARE.The promoter constitutes several *cis* elements involved in abiotic stress response like HD-Zip 1, HD-Zip 2, MBS, W-box, ABRE etc. 5' serial deletion fragments were designed, cloned in pCAMBIA1301 and transformed in tobacco. The full-length promoter showed expression in different parts of flowers like petals, the junction between anther lobe and filament, dehiscence slit and whole seedling. MUG Assay was performed in T1 seedlings to study the regulation of promoter deletions under different stress conditions. The compound, 4-methylumbelliferyl glucuronide (4-MUG) is a GUS substrate, which upon hydrolysis produces the fluorescent 4-methylumbelliferone (4-MU). Deletion 2, possessing MBS, W-box and ABRE elements, showedhighest GUS activity under different stress conditions at 48 hrs.EMSAanalysiswith stress treated plant protein showed higher binding with D2 probe suggesting that the D2 promoter is the most efficient portion of the HKT promoter.

P2: Kinetin amelioratingeffect on*in vitro* shoot budgrowth and development under salinity stress of *Juncus rigidus*

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Abstract:
Juncus rigidus is important source of material for weaving and traditional handicrafts. *J. rigidus* can play important role in the reclamation of saline land, and clearing polluted water. In addition, *Juncus rigidus* is rich in cellulose content and could be potential source for bioethanol. Shoot buds cultured in liquid MS medium supplemented with 1.11 µM 6-benzyl aminopurine (BAP), 0.57 µM Indole Acetic acid (IAA), and 0.46 µM Kinetin (KN)developed > 80 shoot buds within 30 days of culture. Cultures were treated with NaCl (10 - 200mM) and the culture growth was adversely affected by high salinity treatments. Different concentration of KN was added to the Sodium chloride (NaCl) treated cultures and 1.0 µM KN has ameliorating effect on salinity stress.Elongated shoots cultured in MS medium supplemented with 0.44 µM BAP, and 0.49 µM IBA developed 72 % rooting in liquid medium. Shoots were treated with NaCl (100 - 200mM) and the rooting percentage increased by the addition on salinity. Rooted sapling successfully established in the nursery.

P3: Patterns and analysis of CATGTG cis regulatory element in different plant genomes

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Abstract:
Plant yield closely depends on its environment and is negatively affected by abiotic stress conditions like drought, salinity, heat, cold. Analysis of the stress inducible genes in *Arabidopsi*s has previously shown that CATGTG plays a crucial role in controlling the gene expression through the binding of NAC TFs under various stress conditions mainly drought and salinity. CATGTG pattern is a conserved motif which has been analyzed in this study to find the mechanism of gene expression through spacer specificity, inter motif distance preference, functional analysis and statistical analysis for four different plants namely *Oryza sativa*, *Triticum aestivum*, *Arabidopsis thaliana* and *Glycine max*.The spacer frequency analysis has shown preference for particular spacer lengths among the four genomes and CATGTGNCATGTG pattern was found having higher frequency among the four genomes. The spacer specificity at all the spacer length which predicts dominance of particular base pairs over other was analyzed to find the preference of the sequences in the flanking region. Functional analysis on stress regulated genes for saline, osmotic and heat stress clearly shows that CATGTG motif frequency with inter motif distance (0-30) in the promoter region of *Arabidopsis* is highest in genes which are upregulated by saline and osmotic stress and downregulated by heat stress. Microarray data was analysed to confirm the role of CATGTG motif in stress response pathways.Transcription factors seem to prefer larger motif size with repeated CATGTG element.The common preference for one spacer was further validated through the Box and Whisker's statistical analysis.

P4: Role of reactive oxygen species scavenging system in blast resistance in finger millet

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Abstract:
Blast disease caused by the fungus *Magnaporthe grisea* is a major biotic stress in finger millet cultivation which under congenial conditions causes upto 80% damage. Blast fungus infects the plant at all growth stages causing leaf, neck and finger blast. Oxidative burst and activation of enzyme machinery involved in the detoxification of the reactive oxygen species (ROS) is one of the earliest responses of plants to microbial invasion followed by the expression of many defense-related genes. The change in the activities of anti-oxidant enzymes and genes in blast resistant and susceptible finger millet genotypes was studied for understanding the contribution of ROS scavenging system towards blast resistance. The production of superoxide and hydrogen peroxide and activities of ascorbate peroxidase and peroxidase were followed in the leaves of resistant (GPU67) and susceptible (IE2821) genotypes at two time-intervals, 48 and 96 hai. Gene expression of SOD and APX were followed using quantitative real time-PCR. Histopathological analysis was conducted to study the superoxide radicals and hydrogen peroxide molecules produced. In comparison to the un-infected plants, ROS were produced more in the infected plants. The experiments revealed that in incompatible (resistant) plant-fungus interactions, oxidative burst was more prominent or was maintained for a longer time than in a compatible (susceptible) interaction. Blast resistant finger millet genotypes are assumed to employ reactive oxygen species as a weapon against the progression of fungal hyphae to adjacent cells from the point of infection.

P5: Stress Management in Plants

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Abstract:
Agricultural production, a major contributing factor towards global food supply is highly reliant on field crops which are under severe threats ranging from various biotic and abiotic stresses and changing climatic conditions. Towards abiotic and biotic stress management plant growth promoting bacteria plays an important role in plants. For managing the abiotic stresses, is important to considered the genetic improvements in combination with the proper cultural practices (Wahid et al., 2007). Several cultural practices have been long practiced to cope with abiotic stresses; however, the use of the genetic tools for this purpose is relatively recent inclusion. In past, major focus of the breeders has remained on the development of high yielding varieties and no doubt those varieties performed best under the non-stressed environment. However, on the face of changing climatic conditions where the plants are more prone to abiotic stress, the emphasis should also be given to breeding for stress tolerance. In the recent past, research has been started by using the conventional and molecular breeding approaches to improve the stress tolerance in the plants (Farooq et al., 2009b).Transgenic approaches involve modifications in the qualitative as well as the quantitative traits through transfer of desired genes (Ashraf, 2010). The major emphasis has been on the engineering of the genes which encode growth regulators, compatible solutes, and antioxidants involved in stress tolerance. Inducing stress tolerance by exogenous application of growth regulators and osmoprotectants at different growth stages can play an important role in inducing resistance against various stress.

P6: Predicting stress-responsive promoters in Arabidopsis thaliana using computational methods

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Abstract:
With the increasing threat of global warming and climate change, the role of gene regulation in plants is gaining prominence. Under various stresses, plants respond by altering their gene expression profiles. The experimental elucidation of differentially regulated gene promoters in plants is expensive and time-consuming. In this regard, computational methods to predict the potential plant promoters that undergo differential regulation are the need of the hour. Our initial studies on *Arabidopsis thaliana* plant promoters under osmotic stress have revealed that using just the sequence information alone one could differentiate between promoters that are undergoing differential expression. We further implemented deep learning tools, specifically, a Bi-directional LSTM architecture, to categorise the promoter sequences into primarily 3 categories namely up-regulated/down-regulated/neutral under stress conditions. Using this method, we were able to achieve an f1-score of 0.76, 0.89, 0.92 respectively and an overall accuracy of 87%. We further used the known *cis* -regulatory elements of *Arabidopsis thaliana* as features to generate the predictive models. Surprisingly, we didn't find any discriminatory power of CREs in terms of differentiating between the three classes of the promoters. Currently, we are planning to extend these methods to various plant species under different stress conditions such as heat stress and salinity stress.

P7: Conditional pathogenesis: understanding why potentially beneficial rhizobacteria turn pathogenic under certain environmental conditions

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Abstract:
Plant growth promoting rhizobacteria (PGPR) are beneficial soil bacteria that colonize the rhizosphere and provide multiple benefits to plants. Some PGPR strains can help plants in abiotic stress tolerance. Data represented here discuss the interaction between a drought and thermo-tolerant PGPR, namely, *Pseudomonas putida* AKMP7 and *Arabidopsis thaliana* under drought conditions. Previous studies from our laboratory have found that, inoculation of AKMP7 to the roots of *A. thaliana* seedlings enhances plant growth under well-watered conditions but results in enhanced drying, wilting and depleted plant water content under water stressed/drought conditions. *Pseudomonas putida* AKMP7 was able to withstand extreme drought-like conditions as evidenced by growth under 25% polyethylene glycol supplementation. The bacteria releases phytohormones such as cytokinin (zeatin), auxin (indole acetamide) and auxin amino acid conjugates (IA-Asp, IA-Phe, IA-ala) to the growth media, which in some cases, were higher in concentration under dehydrating (PEG supplemented) conditions than under normal (non-stressed) conditions. It is known that, some of these bacteria- produced phytohormones like indoleacetamide and IA-Asp can contribute to the bacterial virulence and pathogenicity. Hence, based on our observations, we hypothesize that the bacterial phytohormone produced by AKMP7 may have a role to play in this accelerated drought mediated injury of inoculated plants. The precise molecular mechanisms leading to such a phenomenon of conditional pathogenesis is currently under investigation in our laboratory.

P8: SbMYB15 transgenics negatively regulate cadmium and nickel uptake and help in stress tolerance by modulating antioxidative defence system

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Abstract:
Plants faces different types of stresses like salinity, dehydration, high temperature and heavy metals, which affects its growth, productivity and yield negatively. World's major concern about the heavy metal release and accumulation in soil is due to its rapid expansion and industrialization. According to FAO, 500 million ha of land is contaminated with heavy metal pollution globally. Heavy metal stress major components are, zinc (Zn), cobalt (Co), and copper (Cu), cadmium (Cd) and nickle (Ni) which are relatively more poisonous for plants and Arsenic (As), lead (Pb), chromium (Cr) and mercury (Hg) are relatively more toxic to animals. The heavy metals reduced the absorption of mineral and water by disturbing a pathway of mineral translocation in plants. It denatures plants cellular membranes and causes failure in process of photosynthesis. Heavy metal stress hinders the plant physiological activity, growth and yield. *S. brachiata* Roxb. is a succulent halophytic plant grows abundantly in salt marshes near Gujarat coast. The R2R3-type SbMYB15 transcription factor (TF) activates stress signalling processes through interacting with reactive oxygen species (ROS) in transgenic tobacco plants in presence of cadmium (Cd) and nickel (Ni) stress. Transgenics shows high transcript expression in tobacco transgenics with improved growth rate and chlorophyll content towards Cd and Ni stress. Tobacco transgenics showed reduced ROS (H2O2 and O2•⁻) content with increased antioxidant enzymes activity and transcript expression of antioxidative genes towards CdCl2 and NiCl2 stress. This is the first report of R2R3-type SbMYB15 transcription factor overexpression shows heavy metal tolerance in tobacco. Our research findings shows that in future this kind of TF can be overexpressed in crop plants for developing heavy metal tolerant crop plants.

P9: Differential expression of antioxidative enzymes during Arsenic toxicity in *Allium cepa*

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Abstract:

Heavy metal stress is one of the major constraints to crop productivity. Amongst all the heavy metals, Arsenic (As) is one of the most crucial environmental toxins existing in soil. The main source of As in soil are pesticides, mining, irrigation with contaminated water, use of fertilizers with municipal solid wastes. When plants are exposed to As, many morphological, biochemical, metabolic and molecular alterations are witnessed. Generation of Reactive oxygen species (ROSs), is one such event, which is noticed during any heavy metal stress.Since, higher levels of ROS can be detrimental for plants, they have developed mechanisms to scavenge ROS. Therefore, monitoring change in expression of genes, which encode for proteins that can scavenge ROS, would be interesting. We, selected genes that encode for SOD, APX, GPX and CAT and studied their differential expression during As toxicity in *Allium cepa*. We also compared their activity in control and treated plants. Our results demonstrated an increase in the expression levels of SOD, GPX, APX and CAT transcripts and an increase in their activity was also confirmed.

P10: Expression studies of an amino acid transmembrane transporter *(AtAVT6D)* from *Arabidopsis thaliana*

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Abstract:

Amino acid transporters are membrane-localized protein carriers involved in the movement of amino acids from the source to sink tissues. They are important participants in various plant processes related to growth, development, and stress tolerance. Also, reported being inducible in response to environmental signals such as light, osmotic changes, pathogen attack. Hence, amino acid transporters may act as a plausible candidate for crop yield improvement. Genetic manipulation of the amino acid transporter can potentially provide enhanced stress tolerance and improved yield. Hence, the study of a completely unexplored transporter family AtAvt6 family will be of great importance as this family predicted to be involved in the export of amino acids aspartate and glutamate. The AtAVT6 family belongs to the ATF superfamily and comprises of five members in *A. thaliana* (*AtAVT6A*, At3g30390; *AtAVT6B*, At5g38820; *AtAVT6C*, At3g56200; *AtAVT6D*, At2g40420; and *AtAVT6E*, At1g80510). On comparing, the promoter regions of these transporter genes, ***AtAVT6D*** has an intriguing arrangement of *cis*-regulatory elements. There exist as many as 15 ABA-responsive elements that are recognized by the bZIP transcription factors (TFs). The bZIP TFs are synthesized in response to increased ABA levels due to abiotic stress which then activates the stress-responsive genes. This analysis suggests that the *AtAVT6D* transporter gene might have some role in stress tolerance. Hence, the study of this proton-coupled amino acid transporter for glutamate and aspartate can be of great economic importance. The data obtained in the study will be presented.

P11: In Silico Identification and Evaluation of Bacillus subtilis RNA Chaperone (cspB) Homologs in Plants

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Abstract:
RNA chaperones are ubiquitous proteins involved in folding of misfolded RNA. Cold shock domain (CSD) proteins with nucleic acid binding properties act as RNA chaperones in bacteria to higher organisms. Bacterial CSPs (*Escherischia coli*-cspA and *Bacilus subtilis*-cspB) have successfully imparted drought tolerance in transgenic plants; however, these cannot be deployed in food crops due to concerns in social acceptance. Therefore, this study aimed to identify homologs of *Bacillus subtilis* RNA chaperone (cspB) in plants that can be used for developing drought tolerant transgenics. NCBI database search resulted into twelve single domain plant CSPs presenting >40% sequence identity with cspB. All 12 plant CSPs were modeled by homology modeling and refined by molecular dynamics simulation for 10 ns. Selected plant CSPs and cspB exhibited high structural similarity (Tm-score: 0.62–0.85). Molecular docking with three RNA molecules (5U, UC3U, and C2UC) indicates that *Ricinus communis*-csd1 and*Triticum aestivum*-csp1 have a binding pattern and docking scores similar to those of cspB. Furthermore, MD simulations for 20 ns revealed that plant CSP-RNA complexes behave in a similar manner to that of the cspB-RNA complex, making them highly potential candidate genes for developing drought tolerance in transgenic plants.

P12: Rice lectin protein r40c1 forms a multi-protein complex to regulate drought stress tolerance in plants

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Abstract:
Lectin proteins are widely known to play key roles in various environmental stress responses in plants. Although the rice lectin protein, r40c1, has been reported to be regulated by drought stress, the molecular mechanism of how it imparts drought tolerance has not been explored so far. In this study, we have demonstrated that the expression of Osr40c1 gene is positively correlated with the drought tolerance potential of different indica rice cultivars. The Osr40c1 overexpressing rice plants showed significantly improved drought and salt stress tolerance over the wild-type plants. It was also identified that the nucleo-cytoplasmic protein, Osr40c1, interacts with a number of drought-responsive proteins like OsSAM2, OsSAP8, OsMNB1B, and OsH4. In addition, the silencing of each of these protein partners led to drought susceptibility in the otherwise tolerant transgenic tobacco plants ectopically expressing the Osr40c1 gene. This observation indicated that all these partner proteins were indispensable for the Osr40c1-mediated drought tolerance in plants. Fascinatingly, the Osr40c1 protein was found to form a multi-protein complex with its partner proteins specifically under drought stress conditions. Together, our study revealed that the lectin protein, Osr40c1 imparts drought tolerance by regulating the chromatin proteins, OsMNB1B, OsSAM2, and OsH4, which presumably enables OsSAP8 to induce downstream gene expression.

Theme: Plant Biochemistry and Crop Improvement

P1: Crop Improvement Using Seaweed Fertilizers

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Abstract:
As the disadvantages of the chemical fertilizers are more apparent now farmers are looking at organic fertilizer. One among such organic biofertilizers is the seaweed fertilizers which are the extracts of seaweeds i.e marine macro algae.. There are many beneficial reports on seaweed fertilizers, which showed that they have better seed germination, deeper root development, increased resistance to disease plants, crop improvement with high productivity. These seaweed extracts act as an organic fertilizer with high nutrient value, they contain some trace elements, plant growth hormones(auxins, cytokinins, gibberellins), micronutrients i.e vitamins(A,C,E,K), minerals(sodium, zinc, magnesium, calcium,etc) and macronutrients i.e carbohydrates, protein, lipids. The aim is to study effect of seaweed fertilizers on the germination and growth of seeds. Two different species of seaweeds collected i.e. *Cladophora rupestris* and *Ulva lactuca* and washed thoroughly and dried in a shady area. The dried seaweeds are soaked in distilled water and boil them for 30 mins and filtered. The filtrate was taken as 100 %concentration of seaweed fertilizer and from this different concentration can be diluted based on the usage. Seaweed extracts increasing the seed germination and seed growth when the moderate concentration of seaweed extract of *Cladophora rupestris* and *Ulva lactuca* is given to black gram (*Vigna mungo*), green gram (*Vigna radiata*),wheat(*Triticum aestivum*), Rice (*Oryza sativa*),high concentrations of seaweeds extract is given to Bengal gram(*Cicer arietinum*)which showed less germination and growth due to high respiratory activity of seeds.

P2: Screening membrane protein leaders for specific targeting of cyanobacterial bicarbonate transporters to the IEM of C3 plant chloroplasts

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Abstract:
In C3 plants, the oxygenase activity of the primary CO_2 capturing enzyme Ribulose 1,5 bisphosphate Carboxylase/Oxygenase (RubisCO) leads to photorespiration. This process reduces the productivity of C3 crop plants. Cyanobacteria possess a carbon concentration mechanism (CCM) that turbo-charges RuBisCO's CO_2 supply, preventing its oxygenase activity. The installation of a cyanobacterial CCM into C3 plant chloroplasts has emerged as a strategy to increase crop productivity. The first phase of the strategy is the transfer of cyanobacterial bicarbonate transporters to the chloroplast envelope to reduce the deficit of chloroplast stroma CO_2 levels compared to the intracellular leaf levels. BicA and SbtA are single subunit cyanobacterial symporters that utilize the periplasmic sodium gradient to pump HCO_3^- ions into the cytosol. We aim to introduce these transporters to the chloroplast inner envelope membrane (IEM) of model C3 plants through suitable IEM targeting signals. Such signals are not well characterized at present. Transit peptides (TPs) alone are inefficient in targeting foreign polytonic membrane proteins to the chloroplast IEM. The region in between the TP and the first transmembrane domain of IEM proteins, termed the membrane protein leader (MPL), may play a role in targeting. To test this, we have generated constructs with the TP-SbtA/BicA gene fused with the MPL sequence of IEM proteins HP59 and PLGG1 from *Arabidopsis thaliana*. We are in the process of cloning the fusion gene/s into plant expression vectors and generation of transgenic model C3 plants (*Nicotiana tabacum, Nicotiana benthamiana, Arabidopsis thaliana)* to study the subcellular localization of the transporter.

P3: Molecular cloning and *in silico* characterization of novel Lipase gene and exploring their role in rancidity of flour in Pearl millet:The Pearl of Indian Agriculture

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Abstract:
Pearl millet (*Pennisetum glaucum L.*) is termed as "nutricereal" because of its rich nutrient composition. In spite of rich in beneficial nutrients, it is not much popular among the masses due to off odour and low keeping quality of the flour. The rancidity of the flour is caused due to the activity of Lipase, LOX, POX and PPO in the flour. Lipase, being present at pivotal position in the pathway, is considered as real culprit for the flour rancidity. It hydrolyses the acyl chains either at primary or secondary positions and produce free fatty acids (FFAs). Very limited information about the lipase gene from pearl millet is available on public domain. Here, we have identified 97 putative lipase transcripts from pearl millet through de novo transcriptomic approach and further classified into 5 families. The motifs and domains of lipases were observed highly conserved across the species. Based on the digital fold expression, we targeted transcript Tra_1901 for the cloning using gene specific primer. RT-PCR showed an amplicon of ~1.4 Kb which was further validated through Sanger's sequencing.BLASTn search showed maximum homology with the lipase genes reported from rice. The cloned gene was observed to be localized in the cytosol. We analysed the activities of Lipase enzyme in the flour of diverse genotype of pearl millet–White, Purple, Dhanshakti (Complete and decorticated). The maximum lipase activity was observed in white genotype (48 nM/min/mg proteins) followed by decorticated Dhanshakti, whereas minimum was observed in purple genotype (38 nM/min/mg proteins). There is a need to further characterize the kinetics of lipase enzyme in order to develop physiochemical technologies for regulating the activity of lipase enzyme in the flour. The identification of lipase gene will help to use it as potential marker for evaluating the pearl millet germplasm for rancidity.

P4: OsCRY2 regulates flowering time and plant height in an *indica* rice variety, Basmati 370

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Abstract:
Light not only serves as a source of energy for photosynthesis, it also acts catalytically to regulate plant growth and development. Therefore, sensing ambient light conditions is critical for plants to adjust metabolism and to initiate developmental transitions accordingly. The perception of light quality, quantity, periodicity, duration and direction is mediated through various photoreceptors in plants. Cryptochromes (CRYs) are a class of photoreceptors that perceive blue/ultraviolet-A light of the visible spectrum to regulate a number of responses in bacteria, fungi, animals and plants. In the past nearly 15 years, our laboratory has been engaged in the characterization of CRYs from mustard (*Brassica)* and rice (*Oryza sativa* ssp. Indica). During the present study, an alternative spliced form of *OsCRY2* has been characterizedat the molecular level and functionally validated in a partially photoperiod sensitive *indica* variety, Basmati 370. Morphometric analyses of the over-expression and knock-down transgenic lines of *OsCRY2* have clearly indicated that OsCRY2 mediates promotion of floral initiation and inhibition of cell elongation. Sub-cellular localization studies by particle bombardment in onion peel cells showed that *OsCRY2* is localized in both the nucleus and the cytoplasm. Also, yeast two-hybrid (Y2H) and in-vitro pull down assays have established that *OsCRY2*interacts with *OsFBO10*, a rice ortholog of FLAVIN BINDING, KELCH REPEAT, F-BOX1 (FKF1) of *Arabidopsis* ZEITLUPE family of another blue/ultraviolet-A photoreceptors. This interaction broadens the horizon of the co-action of the two different photoreceptors in fine-tuning the various developmental responses in plants.

P5: Analysis of intergeneric cross variants and understanding genome alterations in sorghum

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Abstract:

Sorghum is a multipurpose crop having immense value as food, fodder, feed and fuel. Despite having the same genome, these types express different traits that make themsuitable for specific end-uses. Widening the genetic base for specific traits and understanding the genes that make them suitable for specific end-use have both applied and basic research value. Intergeneric hybridization between sorghum and maize has induced a large *de novo* variationin F_2 generation resulting in grain, sweet stalk and forage types. Some of these variants were identified as promising in all India Coordinated trials. To identify the genes/genomic regions that decide the end-use, we selected two variants each in grain and sweet stalk and one in forage, derived from the intergeneric cross between sorghum (27A) and maize (CM211). Genotyping using simple sequence repeat (SSR) markers showed occasional unique ampliconsto each end-use type. One Mb region flanking these markers wasanalyzedfor the presence of genes. The metabolic role of such genes was known from the functional annotation of the genome to identify any gene (s) related to the end-use types. Unique bandgenerated in sweet sorghum line by SSR marker, SbGM4-10on chromosome4 was found to possessglycosyl transferase gene that plays an important role in transfer of glycosyl (sugar) residues during biosynthesis of polysaccharides, glycoproteins and glycolipids, which also corroborates with other reports for sugar QTLs in sorghum. Further analysis of such genes adjacent to unique amplicons will help in understanding the role of specific genes in creating variations related to specific end uses.

P6: Genome-wide identification and characterization of Trehalose-6-Phosphate Synthase gene family in linseed

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Abstract:

Linseed (*Linum usitatissimum* L.) is second most important *Rabi* oil seed crop in India and is mainly grown for its fiber and seeds oil. Early maturity is considered an important trait as it helps crop to escape several biotic and abiotic stress. T*rehalose-6-phosphate synthase gene is known to have role in flowering time regulation in Arabidopsis. In present study, genome wide identification and characterization of trehalose-6-phosphate synthase have been carried out in silico.* In linseed, a total of 18 TPS genes were identified. Orthologous nomenclature of the TPS gene family was done having *Arabidopsis thaliana* TPS genes as reference. It was found that every *Arabidopsis* orthologue of TPS in linseed has a paralog suggesting gene duplication event. TPS gene family was grouped into two clusters having 4 and 14 genes in cluster I and II, respectively. Subcellular localization prediction showed that most of the TPS are present in the nucleus (11) followed by the cytoplasm (4). Gene length of all the TPS sequences was found between 2.5 to 3.0 KB except TPS1 genes having gene length of more than 5 KB. Protein length of TPS genes was found between 800 to 970 amino acids. In order to study allelic variation in TPS genes, TPS1 gene was PCR amplified from in 2 early and 2 late flowering-maturing linseed germplasm accessions and sequenced. Sequences analysis of gene sequences from all the four accessions revealed a total of 6 SNPs. Present study gives an insight into TPS gene family in linseed.

Key words: Trehalose-6-Phosphate Synthase, gene family, flowering and maturity, linseed

Theme: Genome Editing, Translational Genomics and Plant Breeding

P1: DNA fingerprinting and identification variety specific loci in onion for genetic purity analysis of open pollinated varieties.

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Abstract:
Onion (*Allium cepa* L.) is the second most important vegetable crop worldwide and iswidely appreciated for its health benefits. Arka Kalyan is one of the popular onion variety, extensively cultivated throughout India. Often, elite varieties are contaminated with the off-type pollens of local varieties during seed production that diminish the genetic purity of onion cultivars. Genetic purity testing of onion cultivars by grow out tests is impractical due to its labour intensive and environmental sensitive field screening procedure. To identify the marker loci specific to Arka Kalyan, 57 onion genotypes including popular varieties and local cultivars of Karnataka were fingerprinted with 12 inter simple sequence repeat (ISSR) markers and their resolving power (RP) was calculated. Twelve ISSR primers produced 93 scorable bands with amplicon size ranging from 280 bp to 1600 bp. Maximum scorable bands were observed in the primer UBC820 (11), followed by UBC855 (10) and UBC809 (09). Amplification percentage ranged from 1.75% (band present in only one sample) to 100% (band found in all samples) with a mean of 74.6%. The maximum number of bands was observed in the Kanchanaganga (79), followed by Kumata local and Gokak local (77 each) and the test variety Arka Kalyan produced 70 bands. The resolving power of ISSR markers ranged from 8.25 (UBC856) to 13.58 (UBC855) with mean resolving power of 11.57. Marker bands 1600 bp, 1500 bp and 400 bp of UBC855 differentiated Arka Kalyan from all other varieties and local cultivars. The marker may be further used for genetic purity testing following its validation in the seed lots.

P2: In silico prediction and validation of polymorphic simple sequence repeat markers between monoecious and gynoecious lines of bitter gourd (Momordica charantia L.)

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Abstract:
Bitter gourd (*Momordica charantia* L.) is medicinally adorable vegetable species of Cucurbitaceae family. Use of gynoecious parents in hybrid production enhance the hybrid vigour and helpful in maintaining hybrid purity. Gynoecious trait is mostly found in wild bitter gourd associated with undesirable agronomic traits. Identification of markers linked to gynoecy would hasten the development of gynoecious female parents of elite hybrids through marker assisted backcross breeding. However, linkage mapping requires time and resource intensive screening of hundreds of markers to identify the polymorphic markers between diverse parents. In this study, *in silico* prediction of polymorphic SSRs between gynoecious and monoecious parents using publicly available restriction associated DNA (RAD) sequencing data. Raw RAD sequences of gynoecious parent K44 (ERS2214863) were downloaded from NCBI. Low quality reads and adapters were trimmed using trimmomatic pipeline and assembled into contigs using soapdenovo2 assembler. Polymorphic SSRs between the monoecious line OHB3-1 (NW_019104488) and newly assembled contigs of K44 were predicted by CandiSSR pipeline using PacBio assembly (DRA009109) as a reference sequence. Quality trimmed RAD sequences were assembled into 418832 contigs with an average contig size of 684 bp and N50 contig length of 2383 bp. A total of 3937 SSRs common to both OHB-3 genome and K44 assembly were identified. Among them 52 SSRs were polymorphic between both the lines. Primers of 32 highly polymorphic SSRs were synthesized and tested for their polymorphism in gynoecious and monoecious parents and 12 showed polymorphism. Validated markers will be used for mapping of gynoecy in F2 mapping population of bitter gourd.

P3: Development of F2 mapping population from heterotic hybrid and QTL mapping for root traits of tropical Carrots (*Daucus carota* L.)

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Abstract:

Carrot (*Daucus carota* L.) is a major temperate vegetable rich in carotenoids and other antioxidants. The chromosome number of carrot is 2n=2x=18, belonging to the family Apiaceae. Being a temperate crop, most of the breeding efforts were concentrated on development of high yielding hybrids and varieties of cooler climates. However, global carrot gene pool has a rich diversity in terms of wider adoptability, nutritional quality, resistance to biotic and abiotic stresses. In this study, the attempt was made to understand the heterosis and developed the mapping population for QTL mapping of important root productivity traits in carrot by exploring the contrasting carrot genotypes and molecular markers. Ten F1 hybrids developed from contrasting genotypes identified in the previous generation were subjected to phenotyping for 15 root productivity related traits and genotyping using 60 molecular markers that include genic, genomic microsatellites and gene specific markers. There was a wide range of variation for root length, root width, root weight and for the molecular markers in the F1 populations. Further, two highly heterotic F1s were utilized for development of F2 mapping populations with the population size of 150 (UHSBC-34-3 x UHSBC-66) and 85 (UHSBC-38 x UHSBC-40) respectively. The phenotypic data was generated during 2020-21 and the population is being genotyped using the 30 polymorphic markers for each of the populations. The F2 mapping populations generated in the tropical carrot background is the suitable plant material to generate the draft linkage map and identification of marker-trait association for the root productivity traits in carrot. The data obtained from the F1 and F2 populations would provide the basis for understanding of heterosis/ inbreeding depression and QTL mapping respectively for the economic traits.

Theme: Conservation of Genetic Resources, IPR and Biosafety issue

P1: Biosensing of Hepatitis C Viral RNA from Clinical specimens

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Abstract:

Hepatitis C, a liver disease and leading cause for liver cirrhosis and hepatocellular carcinoma, is caused due to Hepatitis C Virus (HCV). Globally, more than 150 million people are infected with HCV.RTqPCR based molecular testing is the gold standard and confirmatory diagnostic test for HCV detection. However, this molecular testing is expensive, has high turn-around-time requiring sophisticated equipment and highly skilled personallimiting its application in resource-limited settings. In this backdrop, an affordable simple diagnostic test is the need of the hour. Gold nanoparticles (AuNPs) based pathogenic detection holds promising approach. Hence, in the current study, we present a rapid, simple and sensitive colorimetric detection system to detect HCV RNA from clinical samples using oligonucleotide probes and AuNPs. The AuNPs in HCV RNA positive sample retain a stable red color on salt-induced aggregation. Contrary, AuNPs in HCV RNA free negative sample aggregate to purple on salt-induced aggregation. A sharp absorption peak at 520 nm is observed for HCV RNA positive samples whereas negative samples show a shift in absorption peak to higher wavelength with broader peak confirming the aggregation of AuNPs. A HCV positive RNase A treated sample aggregated to purple while sample without RNase A digestion retained red color. This study validated the AuNPs stability in positive sample due to hybridization of HCV specific probe to HCV RNA. The assay has a turn-around-time of ~30 min after RNA extraction and has a LOD of 100 IU/mL.

P2: Production of *Shigella flexneri* polysaccharide and its conjugation with CRM_{197} protein as potential vaccine candidate

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Abstract:

The polysaccharide (PS) from the Gram negative pathogenic bacterium, *S. flexneri* is considered as a major disease causing component (anti-gen). To increase the human immunological efficiency, conjugates are discovered, where these polysaccharides are a major component of the conjugates. A robust process is developed in the present study using synthetic media and chromatographic filtration technique along with the novel silicate treatment to produce significant quantities of polysaccharide (PS) from *S. flexneri* in reduced cost and time, which could be further conjugated to a suitable carrier protein, CRM_{197} to generate a potential *Shigella* conjugate antigen. CRM_{197} is a non-toxic mutant of diphtheria toxin which is currently used as a carrier protein for purified *S. flexneri* PS. Conjugation method utilizing adipic acid di hydrazide (ADH) linker to generate *Shigella* PS-carrier protein conjugates is employed in the current study. Polysaccharide carboxylates (-COOH) were activated with EDAC[1-Ethyl-3-(3-dimethylaminopropyl) carbodiimide] in presence of N-Hydroxysuccinimide (NHS), by forming an active ester intermediate which further increases the efficiency of conjugation with CRM_{197} derivatized with ADH linker. The conjugation efficiency has been explored by estimating the free protein, free polysaccharide and PS:CRM197 ratio using size exclusion chromatography, high-performance anion exchange chromatography and slot-blot techniques. The produced glycoconjugates exhibited enhanced shelf-life for over four weeks. The cytotoxicity/cell viability studies with Vero/MRC-5 cell lines have confirmed the non-toxic nature of the conjugate. This glycoconjugate with enhanced bioconjugation could serve as a potential vaccine candidate for shigellosis.

P3: Simultaneous saccharification and fermentation of lignocelluloses: Review

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Abstract:
Bioethanol derived from petroleum as an alternative to transportation fuels that is concentrating worldwide to address energy security, energy costs, and global warming shortcomings associated with liquid fossil fuels. Fossil fuels have already caused a lot of damage to the environment and contributed to increasing global warming. To some extent, partial replacement of gasoline for biofuels has improved the situation. But technically, compression-based engines are considered suitable for biodiesel and DME, while spark-ignition engines are suitable for bioethanol. In addition to political (energy security), climate (global warming) and economic (saving foreign treasury) production of bioethanol may be important for many developing countries for many reasons. Biomass can be produced in developing countries for bioethanol on wastelands, creating employment opportunities, as well as reclaiming wastelands and the environment can also benefit. The ability to produce rural income from the production of high-value products (such as liquid fuels) is attractive. In this, the possibility of export earnings through the sale of industrial bioethanol to the countries is strong.

Thank you!