3rd Global Congress on

PLANT BIOLOGY AND BIOTECHNOLOGY

MARCH 11-13, 2019 | SINGAPORE

Theme: *To Disseminate the Research and Advancements in Plant Biology and Biotechnology*

VENUE

VILLAGE HOTEL CHANGI
1 NETHERAVON ROAD SINGAPORE 508502

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BOOK OF ABSTRACTS

3rd Global Congress on

PLANT BIOLOGY AND BIOTECHNOLOGY

Theme:

To disseminate the research and advancements in Plant Biology and Biotechnology

MARCH 11-13, 2019
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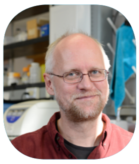

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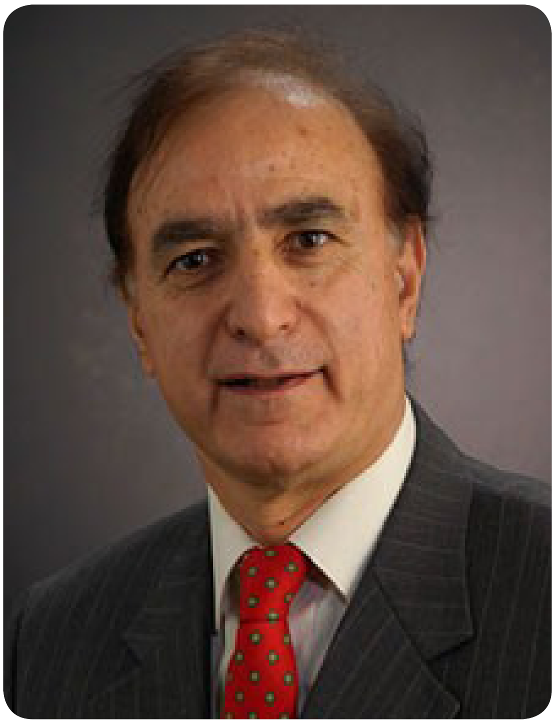
Thank You
All...

Welcome Message



Did you know that millions of people are suffering from hunger and malnutrition?

Did you know that the world would need to provide food for more than nine billions of people in by 2050?

Did you know that the lack of sustainable food security is seriously threatening world's peace?

Did you know that more than 30% food crops and products are lost to pests and post-harvest problems?

Did you know that Singapore has been among the fastest growing countries in science and technology?

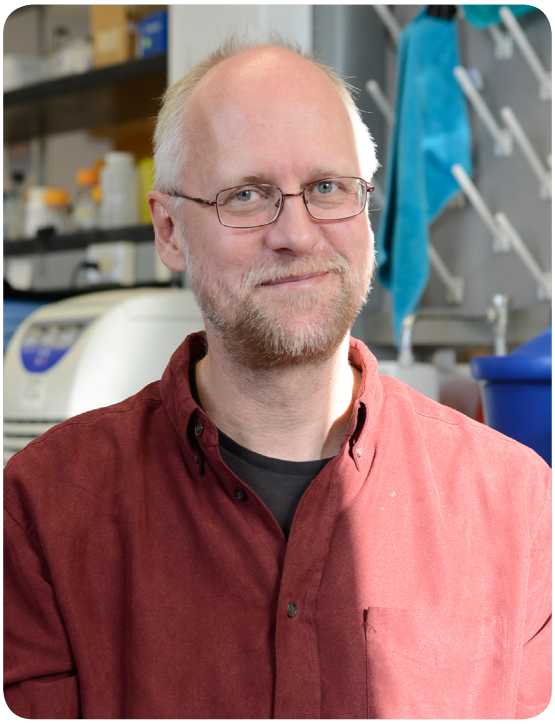
Did you know that Singapore Airlines has been determined the best service proving airlines in the world in 2018 and for 2019?

If you are a plant scientist and are concern about food security in the world, you should not miss the 3rd Global Congress on Plant Biology and Biotechnology (GPB 2019), schedule for March 11-13, 2019 at Singapore.

M. Babadoost

Prof. Mohammad Babadoost
Professor of Plant Pathology and Extension Specialist
University of Illinois
USA

Welcome Message



On behalf of the Scientific Committee and the Magnus Group, we would like to welcome you to the 3rd Congress on Plant Biology and Biotechnology 2019 in Singapore.

Plant biology is a rapidly developing field that has become more and more relevant to secure food productivity and human health in these times of climate change, increasing population growth, and destruction of natural habitats. This international meeting covers a broad range of important research topics including molecular and developmental biology, different 'omic' approaches, biotechnology, plant pathology, and environmental aspects. With experts coming from Asia, Africa, Australia, Europe, and the Americas, this congress represents a great opportunity to meet and exchange knowledge with researchers from around the world. By sharing new ideas and developing fruitful collaborations, we can continue to create innovative solutions to address the current and future global issues in order to benefit everyone.

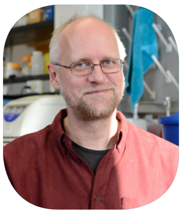
We are looking forward seeing you at the meeting in this exciting city of Singapore.

Dr Hanjo Hellmann Ph.D.
Associate Professor
Plant Stress Physiology
Washington State University, USA

Keynote speakers

Jeff Bennetzen
University of Georgia
USA

Mohammad Babadoost
University of Illinois
USA



Hanjo Hellmann
Washington State University
USA

Yinghua Huang
USDA-ARS and Oklahoma State University, USA

Petr Karlovsky
University of Goettingen
Germany

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University of Novi Sad
Serbia

Sadasivam Sankaranarayanan
Tamil Nadu Agricultural University, India

About
MAGNUS GROUP

Magnus Group (MG) is initiated to meet a need and to pursue collective goals of the scientific community specifically focusing in the field of Sciences, Engineering and technology to endorse exchanging of the ideas & knowledge which facilitate the collaboration between the scientists, academicians and researchers of same field or interdisciplinary research. Magnus group is proficient in organizing conferences, meetings, seminars and workshops with the ingenious and peerless speakers throughout the world providing you and your organization with broad range of networking opportunities to globalize your research and create your own identity. Our conference and workshops can be well titled as 'ocean of knowledge' where you can sail your boat and pick the pearls, leading the way for innovative research and strategies empowering the strength by overwhelming the complications associated with in the respective fields.

Participation from 90 different countries and 1090 different Universities have contributed to the success of our conferences. Our first International Conference was organized on Oncology and Radiology (ICOR) in Dubai, UAE. Our conferences usually run for 2-3 days completely covering Keynote & Oral sessions along with workshops and poster presentations. Our organization runs promptly with dedicated and proficient employees' managing different conferences throughout the world, without compromising service and quality.

About GPB 2019

GPB Singapore is the International conference which brings together the collection of investigators who are at the forefront in the field of Plant Biology and Plant Biotechnology. The scientific program will include oral presentations of sub-disciplines, keynote sessions led by eminent scientists and poster sessions presented interactively by junior scientists and graduate students. It is the ultimate meeting place for all the experts worldwide for new interdisciplinary scientific collaborations and networking. With different scientific sessions, you are provided assurance to explore the latest technologies and breakthroughs that are specific to your area of work. No doubt the event has a broad scope of topics and continued in parallel sessions relative to the specific area of research.

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Biography

Dr. Bennetzen received a Ph.D. in 1980 from the University of Washington in Seattle for investigations of gene function and evolution in brewer's yeast. After a one-year postdoctoral fellowship and two years in industry, he joined Purdue University as a faculty member in 1983. In 2003, he moved to the University of Georgia as the Giles Professor. He is an elected fellow of the US National Academy of Sciences and the American Association for the Advancement of Science. Dr. Bennetzen has published more than 200 refereed research articles.

Vertically and horizontally transmitted genetic information in plant::plant and plant::Microbe interaction

Jeffrey L. Bennetzen
University of Georgia, Athens, USA

Plants are inundated by seas of microbes in every tissue, in every environment and at every stage of development. Some of these microbes cause disease, while a few are known to enhance plant performance by preventing disease or by improving nutrient acquisition. Perhaps because the microbial diversity of all microbes (including beneficials) is much lower on the aerial parts of plants, diseases of these tissues are much more common than are root diseases. Because microbes have very high population numbers and short generation times, they are expected to be the routine winners in the never-ending evolutionary arms race between virulence of pathogens and disease resistance in host plants. However, recent work has shown that plants have more sources of genetic variation than previously expected, including horizontal gene transfer and site-directed recombination. Moreover, the microbial community in any given environment is uniquely established by each unique plant genotype, providing the opportunity for plant scientists to design host genotypes that create an optimal microbial community to improve plant performance and crop yield. This presentation will describe our experiments to map and identify the plant genes responsible for the determination of microbial composition associated with several different plant species and plant tissues. These studies are also uncovering previously unknown beneficial microbes, and laying the groundwork for breeding crops that show excellent and durable productivity without the need for fertilizers or pesticides.

Take Away Notes:

- A greater understanding of the nature and rate of plant genome instability, particularly as it relates to the evolution of new gene function.
- A strategy for identifying the plant genes that contribute to plant-associated microbial composition.
- A model for plant breeding to control the microbial composition that provides optimal plant services to its crop hosts in both stress resistance and nutrient use efficiency.

Biography

Mohammad Babadoost received his Ph.D. in plant pathology from North Carolina State University. In 1999, he joined the faculty of the University of Illinois at Urbana-Champaign, where he is now a Professor of Plant Pathology and Extension Specialist. Mohammad conducts research and extension programs on the biology and management of vegetable and fruit crops diseases, and teaches “Plant Disease Diagnosis and Management.” Dr. Babadoost has published 57 peer-reviewed and more 400 extension articles. He has developed a profound commitment for improving crop production in the developing countries and establishing food security in the world.

Improving identification of plant pathogens by molecular analysis

M. Babadoost
University of Illinois, USA

Using molecular analysis has helped to accurate identify plant pathogens and determining variation among their isolates. We have used molecular methods to identify species and variations among their isolates of pathogens causing cucurbit powdery mildew, Phytophthora blight of peppers and cucurbits, and internal discoloration of horseradish roots. Several other studies on determining species of fungi (e.g., *Fusarium* and *Phytophthora*) have also been published. After sequencing the internal transcribed spacer of nuclear ribosomal DNA (nrDNA) region of 119 isolates of powdery mildew fungi collected from six species of cucurbits in the United States, Italy, and Chile, *Podosphaera xanthii* was found the only species causing powdery mildew of cucurbits. Genetic variation among the isolates showed significant clustering trend of isolates. Random amplified polymorphic DNA markers were employed to assess genetic variation among 24 isolates of *Phytophthora capsici* in Illinois. Mean pair group analysis clustered isolates into six distinct groups. Original study showed that *Verticillium dahlia* caused internal discoloration of horseradish roots. Using molecular methods, it was revealed that the internal discoloration of horseradish roots is a disease complex and can be caused by one or any combination of five fungal species, including *V. dahlia*, *V. longisporum*, *Fusarium solani*, *F. oxysporum*, and *F. commune*. “Die Fusarien,” published in 1935, described 65 species, 55 varieties, and 22 forms of *Fusarium*. Using morphological characteristics, number of species of *Fusarium* was reduced to nine in 1945. The application of phylogenic species concept based on the DNA sequencing resulted in describing 70 species of *Fusarium* in 2006.

CONTENTS

Cullin 3 Plant E3 Ligases: A perspective on improving agricultural traits by controlling protein stability

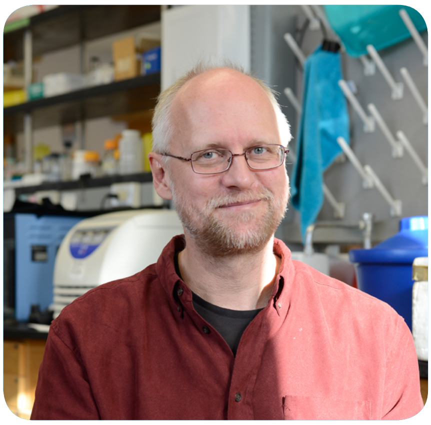
Hanjo Hellmann

Washington State University, USA

Plant development depends on a complex and flexible regulatory network that integrates environmental cues with specific developmental programs. A mechanism that provides plants with the ability to quickly and precisely respond is given by the ubiquitin proteasome pathway. Within the pathway, E3 ligases are key regulators that recognize specific substrate proteins and mark them for degradation through the 26S proteasome. A particular class of E3 ligases, CRL3^{BPM}, is composed of a scaffolding protein, Cullin3 (CUL3), and substrate adaptor proteins that contain a MATH-BTB/POZ domain (BPM). *Arabidopsis thaliana* encodes for six BPM (BPM1 to 6) and two CUL3 (CUL3a and 3b) proteins. Here we show that CRL3^{BPM} E3 ligases are widely involved in transcriptional processes by affecting stability of members of major transcription factor families in Arabidopsis. As a consequence, these E3 ligases alter diverse processes such as fatty acid biosynthesis, flowering time point control, and abiotic stress tolerance. Our work establishes CRL3^{BPM} E3 ligase as a major regulatory tool plants can use to facilitate controlled gene expression through specific protein degradation: a mechanisms that allows plants a high degree of flexibility to quickly modulate their physiological and developmental processes as needed.

Take away note:

- The presentation will introduce the ubiquitin proteasome pathway as one of plants' central regulatory systems.
- It will specifically address findings for a specific class of E3 ligase and what regulatory steps and substrates are known.
- Such findings provide valuable information to design novel approaches in bioengineering crop plants with improved traits.



Biography

Dr. Hellmann studied biology at the Technical University in Kaiserslautern, Germany. He started his PhD thesis in the group of Prof. Wolf Bernd Frommer in Berlin, Germany, on sugar and amino acid signal transduction, and received his Ph.D. degree in 1997. He went for two years to the group of Prof. Mark Estelle, University of Texas at Austin, USA, as a postdoctoral researcher to work on auxin and plant E3 ligases. In 2002 he started his own group as an Assistant Professor at the Freie University in Berlin, Germany, with a focus on plant E3 ligases as well as on steps that control vitamin B_6 biosynthesis in plants. In 2007 he moved to Washington State University, Pullman, USA, and was promoted to Associate Professor in 2013. He has published more than 45 articles reaching an h-index of 28.

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DAY 1

SPEAKERS

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Two mechanisms of lincosamide tolerance function as nuclear and plastid markers in higher plants

Massimo Bosacchi*, **Kliment Todosov, Daniel Ilg, Zora Svab and Pal Maliga**
Waksman Institute of Microbiology, Rutgers, The State University of New Jersey, Piscataway, NJ, USA

Lincosamide antibiotics inhibit the regeneration of plants in tissue culture. Resistance to lincosamides can be conferred by a mutation that modifies the ribosomal target site in the plastid genome, or by a transgene that encodes detoxification activity. We exploited both mechanisms to recover lincosamide-tolerant events in tissue culture. We identified several lincosamide nucleotidyltransferase (*lnu*) genes from medical studies and modified them for expression in plants. Four of these genes, the *lnuAN2s*, *lnuBs*, *lnuDs* and *lnuFs* function as highly efficient selectable markers for nuclear transformation of multiple dicot species. Under lincosamide pressure, we recovered transgenic tobacco, potato and Arabidopsis events with similar transformation frequencies as reported with kanamycin selection using the *nptII* gene. In the absence of a transgene, lincosamide tolerant lines developed in tobacco tissue culture over several weeks. Analysis of the plastid *rrn23* sequence of these events revealed point mutations or 1nt insertions at the putative lincosamide binding site. The efficiency of the lnu marker genes makes them useful additions to the toolkit of plant biologists. Furthermore, our ability to select for a plastid trait using lincosamide antibiotics sets the stage for the development of lnu genes as plastid markers in genotypes with increased antibiotic susceptibility.

Take away notes:

- My presentation will describe the discovery and development of highly efficient selectable marker genes for plant transformation.
- Other researchers are welcome to make use of these genes in their own research, and my presentation will highlight how to maximize their potential
- This work will be put in the larger context of our work towards maize chloroplast transformation. There will be a molecular component about our development of the expression signals driving these genes.

Biography:

Massimo Bosacchi is a Research Scientist at the KWS Gateway Research Center. As a member of the Cell Technologies team, he runs the maize transformation pipeline and researches cell culture based strategies to facilitate gene editing. He obtained his PhD from Rutgers University in 2016. Prior to this he spent 4 years as a Research Associate with the Monsanto Company.

Rice genome editing: A contribution to climate change mitigation and achievement of food security in Costa Rica

Marta Valdez-Melara*[1], Randall Rojas-Vásquez[1], Federico Albertazzi-Castro[2], Alejandro Hernández-Soto[3], Griselda Arrieta-Espinoza[2], Andres Gatica-Arias[1]
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[2]Center for Research in Cellular and Molecular Biology, University of Costa Rica, 2060 San Pedro, Costa Rica
[3]School of Biology, Technological Institute of Costa Rica, Cartago, Costa Ric

Abiotic factors, such as drought, salinity and high temperatures are limiting agricultural production. Also, under the pressure of rapid population growth, climate change and evolution of agricultural pests and diseases, new genome-editing technologies are the next green revolution and provide new genetic variations to improve yield, quality and resistance to biotic and abiotic factors in cultivated plants. In this sense, our study focuses on the modification of the active site of the enzyme trehalase using CRISPR/Cas 9 to confer tolerance / resistance to salinity in rice. As a result, a protocol for genetic transformation of rice embryogenic calli using *A. tumefaciens* was established. Four plasmids with the RNAg for the trehalase gene (Os10g0521000) were developed. However, the diverse applications of modern biotechnology arouse enthusiasm and mistrust in society, so it has both advocates and adversaries. These concerns could impact on national and international policies. In this sense, the public perception of society must be taken into account if it is considered that the new genome editing strategies can contribute to food security by introducing new traits in the crops. For this reason, the present study aims to investigate the role of collective communication in shaping a certain perception towards new genome editing strategies in plants, as well as to analyze the perception and attitude of Costa Rican society to new strategies of editing genomes in plants. Also, with respect to these new genetic improvement strategies, governments should consider their regulatory status and establish appropriate regulations if necessary. That is why in the present research is proposed to analyze the regulatory framework of Latin American countries around the new genome editing strategies in plants. This would allow the strengthening of regulatory frameworks and science-based decision-making to foster innovation, research and trade in products derived from new genome-editing technologies.

The University of Costa Rica financed this work (801-B7-294).

Take Away Notes:

- The audience will learn how to address an agricultural problem: the effect of drought and salinity in tropical crops such as rice, from a multidisciplinary perspective.
- The audience will know how we investigate in a developing country, with few economic resources but with a great inter and multidisciplinary effort. Also will learn how to edit the rice genome, which could be applied to other agricultural crops.
- Of course, our research may be used by professors in fields such as biotechnology, genetic engineering, communication, regulatory framework, among others.

Biography

She obtained a Doctorate on natural sciences from the University of Paris VI, France, in 1986. Her area of specialization is genetics, plant biotechnology and biosafety. She Is a professor at the School of Biology of the University of Costa Rica since 1990. Also she was the founder and first Director of the National Center for Biotechnological Innovations in Costa Rica and is a corresponding member of the French Academy of Agriculture. She has received two decorations: "National Order of French Merit" in 2014 and "Order of the Liberator of Slaves José Simeón Cañas" of the Government of El Salvador in 2015.

Cultivation, market and uses of Nepal's medicinal and aromatic plants: Reflections on local and national policy

Joel T. Heinen[*1], **Prakash Paudel**[2]
[1]Department of Earth and Environment, Florida International University, Miami, USA.
[2]Center for Conservation Biology, Kathmandu Institute of Applied Sciences, Kathmandu, Nepal

Nepal is a least-developed land-locked country with spectacular scenery and very high species diversity of many taxonomic groups. It is a center of adaptive radiation for many animal and plant families. The country boasts over 2,500 species of non-timber forest products of all kinds (NTFPs) and at least 160 species of medicinal and aromatic plants (MAPS) that are used in trade. Traditionally, Nepal has supplied raw, wild materials for the large Ayurvedic industry (traditional South Asian plant-based medicines) based in India. Since Ayurvedic products are also widely used in Nepal, and some species can be cultivated, much more revenue could be generated in-country if at least some popular species were cultivated at large scales and if at least some final products were manufactured locally.

For these reasons, the Government of Nepal proposed a national NTFP policy in the early 2000's and has been implementing the policy since that time with a goal of improving rural livelihoods in impoverished districts of the Himalayas. One main objective is to study up to 30 species of MAPs that show some promise for cultivation on small farm plots, and thus improving local livelihoods in rural areas. Another objective is to develop national industries, where feasible, to produce Ayurvedic medicines directly as opposed to exporting raw materials to India, only to import value-added medicinal products from India. Here we assess Nepal's NTFP Policy and consider its strengths and weaknesses as currently implemented. We conclude that it shows a great deal of promise and potential. It is clearly a step forward in meeting millennial development goals and in meeting some of the criteria for the implementation of the Convention on Biological Diversity. It has also attracted a good deal of interest and funding from several international and national-level non-governmental organizations (NGOs) due to its potential. However, our review shows that that some concerns remain and we end with several recommendations to improve this sector.

Take Away Notes:

- The audience will learn about a viable case study relevant for other developing countries, in how the sustainable use of biodiversity can ben managed to improve rural livelihoods, and how the policy is addressing the national-level economy though intense study of potentially cultivatable MAPs. The approach of this case study can be applied to a number of renewable resources that are locally collected for broader markets.

Biography

Dr. Joel T. Heinen received his PhD from the University of Michigan's School of Natural Resources and Environment in 1992 and has been on the faculty of Florida International University's Department of Environmental Studies, now the Department of Earth and Environment, since 1993. He served as an American Peace Corps Volunteer in Nepal from 1984 to 1988 and Fulbright Senior Scholar in Kyrgyzstan in the 1999-2000 academic year. His main research focus is in biodiversity conservation policy studies in developing countries of Asia and Latin America and he has published well over 100 academic to date, I addition to numerous other works including reports, book reviews, chapters, abstracts, etc. He lives and works in Miami, FL USA.

Plant proteomic responses to signal compounds lipo-chito-oligosaccharide and thuricin

Sowmyalakshmi Subramanian* and Donald L Smith
Department of Plant Science, Macdonald Campus, McGill University, Sainte Anne de Bellevue, Quebec, Canada

Lipo-chitooligosaccharides (LCO) and thuricin 17 (Th17) are bacterial signal compounds secreted by the rhizosphere bacteria of soybean, *Bradyrhizobium japonicum* 532C and *Bacillus thuringiensis* NEB17. At femtomolar concentrations these signal compounds promote plant growth and impart salt stress tolerance to *Arabidopsis,* soybean, corn and tomato. In all these studies, seeds and plants at the vegetative stage of growth were the most positively and visually affected. In each of these plants, the proteome responses vary depending on the abiotic stressors such as salt, drought and low temperature stress; the carbon, nitrogen and energy metabolic pathways were affected. Some of the key upregulated proteins in LCO and Th17 treated samples, in comparison with control, were ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, ribulose-1,5-bisphosphate carboxylase small subunit, ATP synthase β-subunit and chlorophyll a/b binding protein type II, along with shifts in stress proteins specific to each of these stressors. In soybean plants, the protein shifts were circadian specific under optimal plant growth conditions. The specificity of these responses plays crucial roles in organ maturation and transition from one stage to another in the plants' life cycles. This understanding of the response of biostimulants is a crucial component in agriculture and to address global food production. This talk summarizes some of the key findings of the proteomics work done on these two signaling compounds.

Take Away Notes:

- Learn the response of plants proteins to biostimulants under optimal and stressed conditions.
- From the research perspective, the research adds to functional interpretation to protein modulation during a biostimulant response.
- From the industrial perspective, this is another step to identify why the biostimulant is working the way it is under a given condition. This will further help address biostimulant formulation strategies and the crops that might be benefitted according to soil conditions.

Biography

Dr. Sowmya Subramanian did her BSc, MSc (Botany, Cytogenetics) from Bangalore University and Master of Technology (M. Tech) from Indian Institute of Technology, Kharagpur, India. She moved to Canada in 2006 and obtained MS (Agriculture) from Dalhousie University and PhD (Plant Science) from Department of Plant Science, Macdonald Campus/McGill University, Canada, where she continues to study Plant-microbe interaction as a Post-doctoral fellow in Prof. Donald Smith's lab. Her primary research interests include Plant stress physiology and 'Omics' (Transcriptomics, Proteomics and Metabolomics) of both plants and microbes in Plant-Microbe interactions with emphasis on biostimulants from rhizosphere bacteria.

Plants and radionuclides: From hazard to biotechnology

Pierre Chagvardieff*, Prat-Leonhardt N.
Biosciences and Biotechnologies Institute of Aix Marseille (BIAM), French Alternative Energies and Atomic Energy Commission (CEA) CEA Cadarache -Bât 177, 13108 Saint –Paul Lez Durance cedex, France

Plant nutrition takes off various minerals from the soils; these minerals are necessary to growth but in some cases these minerals are radioisotopes of essential elements but may be also exotic elements derived from industrial activities. The biological responses of plants to radioisotopes will be analysed, from the absorption in roots, the translocation to upper parts in stalks and leaves and their accumulation or storage. The limits of toxicological concentrations will be also discussed. Examples will be developed at a physiological, biochemical and genetic levels concerning Uranium, when this element is derived from uranium ore-bearing sedimentary bedrock, and Cesium (mainly 137Cs) as one of the element released after a nuclear accident. The importance of their bioavailability in the soil is a driven parameter for their impact on plants and the interactions in particular with phosphate and potassium will be described. The biological responses of plants to these elements have generated several biotechnological applications, so-called phytoremediation. The objectives are to manage their residual radioactive concentration in soils or in liquid medium, in order to extract them from the environment through depleting the soil concentration, or at the opposite to repress their accumulation generating edible crops so-called "safe food". An overview of the properties of various crops to radioactive elements will be presented. Finally, some economical applications will be considered.

Take Away Notes:

- Nuclear industry is very sensitive to its impact on environment, not only in case of accident. The increasing production of nuclear energy on the world market will generate increasing volume of wastes that will have to be treated. Dismantling and decommissioning of closing reactors should reinforce the cleaning of the local environment, so that soft technics are promising.
- The presentation should provide practical knowledge and experimental solutions to the reclamation of contaminated sites, as well as opportunities of collaboration.

Biography

Dr Pierre CHAGVARDIEFF has long expertise in biological science and R&D management on plant physiology, plant x microorganisms interactions, toxicological effects of metals. International expert in biotechnologies at CEA, scientific leader of CEA R&D "impact of technologies on humans and environment", he is representative in French Union of Research Institutes on environment (www.allenvi.fr). Formerly Director of Biosciences and Biotechnologies Institute of Aix-Marseille (BIAM/CEA/Cadarache), he is manager of DEMETERRES project devoted to the "Development of bio- and eco- technologies for effluents and soils remediation in support to a restauration strategy following a nuclear accident". He is also part of the SCARCE project (Singapore CEA Alliance for Research in Circular Economy).

Green algae *Cladophora* in the Crimean hypersaline waters as an ecosystem engineer and valuable resource

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Hypersaline waters are among the most extreme habitats on Earth. To exist in such harsh environment organisms must develop different adaptations including biochemical. Due to this they have unique components in biomass. *Cladophora* spp. may reach high biomass and play a very important functional role in productivity and nutrient cycling in the hypersaline water bodies worldwide. In the numerous Crimean hypersaline lakes and lagoons, floating and bottom *Cladophora* mats occupies large areas, and its biomass reaches up to 2-3 kg m^{-2}. These mats influence on regimes of salinity, temperature, oxygen, pH, and other factors in the water bodies, as well as create habitats for different organisms (bacteria, microalgae, animals), which reach highest abundance in the mats. Composition of *Cladophora* biomass was studied. Average composition: dry weight - 33%, organic matter in dry mass - 61%, protein - 69 g kg dry $mass^{-1}$, carotenoids 367 µg / g dry $mass^{-1}$, chlorophyll "a" - 523 µg / g dry $mass^{-1}$, chlorophyll "b" - 245 µg / g dry $mass^{-1}$, phaeopigments - 127 µg / g dry $mass^{-1}$, total carbohydrate -142 mg / g dry $mass^{-1}$, including ethanol-soluble - 12.3 mg / g dry $mass^{-1}$, water-soluble - 21.3 mg / g dry $mass^{-1}$, acid soluble - 95.4 mg / g dry $mass^{-1}$, and alkaline soluble - 12.5 4 mg / g dry $mass^{-1}$. Content of essential polyunsaturated fatty acids is high. An example, in *Cladophora* biomass, a relatively high content of eicosapentaenoic acid (EPA; 20:5n−3) (4.14 mg g^{-1} C), whereas other green algae *Ulva. intestinalis* had a lower value (0.45 mg g^{-1} C). All available data suggest that *Cladophora* have high productivity, and its biomass may be a valuable resource for different industries, agri-aquaculture, medicine, etc.

This study was supported by the Russian Science Foundation (grant 18-16-00001).

Take away notes:

- It provides new information, gives new data and ideas on a biotechnological and agri-aquacultural use of green algae *Cladophora*.

Biography:

Dr. Shadrin studied biology/hydrobiology at the Leningrad (now St.-Petersburg) State University, Russia and graduated as MS in 1974.). He received his PhD degree in 1982 at Institute of Biology of the Southern seas, Sevastopol, Russia. He was a head of several international projects. He published more than 200 research articles in Russian and English.

CONTENTS

Regeneration strategies in native woody species from disturbed South American dry tropical forests: The of aerial bud bank and soil seed bank

Sandra Bravo*[1], **Roxana Abdala**[2], **Valeria Ibáñez-Moro**[3]

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[2]Cátedra de Protección Forestal, Facultad de Ciencias Forestales, Universidad Nacional de Santiago del Estero, Santiago del Estero, Argentina

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The resilience of dry tropical forests is one of most central goal for scientists, environmental managers and politicians in South American countries due to the climate and land-use changes and to the great human population living to expenses forest resource at these latitudes. South American Chaco region forests are strongly modified by anthropic disturbances as wildfires, logging, livestock, rolling chopper to silvopastoral systems. Studies about regeneration strategies of native flora are yet scarce and fragmentary. The recruitment of new individuals and resprouting after disturbances are dependent from bud bank and seed bank of native species, respectively. The native vegetation responses to anthropogenic disturbances are been studied through functional approach in order to assess their effects on plant persistence and community dynamic. The native woody species have a high resprouting ability from aerial and subterraneous organs, which allow the maintenance of the species composition of forests after disturbances. However, structural changes related to resprouting, spinescence and growth habit occurred in disturbed forests of Chaco region. The resprouting pattern (basal vs/epicormic) is influenced by fire intensity and aerial bud bank of species. Disturbances drove the forest structure with three strata towards dense and thorny shrublands, with low potential for wood production, non-timber forest products as forages, medicinal plants, tinctures, among other environmental services. The seed density in soil decreased in forests disturbed by roller chopping and logging respect to forest under closure over the last three decades which could be related to biomass remotion and disturbance synergism. The studies about seed viability of dominant forest species showed a low persistence into the soil seed bank and low tolerance to heat shock at lab and in experimental fires. The assessment of soil seed bank of the six dominant species in Chaco region forests under closure and under synergic disturbances (wildfires and rolling chopping) are in course. Dominant species of Chaco region forests are wind-dispersed and their dispersion units are common components of leaf litter. This location exposes them to a greater degradation than those secondary species whose dispersion units remain immersed in soil upper horizons. There were no recruitment from seeds located in leaf litter, two years after medium to high severity experimental burns suggesting the importance of soil protection during wildfires and prescribed fires and the adverse environmental conditions for germination. The difficulties for native woody species recruitment in Chaco forests environments could reduce genetic diversity of their populations representing a great risk under climate change landscape. Our results suggest that disturbance frequency must be closely controlled to avoid losing of forest structure, genetic diversity and environmental services

Take Away Notes:

- The wide audience of congress will recognize common aspects and knowledge needs related to management of dry tropical forests of the World.
- The functional approach based in the relative importance of both woody species regeneration strategies can guide similar researches in other semiarid areas of World; as well this work can give an example to analyze in ecology classes.
- Early results of this work can improve models about dry tropical forest dynamics in disturbed landscapes and provide information to enhance the experimental design of other researches.

Biography

Dr. Sandra Bravo studied Biology at the Universidad Nacional de Tucumán, Argentina and graduated as Licenciada en Ciencias Biológicas in 1990. After 4 years of doctoral fellowship, she received her PhD degree in 2006 at the same institution. Her expertise area is fire ecology, regeneration strategies and dispersion in native woody species from Argentine Chaco region. Currently She works as Research/ Professor in Instituto de Silvicultura y Manejo de Bosques, Facultad de Ciencias Forestales, Universidad Nacional de Santiago del Estero, Argentina. She is Director of 3 doctoral fellowships and Co-director of 3 doctoral fellowships. Their current research projects are: - Ecological studies on soil seed banks of native woody species from Argentine Chaco region and effects of disturbances. - Vegetative regeneration strategies of native woody species from Argentine Chaco region and effects of disturbances. - Disturbance regimes in native forests from Argentine Chaco region.

Glomalin content of soil in relation to soil organic carbon under long term fertilizer studies in finger millet – maize cropping system

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An experiment conducted in an ongoing Long Term Fertilizer Experiment at Zonal Agricultural Research Station, UAS, GKVK, Bengaluru, Karnataka, India to study the dynamics of soil organic carbon and glomalin content of soil under finger millet-maize cropping system. Glomalins are a thermo stable, water-insoluble soil glycoproteins produced by arbuscular mycorrhizal fungi measured in soil as glomalin related soil protein. These proteins perform a fundamental role in making soil structure and they live relatively long in soil and play a structural role in soil carbon dynamics. The results of two years study (2013 and 2014) revealed that continuous application of inorganic fertilizers along with organic manure had significant effect on glomalin content which was significantly higher in 100 % NPK + FYM + Lime (3.83 g kg^{-1}) applied plot followed by the treatment receiving 100 % NPK + FYM (3.72 g kg^{-1}) as compared to the treatments receiving only inorganic fertilizers, while lower glomalin content was recorded in control (1.21 g kg^{-1}). Among different depths, surface layer (0 to 15 cm) recorded significantly higher glomalin content in soil (2.53 g kg^{-1}). Generally in cultivated land plant roots were more heavily colonized with almost the whole root filled with mycorrhizal material (hyphae, arbuscules, vesicles or spores). The content of glomalin in the soil is something that builds up over time and is not always measurable in the first year after treatment imposition. Therefore, long term application of fertilizers had significant impact on glomalin content. Total organic carbon was also significantly higher in the treatment receiving 100 % NPK + FYM + Lime (5135 mg kg^{-1}). The pooled data of two years revealed that irrespective of depth soil organic carbon content was significantly higher in the treatment receiving 100 % NPK + FYM + Lime (4.99 g kg^{-1}) followed by treatment receiving 100 % NPK + FYM (4.85 g kg^{-1})). In the present study it was observed that the values of glomalin content had a positive and significant relation with soil total organic carbon. Application of FYM increased the soil organic carbon content to a greater extent than that of inorganic fertilizer alone. This may be attributed to enhanced crop growth which in turn, resulted in increased above and below-ground organic residues and thus raised the organic carbon content. Aggregate stability of soil was also significantly higher in 100 % NPK + FYM + Lime (79.53%) followed by 100 % NPK + FYM (77.98%) as compared to treatments receiving only inorganic fertilizers and unfertilized control. Significantly higher maize yield was recorded in 100 % NPK + FYM + Lime (50.49 q ha^{-1}) and finger millet in 150 % NPK (34.51 q ha^{-1}) was mainly due to more organic carbon and improved glomalin content which enhanced the good soil aggregates which helped in better moisture and nutrient supply there by enhanced the crop yield.

Take away notes:

- Can know the significance of glomalin content in soil aggregate formation, maintaining soil fertility and soil organic carbon content in soil.
- The data generated is only after 28 years of experimentation. Long term impact of organic manure and fertilizers on glomalin content and carbon sequestration can be studied over the years.
- Long term impact of organic manure and fertilizers on annual C input required to maintain SOC in equilibrium can be studied by carbon modeling.

Biography:

Dr. P. K. Basavaraja, completed his MSc (Agri) at University of Agricultural sciences, Bangalore, Karnataka and PhD at Forest Research Institute, Dehradun, India, is presently working as Professor & Scheme Head, AICRP on STCR, UAS, and Bangalore. Since thirty years he is working on Soil Fertility, Micronutrients, Salt affected soils, Organic residue management, Watershed management, Soil test crop response studies. He operated Thirteen research projects and guided /guiding Five PhD and Ten MSc(Agri) students and Ninety students as Co-guide. He published more than 200 publications including 53 peer reviewed research papers, bulletins, abstracts, book chapters. Officially he visited Crete, Greece, Wageningen, Netherland, Dubai and presented four research papers in international conferences.

CONTENTS

LED technological possibilities: Tool for management of metabolic changes in microgreens

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Owing to high nutritional value and improved bioavailability of essential elements, microgreens are promising targets for nutrient enrichment using technological aspects of light-emitting diodes. This study determines changes in metabolism of certain prebiotic carbohydrate (hexoses and sucrose), ascorbic acid, β-carotene; nonheme iron (Fe) enrichment and interaction with inorganic catalysts, such as magnesium (Mg) or calcium (Ca) in *Brassicaceae* (kohlrabi *Brassica oleracea var. gongylodes*, broccoli *Brassica oleracea* and mizuna *Brassica rapa var. Japonica*) microgreens. Plants grew under main LED lighting spectrum (combination of blue 447 nm, red 638 and 665 nm and far-red 731 nm) or supplemented with green 520 nm, yellow 595 nm and orange 622 nm LEDs. Photoperiod of 16 h and total PPFD of 300 μmol m^{-2} s^{-1} was maintained. Obtained results highlight the impact of supplemental LED components and provides key information to improve microgreens nutritional quality. Supplemental 595 nm significantly increased content of prebiotic carbohydrates in mizuna and broccoli. Significantly positive effect of supplemental components on β-carotene accumulation was observed only in mizuna, whereas kohlrabi distinguished in significant accumulation of ascorbic acid. Supplemental 622 nm component led to a significant increase of Fe, Mg and Ca in all microgreens. Generally, the accumulation of Fe was highly dependent on promoters and inhibitors of Fe absorption, as very strong positive correlation between Fe and Ca, Fe and Mg was found in kohlrabi and broccoli, whereas, strong negative correlation between Fe and β-carotene, Fe and prebiotic carbohydrates was found only in kohlrabi. Thus, metabolic changes that occurred in treated microgreens increased the bioavailability of essential nutrients. Therefore, selected supplemental LEDs, might be a preferred option for *Brassicaceae* microgreens cultivation to preserve and accumulate certain nutritionally valuable metabolites.

Biography:

Giedrė Samuolienė has completed her PhD at the age of 30 years from Aleksandras Stulginskis University (biomedical sciences, agronomy). She is the Chief Researcher of Laboratory of Plant Physiology and Deputy Director for Research of Lithuanian Research Centre for Agriculture and Forestry, Institute of Horticulture, and docent at Aleksandras Stulgisnkis University. She has published 27 in CA WoS data base journals with impact factor, 24 publications in CA WoS data base journals without impact factor. She has National science award (2014, with co-authors), Silver medal of Vytautas Magnus university (2015), Scholarship of the Lithuanian Academy of Sciences (2012-2013). She is Guest Associate Editor for Crop and Product Physiology in Frontiers in Plant Science. Is a leader or participates in Horizon2020 and national High-level R&D projects. The main research topics are: biology of plant morphogenesis and flowering initiation; plant photophysiology: the manipulation of photosynthesis photomorphogenesis and metabolism, the creation of plant irradiation principles; plant ecophysiology: modulation of differential and complex impact of changing climate and anthropogenic factors; plant productivity physiology: optimization of crop or plantation physiological parameters by technological means, the formation of biopotential and realization in ontogenesis.

In vitro multiplication of plum cultivars (*Prunus domestica* L.)

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In 2016, a project has been started to preserve the diversity of older plum cultivars grown on the territory of the Czech Republic. The purpose of this study was to develop an efficient in vitro system for rapid propagation of plum explants as an initial plant material for sanitation from viral contamination by chemotherapy and long term storage by cryopreservation experiments. Due to the fact that different species and subspecies of genus *Prunus* contributed to the diverse gene constitution of existing plum cultivars, the response of particular genotypes can vary in in vitro culture environment. Despite increasing numbers of reports of successful micropropagation more research is still needed to identify appropriate in vitro media compositions and concentrations of phytohormones for particular cultivars. The donor shoots were obtained in March from mature trees grown at the Research and Breeding Institute of Pomology (RBIP) Holovousy Ltd., Department of Fruit Genebanks. Selected plum genotypes 'Svestka domaci', 'Hamanova' and 'Chrudimska' were successfully established in vitro using 0.15% mercuric chloride as a disinfection solution. Developing shoots were serially subcultured onto fresh media for six consecutive 4-week passages. This provided a stock collection of shoots for proliferation studies. To assess the effect of plant growth regulators on multiplication, in vitro shoots were assigned to the basal MS medium supplemented with 1, 2 and 4 mg L^{-1} BAP (6-benzylaminopurine) or 0.5 and 1 mg L^{-1} TDZ (thidiazuron). All cultures were incubated in a growth room under 16 h of cool-white fluorescent light provided by Sylvania/Germany tubular lamps (F18W/840-TB) at 22 ± 1°C. The irradiance was 40 μmol m^{-2} s^{-1} at plant height. Multiplication rate was defined as the number of newly formed shoots (>10 mm) per initial shoot tip after four weeks of culture. Each combination of genotype and treatment involved 25 shoot tips and each experiment was repeated four times. Data from four independent experiments were pooled and expressed as the mean. Treatment means were compared with the standard error (SE) of the mean. Cultivars in the study differed in their proliferation and development potential in MS medium according to hormone level between 1.1 and 5.9. Generally, the highest proliferation rate (5.9) in our experiments was obtained for cultivar 'Hamanova' on MS medium with the highest concentration of BAP 4 mg L^{-1}. Concerning cytokinin TDZ, sufficient multiplication rate 5.1 was obtained only for 'Hamanova' on medium with higher concentration 1 mg L^{-1}. Results obtained in our study confirmed preliminary findings that BAP was an important plant growth regulator for proliferation and growth in plum micropropagation. During in vitro multiplication phase, for all tested cultivars, any morphological abnormalities such as excessive callus formation, hyperhydricity or production of abnormally narrow leaves were not noted. The observed differences in multiplication and morphology among plum genotypes under the influence of an exogenous BAP or TDZ could result from the genetic control of different auxin and cytokinin metabolisms of plant tissue. Examination of rooting of in vitro propagated plants is now in progress.

Take away notes:

- The described technique enabled us to multiply and maintain sufficient amount of in vitro plants of three plum cultivars for research experiments with in vitro virus elimination and cryopreservation. Moreover a successful *in vitro* culture technique would provide an alternative method, which can potentially multiply selected plum genotypes including rootstocks more rapidly than traditional nursery systems. Micropropagation techniques described in this paper may also be applied to other *Prunus domestica* cultivars. Advanced vocational schools and universities could also use obtained results to expand their teaching or research.

Biography:

Jiri Sedlak studied at the Mendel University of Agriculture and Forestry in Brno, the Czech Republic and graduated as MSc in 1996. He received Ph.D. at the Czech University of Life Sciences in 2007 (postgraduate study). Since 1998, he has worked as scientific worker in the Department of Fruit Genebank. Currently he specializes in biotechnology, plant tissue cultures and cryopreservation. He has published more than 50 scientific and research articles in the past ten years.

Massive growth of super dwarf rice plant in a fully closed type plant factory for poly lactic acid production

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A natural strain of dwarf rice (*Oriza rufipogon* G. subsp. *nunus,* M. N.) is discovered. It is just ordinary rice except its plant length. The length of the rice plant is about 20 cm. Since the size of the discovered rice plant is so small, those conventional machineries for rice production are not usable to this plant and the conventional paddy field culture method cannot be applicable either. The plant size just fits for a multi-layered shelf type plant factory. It can be harvested 4 to 6 times in a year under controlled environment depending on control strategies. Since this grain production system can be fully closed, the amount of recycled and circulating water requirement to produce dried rice grains is remarkably small compering to the open paddy field system. This dwarf rice plant requires just 300 PPFD. By using LED for radiating the plant, it is easy to sustain proper plant temperature at around 28℃. Most of the conventional closed type plant factories have been utilized to grow perishable vegetables. It is often difficult to find proper consumers in order to sell those short shelf-life vegetables. This plant factory grown rice grain is edible naturally. However, a variety of industrial applications at very low price is more expected. For example, the global demand for the poly lactic acid production is becoming very much sizable in the world environmental issues. The bio-ethanol production is another market for this material. It should be reminded that this factory production of grains can be robotized easily by modifying conventionally mechanized paddy system. This leads us to 5G and IoT era in the near future.

Take away notes:

- Not only rice but also wheat and corn will be introduced.
- Many fully closed type plant factories currently available can be easily modified for grain factories.
- There are many application examples for the factory grown grain products including possible locations where grain factories can be built.

Biography:

Dr. Murase studied Agricultural Engineering at Michigan State University, USA and obtained Ph.D. in 1977. He then became a professor at Osaka Prefecture University, Japan. Currently he is a retired Professor and a CEO of Mspore Corporation.

Towards C4 rice; Overexpression of C4 genes in *Arabidopsis thaliana* and *Oryza sativa* enhances photosynthesis, plant productivity and water use efficiency

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Plants with C4 photosynthesis are not only efficient in carbon assimilation, but they also have an advantage under unusual growth conditions. In C4 photosynthesis, the primary CO_2 fixation is catalyzed by phosphoenolpyruvate carboxylase (PEPC). It is shown that overexpression of, both PEP Carboxylase and PEP Carboxykinase in *Arabidopsis thaliana* to have increased CO_2 concentration in the vicinity of Rubisco. resulted in higher electron transport, carbon assimilation, increased biomass coupled with better water use efficiency. Carbonic anhydrase (CA) catalyzes the inter-conversion of CO_2 and bicarbonate used by the primary carboxylating enzymes of C3 and C4 plants respectively. Overexpression of cytosolic carbonic anhydrase (b-CA3) of the C4 dicot *Flaveria bidentis* in C3 *Arabidopsis thaliana* increased the photosynthetic efficiency of the transgenics. Due to higher concentration of HCO_3^- in CA overexpressors, their PEPC activity increased generating more oxaloacetic acid and amino acids. Consequently, their total protein content increased resulting in higher Chl synthesis. The electron transport rate, CO_2 assimilation rate, starch content, plant fresh weight and dry weight increased by 10-20% in CA overexpressors. Transgenic plants had lower stomatal conductance, reduced transpiration rate and higher water use efficiency. Like C4 plants all the transgenics were tolerant to abiotic salt stress. Transgenics had higher electron transport rate, better performance index and reduced generation of reduced generation of reactive oxygen species in stress environment. These approaches are being replicated in rice (*Oryza sativa*) to have increased photosynthesis, plant productivity and grain yield.

Take away notes:

- Work presented shall be helpful to researchers working in the field of Plant Biology and Biotechnology. The approach could be replicated in other plants to increase plant productivity and grain yield.

Biography:

Professor Baishnab C Tripathy studied Botany for his master's degree. Subsequently, he joined PhD program in Jawaharlal Nehru University, New Delhi and did his PhD on Primary Processes of Photosynthesis in 1981. Subsequently, he did his post-doctoral research on chlorophyll biosynthesis and membrane bioenergetics in Ohio State University, Columbus, Ohio and University of Illinois, Urbana, USA from 1981-87. After returning to India, he joined Jawaharlal Nehru University, New Delhi as Assistant Professor in 1987 and promoted to full professor in 2001. He has contributed a lot to Photosynthesis Research and has more than 100 research publications.

CONTENTS

Precision Nitrogen management through crop sensors on growth and yield of aerobic rice (*Oryza sativa* L.)

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Aerobic rice is grown in well drained, non-puddled and non-saturated soils just like wheat and maize. Experimental results showed that water requirement of aerobic rice was 30 – 50 % less than flooded system which yields almost same as obtained in case of transplanted rice. N fertilization is the major agronomic practice that affects the yield and quality of aerobic rice. The fertilizer N use efficiency by rice is very low as partial factor productivity has decreased exponentially. Nowadays crop sensors are becoming popular for nitrogen management. Hence field experiment was conducted to standardize the precision nitrogen management using crop sensors during kharif 2017 and 2018 at Zonal Agricultural Research Station, UAS, Bengaluru in sandy loam soil (pH 6.0; OC 0.51 %) with medium available nitrogen (318.13 kg ha-1), phosphorous (34.18 kg ha-1) and potassium (284.28 kg ha-1). The experiment was laid out in RCBD with nine treatments, replicated thrice and cultivar used was MAS 946-1. The results revealed that nitrogen management through SPAD sufficiency index 96-100 per cent recorded significantly higher plant height (70.0 cm), number of tillers (42.8 hill-1), leaf area (2720 cm2 hill-1), total dry matter (133.8 g hill-1), higher productive tillers hill-1 (34.0), panicle length (23.2 cm), test weight (24.8 g) and resulted in higher grain (7189 kg ha-1). The nitrogen management through SPAD sufficiency index 96-100 per cent recorded higher nutrient uptake (130.5, 24.0 and 120.0 kg NPK ha-1, respectively), gross returns and net returns. Whereas, higher B: C ratio was found with GreenSeeker based nitrogen management.

Evolutionary epigenomics of mangroves reveals the homeostatic role of gene body methylation in stress adaptation

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DNA methylation plays an important role in plant stress responses whereas little is known about its role in long-term stress adaptation. In this study, we used mangroves well-adapted to tropical intertidal environments as a model system to understand the role of gene body methylation, i.e., CG methylation in coding regions, in plant stress adaptation. Using whole-genome bisulfite sequencing, we compared patterns of gene body methylation between pairs of mangrove and non-mangrove species using rice as outgroup. We found massive gains of gene body methylation specific to mangrove lineages. The estimated gain-to-loss ratio of gene body methylation in mangroves is magnitudes higher than that in non-mangroves. We estimated that more than a thousand genes exhibited convergent body methylation in mangrove genomes (convBMM) but only tens of genes in the non-mangroves (convBMN). In comparison with non-convergent gbM genes, covBMM but not convBMN genes showed reduced gene expression variation in response to salt and UV-B stresses. We found little overlap between convBMM genes and loci with signatures of convergent DNA sequence evolution. Our results suggest that positive selection acts on natural gbM variation to increase gene expression stability. This may allow rapid accumulation of genetic variation and thus accelerate long-term adaptation to environmental stresses.

Take away notes:

- This study indicates that epigenetics independent of genetics plays a significant role in adaptive evolution.
- Our results suggest that gene expression homeostasis is crucial for plant long-term adaptation to environmental stresses.
- Genes with mangrove-specific convergent gene body methylation would provide a valuable resource for unraveling the molecular mechanisms underlying plant adaptation in general.

Biography:

Dr. Tang received her Ph.D. from Sun Yat-Sen University in 2004 and has been working there ever since then. She was promoted to Professor in 2013. Previously, she was a visiting scholar at the University of Chicago where she studied functional evolution of microRNAs. Dr. Tang is interested in small RNA evolution and function. Her current research themes include: microRNA evolution and sex antagonism, siRNAs in epigenetic inheritance and stress adaptation, genetic conflict between transposable elements and host small RNAs, evolution of small RNA pathways.

Qualitative analysis and anti-bacterial investigation of *Plumbago zeylanica*

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Plant Biotechnology Laboratory, Department of Biotechnology, Delhi Technological University, India

Plumbago zeylanica commonly known as 'Chitrak' is a medicinal plant which contains a wide range of phytocompounds like flavonoids, alkaloids, napthoquinones, saponins, steroids, tannins, tri-terpenoids, etc. Utilization of *in-vitro* culture has an advantage over wild type as it possesses high growth rate and independent from seasonal changes. The present investigation was performed to identify presence of different bioactive compounds in three different extracts of *in-vitro* grown roots of *P. zeylanica*. Root of the plant was air dried and extracted with methanol, ethanol and chloroform by 72 hours maceration. Seven different phytochemical studies have been conducted i.e. flavonoid, terpenoid, alkaloid, steroid, coumarins, saponin and tannin. Methanolic extract showed presence of flavonoid, terpenoid, steroid and coumarins, ethanolic extract showed presence of terpenoid, steroid, and alkaloid whereas chloroform extract showed presence of only flavonoids and tannins. Further antibacterial activity of different extracts was tested against two bacteria i.e. *E.coli and Staphylococcus aureus*. Antibacterial activity was determined using zones of inhibition, which were measured by using disc diffusion method. Maximum antibacterial activity was against *Staphylococcus aureus*. Methanolic extracts of *Plumbago zeylanica* were found to be more potential for antibacterial activities followed by chloroform and ethanolic extract.

Take away notes:

- This study provides the information about application of *P. zeylanica* in antibacterial activity and shows the presence of different phytocompounds.

Biography:

Arpita Roy is pursuing her PhD (3rd year) from Delhi Technological University. She has published more than 25 papers in reputed journals. She secured first rank and received Gold medal in M.Tech. Her area of expertise includes plant tissue culture, antibacterial studies, phytocompound analysis, microbial & fungal culture handling, biosurfactant production, nanoparticles synthesis, etc.

CONTENTS

Population status, soil properties and microbial colonization in Himalayan Silver Birch (*Betula utilis* D. Don)

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The Himalayan silver birch (*Betula utilis* D. Don), commonly known as bhojpatra, is a multipurpose and broadleaved deciduous tree. It grows up to 4500 m asl and represents one of the dominant species of the tree line in Indian Himalayan region (IHR). It often grows in association with *Abies pindrow*, *A. spectabilis*, *Prunus cornuta*, *Acer accuminatum, Sorbus foliolosa, Pinus wallichiana* and *Rhododendron campanulatum*. Its bark is a striking feature which is smooth, shining and reddish white bearing numerous paper-like layers with broad horizontal rolling nature. *B. utilis* grows efficiently in acidic, neutral and alkaline soils and shady moist habitat. The tree is a source of many biochemical compounds which possesses anti-cancerous, anti-HIV, antimicrobial, antioxidant, and antifertility properties. Factors such as over exploitation, deforestation, overgrazing, natural calamities, snow drift, forest fire, landslides, etc., influence the regeneration of *B. utilis*. The species has also been reported for a suppressive effect on microbial population in its rhizosphere.

The aim of the present study is (1) to assess its population status in IHR, and (2) to evaluate soil and plant growth related properties including physico-chemical and enzyme activities in rhizosphere soil along with the root associated microbial communities. The study sites were located at Rohtang Pass, Solang Valley and Hamta Pass in Himachal Pradesh, North Western Himalaya, India. Ten quadrates (10x10) were laid for the assessment of birch population. The physicochemical properties and activities of six soil enzymes (arylsulfatase, acid and alkaline phosphatase, β -glucosidase, dehydrogenase, and urease) were estimated following standard procedures in two, active (summer) and dormant (winter), seasons. Root associated microbial communities were studied following microscopy using trypan blue staining method.

The highest total tree and *B. utilis* density recorded was 1430 Ind ha^{-1} and 700 Ind ha^{-1}, respectively. The soil moisture content, pH, organic carbon, available phosphorus, nitrogen and potassium were recorded ranging from 15.17- 43.92%, 5.17 - 6.03, 1.64 ± 0.06 - 3.36 ± 0.01 %, 0.005 ± 0.001 – 0.0375 ± 0.002 ppm, 11 ± 3 - 57 ± 3 ppm and 140 ± 1 - 477 ± 7 ppm, respectively. Higher alkaline phosphate (411.21 ± 7.49 μg pNP/g), β –glucosidase (48.77±1.69 μg pNP/g) and dehydrogenase (0.84 ± 0.03 μg TPF/g) activities were recorded in dormant season, while higher urease (28.40 ± 0.33 μg N/g dry soil/h), aryl sulfatase (24.16 ± 0.88 μg pNP/g and phosphatase (331.63 ± 5.41μg pNP/g) activities were recorded in active season. Microscopy revealed colonization of a variety of microbial endophytes (both bacterial and fungal) in birch roots, being higher in active season. Fungal endophytes were majorly consisted of fungal mycelium and dark septate endophytes. Some nematode-like structures were also observed in the cortical root cells of birch.

Frequent monitoring of the populations might form the baseline for conservation and management of birch forest. Soil microbial communities are responsible for the variation in various ecological processes through biogeochemical cycling under low temperature environment. Further, the association of specific groups of microorganisms and activity of soil enzymes my be considered as the health indicators of soil, plant and the environment.

Take away notes:

- Ecological importance of a timber line tree species (Himalayan birch) of IHR along with its population status.
- The economic importance of Himalayan birch for its bioprospection.
- The role of soil microbial and enzyme activities as indicators of a specific climate.

Biography:

Ms Khashti Dasila is a Senior Project Fellow at G.B. Pant National Institute of Himalayan Environment and Sustainable Development, Kosi-Katarmal, Almora, India. She has obtained MSc degree in Microbiology and perusing PhD in Biotechnology on "Bioprospection of root-associated endophytes in Himalayan Birch (*Betula utilis* D. Don) from North Western Himalaya".

Trichome formation and insect tolerance in tomato

Wei Deng*, Yujin Yuan, Zehao Gong, Yingqing Luo
School of Life Science, Chongqing University, Chongqing, China

Tomato trichomes, with unicellular and multicellular types, function as mechanical and chemical barrier against pests. Knock-down and over-expressed lines of *SlARF4* were obtained to study the function in trichome formation in tomato. *SlARF4*-up-regulated plants exhibited increased density of type I, V and VI trichomes, whereas down-regulation of *SlARF4* decreased density of type I, V and VI trichomes, indicating *SlARF4* positively regulated the formation of unicellular and multicellular trichomes in tomato. Over-expression of *SlARF4* increases the excretion of α-terpinene, β-phellandrene, γ-elemene, β-caryophyllene and α-humulene, and confers tolerance to spider mites. Down-regulation of *SlARF4* decreased the terpenoid excretion and cause susceptibility to spider mites. Knock-down of SlTHM1 gene increase the density of type I and VI trichomes of leaves, indicating SlTHM1 negatively regulates the multicellular trichome formation. SlTHM1 knock-down plants exhibited increased the terpenoid excretion and tolerance to spider mites. SlARF4 targets the AuxRE motif of SlTHM1 genes and inhibits its expression. Knock-down of SlMYB52 gene increase the density of type V trichomes, which demostartes SlMYB52 negatively regulates the unicellular trichome formation. SlARF4 targets the TGA motif of SlMYB52 gene and inhibits its expression. Moreover, SlTHM1 and SlMYB52 target the promoter of SlCycB2 gene and increase its expression. Taken together, our results prove the SlARF4-SlTHM1/SlMYB52-SlCycB2 cascade in transcriptional regulation of the formation of unicellular and multicellular trichomes in tomato. Our results also provide a novel strategy for insect resistance in plants.

Take away notes:

- This presentation provides molecular mechanism about the formation of unicellular and multicellular trichomes.
- SlARF4-SlTHM1/SlMYB52-SlCycB2 cascade plays important role in transcriptional regulation of the formation of unicellular and multicellular trichomes in tomato.
- This presentation provides a new strategy for insect tolerance in plants.

Biography:

Dr. Deng studied horticulture at the Southwest University, China and graduated as bachelor in 2000. He received his PhD degree in 2006 at Department of Plant Science, University of Connecticut, USA and Southwest University, China. He is a postdoctoral fellow at Department of Agricultural, Food and Nutritional Science, University of Alberta, Canada from 2011 to 2012. Now, he is a professor at School of Life Science, Chongqing University, China. He has published more than 30 research articles in SCI journals.

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DAY 2

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Biography

Dragutin T. Mihailovic is Professor in Meteorology, Biophysics and Environmental Fluid Mechanics at the University of Novi Sad (Serbia). He was the Visiting Professor at University at Albany, The State University of New York at Albany, Visiting Scientist at University of Agriculture, Wageningen and Norwegian Meteorological Institute. He has more than 100 peer-reviewed scientific papers in SCI(E) journals. He edited and wrote seven books and one monograph. He was the member of the Editorial Board of Environmental Modeling and Software (1992-2010) and reviewer in 15 scientific journals. He was principal investigator in many international projects with U.S.A and several European countries.

Stability of synchronization in the process of biochemical substance exchange in a diffusively coupled ring-like arrangement of cells in plants as a potential source for autoimmune diseases

Dragutin T. Mihailovic*[1], Darko Kapor[2]

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Understanding how local intra-cellular biochemical exchange processes and global features, like environment and system size, influence the robustness, adaptability and evolution of the collective behavior of multi-cell systems is one of the most challenging topics in the biology of complex systems today. Information coupling and the exchange of biophysical substances among the components of multi-cell systems are both driven by a range of intrinsic and extrinsic factors. Many authors have invested significant contributions to the understanding of multi-cell system dynamics through studies of the stability of the synchronized state, which is required for robust functioning of the multi-cell system in the face of noise and perturbation. However, they considered cells as completely uniform particles, without internal structure and without the ability to change their behavior. In actuality, it is well known that in natural conditions, cells spend most of the time in the stationary phase which is characterized by a decrease in growth rate, slowdown of all metabolic processes and increase in resistance to several stress conditions. Since these and many other processes in a cell are defined as diffusion-like, it is important to see: (i) how these processes can be better represented in models, by introducing affinity in the diffusive coupling associated with biochemical substance exchange; and (ii) how intra-cellular dynamics are affected by the perturbation of parameters that represent the influence of the environment, cell coupling and cell affinity. In this study we numerically investigate a model of a diffusively coupled ring-like arrangement of cells in plants (specifically in roots). To model the dynamics of individual cells we propose a map with cell affinity, which is a generalization of the logistic map. First, the basic features of a one-cell system are studied in terms of the Lyapunov exponent, Kolmogorov complexity and Sample Entropy. Second, the notion of observational hierarchy, which is a perpetual negotiation process between different levels of the description of a phenomenon, is reviewed. After these preliminaries, we study how the active coupling induced by the consideration of the observational hierarchy modifies the synchronization property of the model with $N=100$ cells. It is shown numerically that the active coupling enhances synchronization of biochemical substance exchange in several different conditions of cell affinity. For the end we shortly elaborate our conjecture that desynchronization in the process of biochemical substance exchange could be one of potential triggers for autoimmune diseases in plant diseases.

Take away notes:

- Understanding how local intra-cellular biochemical exchange processes and global features, like environment and system size, influence the robustness, adaptability and evolution of the collective behavior of multi-cell systems in plants
- Since the information coupling and the exchange of biophysical substances among the components of multi-cell systems are both driven by a range of intrinsic and extrinsic factors it will help to audience in their theoretical work as well as in designing experiments
- This research could be used at universities and research institutions to expand their research and teaching.

AP-MS and organ growth in plants: From cells to tissues

Geert De Jaeger, Ph.D.

VIB-Ghent University, Belgium

At the very basis of cellular structure and function lie networks of short- and long-term molecular interactions. My research team develops interactomic tools for plants and runs a state of the art AP-MS platform for protein complex isolation. Through its high specificity and explanatory power, our platform steadily became a central –omics tool in our research department. Complexes got isolated for hundreds of proteins involved in cell growth and proliferation control leading towards protein discovery, functional analysis of protein complexes, and the mapping of protein networks involved in plant organ growth. We started in cell cultures, but steadily moved towards Arabidopsis seedlings, to finally end up into crop plants. Their bigger organs make them particularly suitable for the study of the complex regulation of organ growth in a developmental context. We obtained proof of concept for the study of protein complex dynamics during leaf growth and demonstrate its use for organ growth engineering.

Biography

Geert De Jaeger is an associate professor at Ghent University and Group leader/Vice-director at the VIB-UGent Center for Plant Systems Biology. He obtained his PhD in 1997 from Ghent University during which he explored technology for targeted gene knock out in plants. During a postdoc at the VIB, he developed transgenic tools that strongly boosted recombinant protein production in seeds. This resulted in a group leader position at the VIB-UGent Center for Plant Systems Biology in 2002. De Jaeger's technology-driven research team obtained high visibility in the plant research field with their state of the art AP-MS platform that maps protein interaction networks in plants. His main research interest is the molecular regulation of plant growth at both the cellular and organ level in Arabidopsis and corn to discover new strategies for the engineering of crop yield with the aim to contribute towards a more sustainable agriculture.

Biography

Petr Karlovsky is professor and head of Molecular Phytopathology and Mycotoxin Research Unit at the University of Goettingen in Germany. Petr studied biochemistry in Czech Republic and worked as a postdoc in Germany and as a visiting professor in the USA before joining DuPont/Pioneer Hi-Bred in the USA as Research Manager for Disease Resistance. He was nominated for two Expert Groups of ILSI (Brussels), acted as Vice President of the Society for Mycotoxin Research, joined editorial boards of several journals and the advisory board of Amity Institute of Microbial Sciences in New Delhi, India and served as a reviewer for grant agencies of nine countries. He was awarded a guest professorship by Zhejiang University in Hangzhou, China, and Senior Visiting Fellowship by the Institute of Advanced Studies in Bologna, Italy. Petr Karlovsky co-authorized 134 publications listed by Clarivate Analytics (Web of Science), more than 200 abstracts and several patents. He lives with his wife in Berlin, Germany.

Take Away Notes:

- Plant biotechnology is more than genetically modified crops.
- Which strategies are available to make crop plants resistant to fungal pathogens?
- Apart from improving resistance to fungal diseases, can plant biotechnology improved food safety?
- Why are food products made from GM maize varieties resistant to pests (so called Bt-maize) healthier than products from non-GM maize?
- How can RNA interference help creating disease-resistant crops?

Plant biotechnology protecting crops against fungi and mycotoxins

Petr Karlovsky

University of Goettingen, Germany

Biotechnology provides indispensable tools for plant protection. Plant cell cultures, in vitro selection for resistance, embryo rescue, protoplast fusion, double haploids and other techniques have advanced resistance breeding long before genetic engineering became feasible in crop plants. Although these techniques are still being used, plant biotechnology is often understood as a synonym for the use of genetically engineered (GM) crops, which will be the focus of this presentation. Many strategies for genetic engineering of crops for resistance against pathogens exist but only few were developed to maturity. Production of enzymes digesting fungal cell walls in GM crops was historically the first strategy, inspired by natural defence of plants. Antimicrobial peptides followed with a ramification to peptides from sources that might frighten consumers (scorpions) and to non-enzymatic effects of enzymes (lysozyme). Fusion proteins consisting of antimicrobial peptides and pathogen-specific antibodies attracted considerable attention, promising to prevent Fusarium head blight in wheat.

Enzymatic detoxification of fungal virulence factors was coined in the 1980th in Japan, targeting fusaric acid. Although fusaric acid acts as a virulence factor in many diseases, in planta detoxification as a resistance strategy has yet to be demonstrated. Detoxification was however exploited successfully against pathogens producing oxalic acid and turned out to be one of the most efficient GM-based resistances available against fungi, entering patent portfolios of major breeding companies. The detoxification of mycotoxin deoxynivalenol was shown to protect grain crops from Fusarium infection. First fungal genes were used; the industrial development of GM wheat resistant to Fusarium failed due to a wrong choice of the gene. More recently genes of plant origin have been employed for the detoxification of deoxynivalenol.

Apart from rendering crops resistant to fungal infection, detoxification of fungal metabolites may improve food safety status of crops when the targeted compounds are mycotoxins. A detoxification strategy aiming at the reduction of exposure to mycotoxin fumonisin was developed by a major seed company to maturity but the GM varieties have not been commercialized, apparently because of concerns about the effect of negatively loaded keywords “GM” and “mycotoxin” on public perception. A surprising effect of a strategy targeting maize pests was discovered in Iowa and confirmed in many countries since: GM maize producing Bt protein, protecting the plant from pests, benefit from significantly reduced content of fumonisins and other mycotoxins.

The most recent strategy of genetic engineering of crops for resistance is transkingdom gene silencing by RNA interference. The efficiency is surprisingly high but there are concerns about the stability of the strategy because fungal mutants impaired in RNA interference are supposed to break the resistance fast. Finally, CRISPR/CAS equipped plant biotechnology with the capability to edit plant genomes in situ in a precise way, offering new options for the enhancement of plant native defence especially against biotrophic pathogens. While in Europe irrational fears and anti-GM lobbies essentially prevented applications of GM in plant production, plant biotechnology will continue advancing plant production in North America, Africa and on the Asian continent.

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DAY 2

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CONTENTS

Prediction of plant protein subcellular locations

Xiangjia Jack Min
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There are many thousands of proteins in a plant cell. The subcellular locations of proteins determine where the proteins play their biological roles. Prediction and curation of protein subcellular locations is essential for protein functional annotation. We evaluated a number of prediction tools and developed an accurate protocol for predicting protein subcellular locations in plants; and then using the protocol we constructed he Plant Secretome and Subcellular Proteome KnowledgeBase (PlantSecKB) for the plant research community to access and curate plant protein subcellular locations. The database is constructed with all the available plant protein data retrieved from the UniProtKB database and plant protein sequences predicted from EST data assembled by the PlantGDB project. The categories of subcellular locations include secretome, mitochondria, chloroplast, cytosol, cytoskeleton, endoplasmic reticulum, Golgi apparatus, lysosome, peroxisome, nucleus, vacuole, and plasma membrane. The data can be searched by using UniProt accession number or ID, GenBank GI or RefSeq accession number, gene name, and keywords. Species specific secretome and subcellular proteomes can be searched and downloaded into a FASTA file. BLAST is available to allow users to search the database based on protein sequences. Community curation for subcellular locations of plant proteins is also supported. This database aims to facilitate plant protein research and is available at http://bioinformatics.ysu.edu/secretomes/plant/index.php

Take Away Notes:

- The audience will learn how to predict the subcellular locations of their proteins.
- The audience will learn how to use the PlantSecKB database to search for their protein subcellular locations.
- The audience will be able to use the system to deposit the subcellular locations of their proteins into the database for public access.
- The database contains 1.4 millions of proteins with predicted subcellular locations and can be a good resource for research and teaching.

Biography

Dr. Min graduated with a Ph. D. degree at the University of Hawaii in 1995. He did the postdoctoral research at the University of British Columbia, Canada, and the Research Institute of Physics and Chemistry (RIKEN), Japan. He worked as a research associate at Concordia University, Canada. He currently works as a professor at Youngstown State University, USA. He has been working in the areas of plant physiology, plant genomics, and bioinformatics. He developed some well used software tools and databases including OrfPrdictor, FunSecKB, PlantSecKB, etc. He has published more than 50 research articles, and served as an editor for several scientific journals such as PlosONE.

ThaliaDB, a tool for data management and genetic diversity data exploration

Steinbach Delphine
Head of ABI-Soft software development group on ABI facility, INRA, France

Diversity and association genetics studies lead to manipulate a large number of individual, lines, clones and/or populations. Moreover, emergence of high-throughput technologies for both genotyping and phenotyping generates a large amount of data. These data need to be stored and managed in order to make requests and to organize datasets to be able to perform genetic diversity data exploration and association genetics analysis. *ThaliaDB*, V3.4, is developed for scientists to facilitate their data management and analysis. The database holds genetic resources data (germplasm/accessions), seed lots, samples, markers and genotyping and phenotyping datasets (fields environments, multiple traits under different conditions). It is well adapted for data useful to apply GWAS or genomic selection methods. It can manage high-throughput results coming from different projects and experiments and propose several views and options to explore these data and to give access to them for reuse. ThaliaDB has since July 2018, a new module to store results from population structure analysis and to represent them with a graphical charts. As new feature, it allows also representation of germplasms on a world map. The Web tool offers to users a Select (Data view) mode and an Admin (Data administration and loading) mode. Data confidentiality is maintained using user accounts and specific levels of rights can be set on data. It enables data extraction in CSV format. The version 3 is operational in our lab since 2017 with maize data that have been produced from projects of A. Charcosset's GQMS team and theirs partners, for 20 years. It contains today data from 23 projects, more than 3000 in bred lines, 1000 populations, 400 hybrids, 6000 seed lots, 48 genotyping experiments (dealing with more than 1 million of markers of recent technologies such as GBS) and phenotyping data coming from 32 experiments. The tool is in test in another lab for tomato and melon data. Perspectives are to test it on wheat and poplar data. ThaliaDB is developed in Python under Framework Django, running under PostGreSQL and MongoDb databases management system. Interoperability is done with external information system such as INRA URGI GnpIS plant information system (D. Steinbach NAR Databases Journal 2013, doi: 10.1093/database/bat058) and GnpIS-GnpAsso tool, through germplasms DOI identifiers. The management of traits ontologies (CropOntology) to improve data quality is currently in development in 3.5 version. The software development project is leaded by ABI-SOFT group (D.Steinbach et al) in collaboration with GQMS team, at INRA GQE-Le Moulon and rgets funds from Amazing, French Investment for the future project and INRA for permanent positions. A paper is in preparation for 2019.

Take Away Notes:

- The talk will illustrate how data produced by a research team or facilities, can be managed for long term use and reuse.
- It will present an example of data produced at large scale, such as genotyping data and how the tool is able to manage the different categories of genotyping technologies (Arrays, GBS).
- It will present a software based on the framework Django and python language, that is simple to learn for young bio-informaticians and a web software that is easy to use for scientists to fill it with data in autonomy and to query it..
- For research purpose, it will show how this tool can be useful either i) to make dashboards and inventories of data, or ii) to store different experiments coming from several technologies and different levels of data (raw and elaborated data) and how iii) to extract data useful for analysis software and for new experimental designs.
- To conclude, it will present a use case for plant breeding and diversity analysis, based on maize data, that allows to combine results coming from genotyping and phenotyping experiments, to help to find in plant germplasm collections, alleles, markers for traits of agronomical interest, to face for example, to challenges such as climatic changes.

Biography

Mrs Delphine Steinbach, studied Biology, Plant Physiology and Computer Science at the Nancy Sciences University, in France. She graduated as software engineer in 1992 (master 2 degree) with a double skill in Physiology. She worked at Genethon, to help scientists to find genes involved in complex genetics disease. She joined the team of J. Weissenbach, contributed to the first genetic map of the Human Genome, Nature 2006 and moved to Genoscope, the national sequencing center. In 2000, she joined INRA, the national institute for agronomical research and was the vice director of URGI research unit, leading its bioinformatics facility. Since 2015, she leads the ABI-SOFT INRA group at Genetique Quantitative and Evolution – The Moulon, on the campus of University Paris-Saclay.

Root morphology, productivity, and photosynthesis of aeroponically grown ice plants (*Mesembryanthemum crystallinum*) with different nutrient spraying intervals

HE Jie*, Ph.D., Chua Ee Lyn, Qin Lin, Ph.D.
National Institute of Education, Nanyang Technological University, Singapore

Mesembryanthemum crystallinum (common name: ice plant) is a succulent plant native to South Africa. It has high nutritional values and has been successfully grown in the greenhouse in Japan and Taiwan under cooling temperature. Recently we have also grown this plant successfully in a tropical greenhouse by cooling the root-zone only or indoor at cooling temperature under different combinations of LED-lighting. Our results also showed that this facultative CAM (crassulacean acid metabolism) plant performed C_3 photosynthesis when supplied with adequate water. Although it is drought- and salt-tolerant species, there is very little work done on the effects of water and nutrient *supply* on this vegetable crop. This project aimed to investigate the impacts of nutrient spraying intervals on root morphology, productivity and photosynthesis. In this project, all seedlings were grown for 4 weeks in small trays before transferring to aeroponic systems with different nutrient spraying intervals. In terms of root morphology and productivity, the longer nutrient spraying intervals such as 30, 60 and 240 min resulted in reductions of total root length, total root surface area and total number of root tips, and smaller mass of root and shoot compared to a shorter interval of 5 min. Decline in photosynthetic light use efficiency measured by chlorophyll fluorescence parameters demonstrated that plants grown under longer nutrient spraying intervals utilized lesser light energy and did not dissipate heat as effectively as those spayed with nutrient solution for 5 min interval. Photosynthetic CO_2 assimilation rate (A_{sat}), stomatal conductance and internal CO_2 concentration were significantly reduced for plants grown under 240 min nutrient spraying interval, indicating signs of drought stress. All other plants had similar values of saturated photosynthetic O_2 evolution rate (P_{max}), A_{sat}, total reduced nitrogen and Rubisco concentrations. However, higher total chlorophyll concentration in plants grown under 240 min nutrient spraying interval imply that chlorophyll could be a mean of storing nitrogen.

Take away notes:

- All vegetable crops including temperate vegetables such as ice plant could be grown in the tropics through manipulation of growth conditions, especially the rhizosphere conditions.
- Ice plant is a facultative CAM plant that performs C_3 photosynthesis when supplied with adequate water.
- Drought stress induced from the longest nutrient spraying interval of 240 min did not switch the photosynthetic mode from C_3 to CAM. However, drought stress resulted in the inhibition of root growth and development, the decline of photosynthetic light use efficiency and the reduction of productivity.
- The findings of this project enhance the understanding of ice plant physiology under different nutrient spraying intervals.
- The findings of this project will help the growers to enhance productivity of ice plants at low production cost through water and nutrient management.

Biography:

Dr. He Jie obtained her PhD from Macquarie University, Australia in 1991. She is currently an Associate Professor at Nanyang Technological University, Singapore. She has more than 30 years of research experience in plant physiology. She has been actively involved in the research on responses of plants to environmental stresses (temperature, drought, light, UVB radiation). Her research interests are 1) photosynthesis (chlorophyll fluorescence, Rubisco protein); 2) shoot-root communication (C partitioning, nutrient uptake and N metabolism; 3) effects of root-zone temperature on aeroponically grown temperate crops in the tropics; 4) impacts of LED quality and quantity on photosynthesis and vegetable production.

CONTENTS

Inheritance of rootstock effects in fruit trees

Andrés J. Cortés*[1], Valeria Velázquez[1], Laura Patiño[1], Oscar Delgado[1], Alejandro Navas[1] Cipriano Díaz[1], Laura Muñoz[2] Paula Reyes[3]

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Mosquera, Mosquera, Colombia

A fruit tree breeding program requires heritable variation at both, the rootstock and the scion level, upon which selection can act. Avocado trees (*Persea americana*) originated in the neotropics and do not exhibit the characteristic genetic bottleneck of many other crops. The incipiency in this domestication has prevented the selection of desirable traits, particularly at the rootstock level. Therefore, our goal was to quantify the inheritance of rootstock effects in scion traits in avocado cv. Hass. We characterized 349 rootstocks from 8 avocado cv. Hass plantations in three regions in the province of Antioquia, in the northwest Andes of Colombia, using 13 microsatellite markers (SSRs). Parallel to this, 21 phenotypic traits (including yield, fruit quality, and morphological and eco-physiological traits) were recorded in the scions during 3 years (2015-2017). Relatedness among rootstocks was inferred through the genetic markers and inputted in an animal-model in order to calculate narrow-sense heritabilities (h2) on scion traits. Heritability estimates were

Significant for 5 of the measured traits and ranged from 0.58 to 0.74 with model fits (R2) ranging from 0.52 to 0.85 across plantations. The results showed significance in the rootstock effects for various quality and ripening traits (i.e. total number of fruits, number of fruits with low weight, number of fruit damaged by trips, and number of fruits with exportation quality), while for morphological traits the only one we found having a significant heritability value was trunk height. These findings suggest the inheritance of rootstock effects on a surprisingly wide spectrum of scion traits in avocado. Furthermore, this research is, up to date, the most cohesive evidence of inheritance of rootstock effects in any fruit tree. Ultimately, this work reinforces the importance of considering the rootstock-scion interaction to enhance our understanding of the consequences of grafting and speed up fruit tree breeding programs.

Physiology and productivity of temperate vegetable crops exposed to sub-lethal heat stress

Lai Cheng-Hsiang*, He Jie
National Institute of Education, Singapore

Commercial cultivars Arugula *Eruca sativa* and lettuce *Lactuca sativa* (Canasta) were grown in aeroponics systems in tropical Singapore with root zone temperature (RZT) kept constantly chilled at 25°C. At 30 days after transplantation (DAT) leaf discs excised from the plants were subjected to heat stress from 26, 30, 34, 38, 42 and 46°C for 1 hour and the magnitude of heat shock protein synthesis was recorded. Based on the heat shock protein kinetic profile a sub-lethal heat shock regime was designed at 38°C. While control plants were kept at RZT 25°C, treatment plants were initially kept at 25°C RZT from transplantation till 10 DAT, and subsequently subjected to a daily 38°C RZT from 1000 hrs to 1600 hrs to simulate a noon-time heating without chiller effect from 11 DAT to 22 DAT. Root scan analysis was performed every 3 days to examine if the sub-lethal heat shock would affect root growth and morphology. From 21 to 30 DAT the plants were divided into four groups: (i) CC: plants were kept constantly at 25°C RZT from transplanting to harvest; (ii) CH: plants kept in 25°C RZT from 0 to 22 DAT and then subjected to a daily heat stress of 45°C of 6 hours (1000 hrs to 1600 hrs) from 23 to 32 DAT; (iii) HC: plants subjected to 38°C RZT sub-lethal heat shock from 11 to 22 DAT and kept in 25°C RZT from 23 to 32 DAT and (iv) HH: plants subjected to 38°C RZT sub-lethal heat shock 11 to 22 DAT and then subjected to a daily heat stress of 45°C of 6 hours (1000 hrs ~ 1600 hrs) from 23 to 32 DAT. Plants were harvested 33 DAT and examined for their productivity, maximal photosynthetic oxygen evolution (P_{max}), chlorophyll fluorescence F_v/F_m ratio and other chlorophyll fluorescence parameters, total reduced nitrogen (TRN) and total sugar content. CH plants initially shows a significantly lower F_v/F_m ratio compared to the other treatment groups (26 DAT), but by 32 DAT there was no significant difference in the four treatment groups. CH treatment group for both vegetables were also significantly lowest for shoot fresh weight, P_{max} and insoluble sugar. Conversely, Arugula HC and CH plants had the lowest soluble sugar and TRN respectively while there were no significant differences between the four treatment groups for Canasta for TRN and soluble sugar. Preliminary results of this study suggests that as long as root zone chilling is applied during the root formative period (0 DAT to 11 DAT) temperature is not a very important environmental stressor for later growth of these temperate vegetables as long as water in the form of nutrient solution is constantly available. A sub-lethal heat shock would also improve crop productivity to approach that of plants constantly kept at chilled RZT despite application of high heat stress (46°C for 6 hours daily).

Take away notes:

- Dosage response of the vegetables to heat stress and optimal thermal window is elucidated.
- Findings of this research could be directly applied in aeroponics practices especially in the tropical regions.
- Energy consumption in aeroponics systems could be reduced by 30~50% with this finding.
- Lethal thermal limit of studied vegetables established.

Biography:

Lai Cheng Hsiang is currently a PhD student with the National Institute of Education, Singapore looking at thermal windows and heat responses of temperate vegetables grown in tropical aeroponics systems. Part of his work involves examining the possibility of thermotolerance conferment via priming events like subjecting vegetable crops to sub-lethal heat shocks and the designing of stress indices of temperate vegetables to heat stress. Previously he was working with marine intertidal organisms on their physiological thermal limits and stress responses to abiotic environmental stressors like temperature and pollution. He has also worked on anti-malaria drug screening from secondary metabolites of gorgonians in Singapore waters.

Cytokinins for immunity; inside and beyond plants

Muhammad Naseem [1, 2]
[1]College of Natural and Health Sciences, Department of Life & Environmental Sciences, Zayed University Abu Dhabi
[2]Department of Bioinformatics, Biozentrum University of Wuerzburg Germany

Cytokinins are small molecule plant hormones that control every aspect of plant growth and development. Their function in mediating plant susceptibility to plant pathogens is well known. We studied the contrary and found that the interaction between cytokinins and salicylic acid pathways promote plant resistance to pathogen infection. We explored ways in which cytokinin signaling could crosstalk with plant immune networks. Some of these networks are modulated by pathogens to propagate disease, whereas others help the host to mitigate an infection. Besides plants, cytokinins are also shown to be involved in animal/human microbial pathogenesis. I would like to highlight these interesting developments in the field of plant cytokinin biology.

Biography

Dr. Muhammad Naseem has been working as Assistant Professor at the College of Natural and Health Sciences Zayed University Abu Dhabi since January 2018. Prior to Zayed University Abu Dhabi Dr. Naseem was working as Assistant Professor at Bogacizi University Istanbul as well as a Fellow Research Scientist at the Department of Bioinformatics, University of Wuerzburg. He completed his PhD in 2009 from the University of Wuerzburg Germany on the role of a small-molecule hormone cytokinin in plant response to biotic stresses. To further study the extensive crosstalk of cytokinin signaling to plant hormone networks, he then joined the group of functional genomics and systems biology of the University of Wuerzburg as a Research Scientist. During his doctoral and postdoctoral stay, he got training opportunities at the International Center of Genetics Engineering and Biotechnology, Trieste and EBI-EMBL Cambridge. He produced a string of publications as principal/corresponding author in high-ranking research journals on the role of cytokinins plant immunity. His research interests involve the accomplishment of Arabidopsis Immune Signaling Network model encompassing factors of the host as well as pathogens, the analysis of large-cellular-interactomes as well as the reconstruction of Genome Scale Metabolic networks to dissect the adaptation mechanisms in plants against environmental stresses. Moreover, he is also interested in investigating cross-kingdom organismal communication mediated by cytokinins.

Impact of wild boar rooting on a soil seed bank of oak-linden-hornbeam forest in the Białowieża Forest

Izabela Sondej
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The wild boar is an omnivorous animal, and by foraging (rooting) disturbs the top soil layer. In some regions of Poland and Europe seasonal fluctuations in rooting have been observed. Wild boars not only eat plants, but also strongly modify their habitat. In Białowieża Forest wild boar most frequently visit oak-hornbeam forests growing on fertile soil. On sites where the forest floor is covered with dense vegetation germination of seeds is difficult, and wild boar rooting can promote the removal of diaspores from deeper layers of the soil seed bank. The aim of this study was to assess the impact of wild boar rooting on the soil seed bank in a natural oak-linden-hornbeam forest. Observations were carried out on permanent plots (100 squares of 8 m x 8 m) in the strictly protected zone of Białowieża National Park (Białowieża Forest). The Białowieża Forest (62 219 ha) is the best preserved forest ecosystem within the temperate zone in Europe, and widely regarded as a model forest, related to observations and research into pristine deciduous and mixed forests. Samples of the soil seed bank were taken from plots which showed varying intensities of wild boar rooting (frequency and average percentage of exposed ground surface). Areas to be sampled were selected on the basis of archival data. Squares were divided into: low (series A), medium (series B) and highly rooted (series C). The series of squares significantly ($P<0,001$) differed in their intensity of rooting. Research was conducted by the seedling emergence method during two vegetation seasons. Altogether, 7985 seedlings (of 67 taxa) germinated from 240 soil samples. The highest number of germinated seedlings and species were found in the highly rooted squared. In all the series dominant species was Urtica dioica. In the soil seed bank 19 species of anemochory germinated, and accounted for 27.5% of all species present in the seed bank of all series. Permanent wild boar rooting increased the species richness in the soil seed bank and increased the amount of species with higher light requirements.

Biography

Dr. Izabela Sondej graduated with a Ph.D. degree at the University of Szczecin in 2015. She is assistant professor in the Forest Research Institute in Poland. Her experience and achievements include: forest ecology, plant-animals interactions, biology and ecology of wood ant, ecology of forest soil seed bank.

CONTENTS

Effect of Boron fertilizer on sunflower seed yield and oil production

P. K. Basavaraja*[1], H. Mohamed Saqeebulla[1], G.V. Gangamrutha[1] and P.Dey.[2]

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Boron concentrations of dicotyledonous plants are several orders of magnitude higher than those of monocotyledonous plants. A study was taken to investigate the effect of different levels of boron application contributing to sunflower yield and oil production. This experiment was conducted during 2016-17 at ZARS, University of Agricultural Sciences, GKVK, and Bengaluru by taking sunflower as test crop in *Alfisol*. Experiment was designed as randomized complete block replicated thrice with five levels of B (2, 4, 8, 12 and 16 kg B ha^{-1}) including control andonly NPK treatments, where boron was applied as borax (Na2B4O7.10H2O) to soil at the time of sowing with required NPK+FYM.The data showed that the highest seed yield (32.89 q ha^{-1}) and dry matter yield (20.77 q ha^{-1}) were observed where 2 kg B ha^{-1}was applied and it significantly reduced with increase in B application rate. The yield reduction was to the tune of 5 to 60 per cent from 4 kg B to 16 kg B ha^{-1}. Boron toxicity was seen at 4 and 16 kg B ha^{-1} application in the sunflower plant, and the toxic effect of B was more pronounced at 16 kg B ha^{-1}. The B toxicity might be due to direct effect of B on pollen viability, fertility and seed set which increases with increase in B concentration in plant. The seed B concentration increased with the increase in B application which ranged from 21.17 per cent (T_3: 2 kg B ha^{-1}) to 27.00 per cent (T_7: 16 kg B ha^{-1}). However, the total uptake was higher in T_2(1444.08 mg kg^{-1}) and it significantly decreased in T_7 (941.93 mg kg^{-1}) as the B concentration increased to 16 kg B ha^{-1}. Higher B application (16 kg B ha^{-1}) resulted in toxic effect, where many cellular activities were partially inhibited, roots which could prohibit the nutrient uptake and plant growth which in turn lower plant growth and yield reduction of sunflower crop. Application of B had significant effect on the seed potassium content, dry matter N and P content. Major nutrients in post-harvest soil did not differ significantly, however B content linearly increased from 0.94 to 3.06 mg kg^{-1}. The oil content and oil yield of sunflower was significantly affected by B. The higher oil content (42.06 %) was observed in 2 kg B ha^{-1} applied plot and lowest was observed in 16 kg B ha^{-1} (23.41 %) applied plot. The oil yield has decreased to the tune of 78 per cent with addition of 16 kg B ha^{-1} to soil. The higher oil content might be due to higher N uptake by seed and decreased as a result of less N uptake. Application of 2 kg B ha^{-1} significantly increased the grain yield and nutrients in sunflower which in turn directly effect on growth and yield of sunflower. As the B application rate increases the relative B toxicity affected on the dry matter, seed yield and oil production by sunflower crop.

Take away notes:

- Through my presentation, audience will understand how the higher doses of boron will affect the crop growth and production, and also know the optimal dose of boron nutrient. Audience will also understand the concentration of boron in sunflower crop without any toxicity symptoms even at higher doses of boron, except reduction in growth and yield. This will be helpful to adopt it in their field or experimental stations for better crop productivity and precautions will be taken to avoid unnecessary application of higher doses of boron nutrient.

Biography:

Dr. P. K. Basavaraja, completed his MSc (Agri) at University of Agricultural sciences, Bangalore, Karnataka and PhD at Forest Research Institute, Dehradun, India, is presently working as Professor & Scheme Head, AICRP on STCR, UAS, and Bangalore. Since thirty years he is working on Soil Fertility, Micronutrients, Salt affected soils, Organic residue management, Watershed management, Soil test crop response studies. He operated thirteen research projects and guided /guiding Five PhD and Ten MSc (Agri) students and Ninety students as Co-guide. He published more than 200 publications including 53 peer reviewed research papers, bulletins, abstracts, book chapters. Officially he visited Crete, Greece, Wageningen, Netherland, and Dubai and presented four research papers in international conferences.

CONTENTS

Molecular characterization of 3-Hydroxy-3-methylglutaryl-CoA reductase (HMGR) multigene family in legume crop *Cicer arietinum*

Renu Kumari*[1] **Gitanjali Yadav**[2]
[1]National Institute of Plant Genome Research (NIPGR), New Delhi, India
[2]Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge, UK

Isoprenoids, the largest and most varied class of plant secondary metabolites, are synthesized either via mevalonic acid pathway (MVA) or the methyl erythritol pathway (MEP) to help the plants to avoid or adapt to unfavorable environmental conditions. The 3-hydroxy-3-methylglutaryl-CoA reductase (HMGR) (EC 1.1.1.34) is the most significant enzyme of the MVA pathway and occurs in plants as a multi-genic family.

Due to its essential role in providing the defense to the plant by producing isoprenoids, the identification and differential expression of three isoforms of HMGR gene (*HMGR1*, *HMGR2* and *HMGR3*) in different tissues of the chickpea (*Cicer arietinum*) legume plant is carried out under different abiotic stress conditions. Out of three isoform, *HMGR1* gene is having constitutive expression and not induced by the stress but the *HMGR2* and *HMGR3* isoforms are highly induced during abiotic stress. So, it suggests that *HMGR1* is having housekeeping function. Besides this, they have variation in their sub cellular localization also. Housekeeping isoform (*HMGR1*) is endomembranous and it is distributed like spherical bodies along the membrane while the other two isoforms (*HMGR2* and *HMGR3*) share the same localization pattern along with nuclear localization. The promoter activity of all the isoforms reveals that they are highly active during reproductive stage of plant development as they have high GUS expression in anthers. The stress induced isoforms have some activity during vegetative growth also. Similarly, phylogenetic analysis also shows that all the stress induced isoforms make separate clades in comparison with housekeeping gene.

So, the outcome of the study will help in elucidating the role and regulation of different isoforms of the *HMGR* gene in the legume plant and provide the new insight for isoprenoid dependent plant response during abiotic or biotic stress condition.

Take away notes:

- It offers an opportunity to study suitable system to understand stress responses in cold season food legume crops through a combination of bioinformatics and molecular biology techniques.
- It will help in crop improvement by altering the plant metabolism.
- Helps in understanding molecular signatures that may regulate isoform activity under abiotic stress.
- Provide information to make changes in the plant system for increased production of volatile compounds.

Biography:

Dr. Renu Kumari studied M.Sc. in Biotechnology at the Jiwaji University, India in 2007. After her post-graduation, she joined the group of Prof. Sushil Kumar at the National Institute of Plant Genome Research, New Delhi, India for pursuing her Ph.D. in Biotechnology. She received her doctorate degree in 2013. She then joined the laboratory of Dr. Gitanjali Yadav, NIPGR, India for working as research associate. She has published more than 15 research articles in reputed journals.

Cryotherapy: Cryogenic technology for virus elimination from infected plants

Ergun Kaya*, **Selin Galatali, Onur Celik, Sevinc Guldag**
Molecular Biology and Genetics Department, Faculty of Science, Mugla Sitki Kocman University, Mugla, Turkey

Plant viruses are the most harmful pathogens causing the most economically damages and harmful product loses in many plant species. Because of xylem and phloem vessels absence, plant meristem tissues used for meristem cultures are virus-free, but sometimes only meristem cultures are not sufficient for virus elimination. Cryotherapy, a new method based on cryogenic techniques, is used for virus elimination. In this technique, 0.1-0.3mm meristems are excised from organized shoot apex of a selected in vitro donor plant and this meristems are frozen in liquid nitrogen (-196 °C) using suitable criyogenic technique. Cryogenic treatments including physical and chemical dehydration process successfully eliminates plant viruses from infected shoot tips with high frequency. Sanitized shoot tips regenerate plantlets that maintained their virus-free status over time and are micropropagated for successful transfer to the field. In this presentation we aimed to determine cryogenic technologies for virus elimination, compare all cryogenic techniques (vitrification, encapsulation-vitrification, droplet vitrification, two step freezing, dehydration, encapsulation-dehydaration) being the best for different kind of plant species (monocotyledone, dicotylodone, woody, herbaceous etc.) and also indicate critical points (meristem size, explant type, regeneration medium, application of procedures, other culture conditions etc.) effecting regeneration, viability of meristems after cryogenic tratments.

Take Away Notes:

- Current presentation will be informative about biotechnological approaches of pathogen elimination from infected plants for the audience.
- The audience will learn different cryogenic techniques and they can compare which application is the best for viability and regeneration after cryotherapy.
- This presentation will provide a practical solution, especially plant biotechnologists and agronomists suffering from plant pathogens can find different and effective solutions in this presentations.

Biography

Assoc. Prof. Dr. Ergun KAYA studied Plant Biotechnology at Mugla Sitki Kocman University, Turkey and graduated as PhD in 2011, Gebze Technical University, Turkey. He then went to USDA-ARS, Co, USA for Post-Doc. research. After one-year postdoctoral fellowship supervised by Dr. Dave ELLIS at the National Center for Genetic Resources Preservation, Fort Collins, Co, he obtained the position of an Assist. Prof. Dr. at the Muğla Sitki Kocman University, Turkey. He has published 17 research articles in SCI(E) journals.

Hormone signaling and alternative splicing in Moso bamboo shoot growth

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International Centre for Bamboo and Rattan, Beijing, P.R.China

Moso bamboo is a large, woody bamboo with the highest ecological, economic and culturalvalue of all the bamboo types and accounts for up to 70% of the total area of bamboo grown. However, the spatiotemporal variation role of moso bamboo shoot during growth period is still unclear. We found that the bamboo shoot growth can be divided into three distinct periods, including winter growth, early growth and late growth based on gene expression and anatomy.

In the early growth period, lateral buds germinated from the top of the bamboo joint in the shoot tip. Intercalary meristems grew vigorously during the winter growth period and early growth period, but in the late growth period, mitosis in the intercalary meristems decreased. The expression of cell cycle-associated genes and the quantity of differentially expressed genes were higher in early growth than those in late growth, appearing to be influenced by hormonal concentrations. Gene expression analysis indicates that hormone signalling genes play key roles in shoot growth, while auxin signalling genes play a central role. In situ hybridization analyses illustrate how auxin signalling genes regulate apical dominance, meristem maintenance and lateral bud development. Our study provides a vivid picture of the dynamic changes in anatomy and gene expression during shoot growth in moso bamboo, and how hormone signalling-associated genes participate in moso bamboo shoot growth.

Alternative splicing (AS) is a key regulatory mechanism associated with proteome and transcriptome diversity. However, the prevalence of AS in the moso bamboo genome is still unclear. Transcriptome sequencing of four different tissues indicated that 36.17% of the genes in the moso bamboo genome undergo AS. The predominant type of AS found in moso bamboo was intron retention (38.70%), followed by alternative 5' (31.86%) and 3' (16.68%) splice sites and exon skipping (11.46%). The number of AS events in every gene was relevant to gene characteristics and gene expression. We also observed that the alternative 5' and 3' splice sites were significantly enriched in the fourth nucleotide downstream or upstream of the dominant splice sites. Furthermore, the frequency of AS types as well as the quantity of AS events significantly varied among different tissues. The findings of the present study provide a comprehensive view of AS events in moso bamboo.

Take Away Notes:

- By the transcriptome analysis to explore the main regulation factors on bamboo shoot fast growth.
- Be helpful to learn alternative splicing in genomic level for the audience in their job.
- This presentation will provide a practical solution to a problem that could simplify farm's job more efficient. It will provide new information to insight in a bamboo growth and development.

Biography

Prof. Dr. Jian Gao studied Forestry in Nanjing Forestry University, graduated as MS in 1993. She then joined the Department of Forestry in Anhui Agricultural University. She received her PhD degree in 2000 in China Academy of Forestry. After one year postdoctoral fellowship supervised by Prof. Dr. Andrea Polle at the Institute of Forest Botany, Gottingen University, Germany. She obtained the position of Professor at the ICBR. She has published more than 40 research articles in SCI(E) journals.

Researches on the radiation induced non-targeted effects in *Arabidopsis thaliana*

Ting Wang*, Wei Xu, Chenguang Deng, Po Bian
Key Laboratory of High Magnetic Field and Ion Beam Physical Biology, Hefei Institutes of Physical Science, Chinese Academy of Sciences, Hefei, Anhui, China

Radiation induced non-targeted effects, which include bystander effects and adaptive effects, have been extensively studied using cell system, multicellular tissues in vitro as well as whole organism in vivo, our aims were to investigate the radiation induced non-targeted effects in plant in vivo, Firstly, using root-localized irradiation, we investigated radiation-induced bystander effects in aerial parts of A. thaliana plants from developmental, genetic and epigenetic aspects by targeting the distal primary roots of seedlings with alpha particles. Then the bystander signaling pathways were studied and results suggested the involvement of the JA signal pathway in the RIBE of plants, the JA signal pathway was shown to participate in both the generation of bystander signals in irradiated root cells and radiation responses in the bystander aerial parts of plants. And we also demonstrated the time course of long distance signaling in radiation-induced bystander effects. Secondly, radiation induced adaptive response was further investigated, we established an experimental method for detecting the effects of gamma-irradiation on the primary root growth of Arabidopsis thaliana, in which adaptive response of root growth was significantly induced by several dose combinations. Lastly, the interaction between adaptive response and radiation-induced bystander effect were studied, the X-ray-localized irradiation of the aerial parts of seedlings (5Gy) initiated obvious adaptive response of root tip cells, exhibiting attenuation of root growth inhibition and cell cycle arrest, reduced level of DNA strand breaks, and promoted repair efficiency of the homologous recombination (HR) and non-homologous end jointing (NHEJ) after the whole seedlings were exposed to 100 Gy of challenging radiation (γ-rays), which suggested the bystander effects mediating the adaptive response in plant.

Take Away Notes:

- Radiation induced non-targeted effects have been well demonstrated in Arabidopsis thaliana.
- Plant is an ideal model for addressing many radiation responses.
- Our studies provided some experimental methods for studying the different response under stress condition.

Biography

Dr. Ting Wang studied biophysics in the research group of Prof. Po Bian at the Hefei institutes of Physical Science, Chinese Academy of Sciences, and received her PhD degree in 2014, then she worked as an associate professor at the same institute, her main research interests are radiation induced non-targeted effects in plant, and she has published over 10 research articles in SCI journals.

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DAY 2

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Arabidopsis SRFR1 dampens defenses against herbivory by *Spodoptera exigua* and parasitism by *Heterodera schachtii*

Phuong Dung T. Nguyen*[1,2,4], Sharon Pike[1,2], Jianying Wang[1,2], Arati Nepal Poudel[1,3], Robert Heinz[1,2], Jack Schultz[1,2], Abraham Koo[3], Melissa Mitchum[1,2], Heidi Appel[1,2] and Walter Gassmann[1,2]

[1]Division of Plant Sciences and Interdisciplinary Plant Group, University of Missouri, Columbia, MO, USA

[2]Christopher S. Bond Life Sciences Center, University of Missouri, Columbia, MO, USA

[3]Department of Biochemistry and Interdisciplinary Plant Group, University of Missouri, Columbia, MO, USA

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Plants are constantly exposed to a variety of pathogenic microbes and pests. Thus, plants have developed diverse mechanisms to fine-tune defense responses to different types of enemies. Cross-regulation between these signaling pathways may allow the plant to prioritize one response over the other. Then, what is the connection between biotrophic microbe- and herbivorous insect–triggered resistance signaling pathways that converge on one gene? In previous work, we identified SUPPRESSOR OF rps4-RLD 1 (SRFR1), as a negative regulator of effector triggered immunity against the bacterial pathogen Pseudomonas syringae pv. Tomato. In the Arabidopsis accession RLD, the recessive srfr1 mutation confers ENHANCED DISEASE SUSCEPTIBILITY1 (EDS1)-dependent resistance to DC3000 (avrRps4) in leaves. Here we examined whether SRFR1 also regulates resistance to a herbivorous insect in leaves and to a cyst nematode in roots. Surprisingly, srfr1-1 plants showed increased resistance to herbivory by the beet army worm Spodoptera exigua and to parasitism by the cyst nematode Heterodera schachtii compared to RLD. Using quantitative real time PCR (qRT-PCR) to measure the transcript levels of SA- and jasmonate/ethylene (JA/ET) pathway genes, we found that enhanced resistance of srfr1-1 plants to S. exigua correlated with specific upregulation of the MYC2-branch of the JA-pathway concurrent with suppression of the SA-pathway. In contrast, the greater susceptibility of RLD is accompanied by simultaneously increased transcript levels of SA-, JA-, and JA/ET-signaling pathway genes. This finding suggests a novel form of resistance in Arabidopsis to the biotrophic pathogen H. schachtii or a root-specific regulation of the SA pathway by EDS1, and places SRFR1 at an intersection between multiple defense pathways.

Seed shattering of *Bromus hordeaceus* L. during the growing season of winter wheat

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Bromus hordeaceus ssp. *hordeaceus* L. is native to Eurasia, where it is most common in the Mediterranean region. It has naturalized in all other continents except Antarctica. It is annual or biennial. The culms are erect or rarely ascending from a decumbent base and can become up to 100 cm high. In Scandinavia, it germinates in the autumn and can be a problematic weed in winter cereals and a severe problem in seed production of ryegrass (*Lolium perenne* L.) because cleansing the seeds of *B. hordeaceus* from *L. perenne* is very difficult. *B. hordeaceus* seeds only survive one year in the soil, and therefore the plant is especially a problem where reduced tillage is practiced or in the headland of the field if ploughing and seedbed preparation had not been done correctly.

In 2018, we investigated the seed production of randomly selected *B. hordeaceus* plants in a winter wheat field. When the plants started to flower, we placed an open cage around the plants to collect all seeds produced during the growing season. Every week the seeds were collected from the cages with a vacuum cleaner and subsequently counted. Just before the wheat field was harvested, we harvested the *B. hordeaceus* plants and counted the remaining seeds on the plants. The purpose was to estimate how large a fraction of the total seed production we potentially would be able to harvest with a combine harvest. We found that on average a single plant produced 849 seeds during the growing season of which in average 41 % were left on the plant at crop harvest time. Consequently, it makes sense to collect the seeds with the combine harvester and remove the seeds with chaff from the field to reduce weed infestation in the coming growing season.

Take Away Notes:

- The audience will get new knowledge about the biology of a cosmopolitan weed species.
- The period of seed shattering of weed plants is an uninvestigated area which needs to be addressed to develop new and better integrated weed management strategies.
- The presentation provides a practical solution which can contribute to reduce a serious weed problem in autumn sown crops.

Biography

Associate Professor Dr Christian Andreasen is Research Group Leader of the Plant Protection Unit at the University of Copenhagen. He got his PhD in 1990 in Weed Science from the Royal Veterinary and Agricultural University (now University of Copenhagen). Since then, he has worked at the same department as a research assistant, Post Doc, Assistant Professor, Associate professor and was in 12 years Head of Crop Sciences. He has published more than 50 per reviewed publications in international scientific journals.

Destroying weed seeds with exhaust gas from a combine harvester

Zahra Bitarafan*[1], Christoph Glasner[2], Johanna Fenselau[2], Christian Andreasen[1]
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Weeds are significant constraints getting high yields of crop plants on arable land. We investigated if exhaust gas from a combine harvester could be used to kill or harm weed seeds. *Centaurea cyanus* L. was chosen as a model plant because it has a high germination percentage and large seeds which a not very sensitive to heat. Combine harvesters cut and thresh both crops and weeds. Chaff containing harvested weed seeds is separated from the crop grains and straw during the threshing and cleaning process in the combine harvester. Afterwards, weed seeds and chaff can be exposed to hot exhaust gas before they are returned to the field to avoid that harvested viable weed seeds are added to the soil seed bank and become a problem in future growing seasons.

In 2017, chaff samples containing 100 weed seeds of *C. cyanus* were treated with exhaust gas with a temperature of around 100 and 150°C for 1, 2, 5, and 10 seconds. Each treatment was replicated four times. Afterwards chaff samples were spread evenly on the soil surfaces in 52 × 26 cm trays and covered by a thin layer of soil/sand. Untreated chaff samples containing weed seeds were used as controls. The boxes were placed in a greenhouse and watered from the bottom. *C. cyanus* treated with exhaust gas at 100°C for 1, 2, 5 and 10 seconds reduced the germination percentage by 15.9, 31.5, 46.6, and 53.3 %, respectively, and seeds treated with exhaust gas at 150°C for 1, 2, 5, and 10 seconds reduced the germination percentage by 4.34, 25.7, 73.9, and 98.8 %, respectively. Consequently, we find that using exhaust gas from a combine harvester could be a valuable new tool in an integrated weed control strategy to reduce weed infestation on arable land.

Take Away Notes:

- The audience will get knowledge about a new approach to reduce weed infestation on arable land.
- This research should stimulate other researchers and companies to develop the method further and think of new ways to make integrated weed management and minimize herbicide use.
- This work shows a new practical solution which can contribute to solving a big problem in agriculture.

Biography

Dr Zahra Bitarafan received her PhD in 2018 from the Shahrood University of Technology, Iran. Since 2017, she has been working as Assistant Researcher on the project: SWEEDHART - Separation of weeds during harvesting and hygienisation to enhance biomass production in the long term. The activity was conducted under the "Joint European research projects in the field of Sustainable and Resilient Agriculture" under ERA-NET Cofund FACCE SURPLUS 2015. She has already published 24 journal papers and 4 international conference papers.

Endophytic bacteria *Bacillus subtilis* and salicylic acid: Biotic strategy to control postharvest diseases of *Solanum tuberosum* L.

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Potato (*Solanum tuberosum* L.) is a valuable food crop with great importance in ensuring food security worldwide. One of the most acute problems of modern agriculture and food industry is the loss of potato tubers (about 40-60% of the total harvest) during storage from diseases. Recently, beneficial bacteria Bacillus subtilis (with the well-known role in plant growth promotion and anti-stress physiological programs induction) generally recognized as safe microorganism to use in the food industry are considered for application as bio-active and eco-friendly agent for controlling postharvest decays. Of special interests are endophytic B. subtilis, living inside plant tissues, which allows them to be less dependent on external environmental factors (compared to rhizosphere and phyllosphere strains) while exhibiting "useful" features. Due to it is difficult to select an individual effective microbial strain with a broad spectrum of activity against range of pathogens an interest is co-application of B. subtilis with other methods (biological, physical) in an integrated vision of disease management. In this work we investigated the effect of endophytic B. subtilis (strains 10-4, 26D) in range of concentrations (103-108 CFU/mL) and its compositions with signalling molecule salicylic acid (SA) on potato tubers' resistance to *Phytophthora infestans* and *Fusarium oxysporum* during storage. The experiments were carried out on virus-free potato mini-tubers (cv. Bashkirsky) grown using hydroponic system. Before storage tubers were dipped into suspensions of Ph. infestans (108 spores/mL) (causative agent of late blight), *F. oxysporum* (106 spores/mL) (causative agent of fusarium wilt and dry rot), water (control) and then dipped into suspension of B. subtilis (strains 10-4, 26D) in concentrations 103, 104, 105, 106, 107, 108 CFU/mL both alone and in composition with SA (0.05 mM), and stored at 18±1°C for 2 weeks and then at 3±1°C. Analysis the effect of B. subtilis (10-4, 26D) and SA on the development of late blight and fusarium of potato during 3 month storage showed dose-dependent manner in the action of B. subtilis (10-4, 26D) both individually and in mix with SA. It was revealed that B. subtilis (10-4, 26D) suppress the development of *Ph. infestans* and *F. oxysporum* starting from 106 CFU/mL and more, however, the most optimal against both diseases was 108 CFU/mL. When B. subtilis (10-4, 26D) used in mix with SA it was sufficient the concentrations of bacterial cells starting from 105 CFU/mL. Nevertheless, the best in suppressing both Ph. infestans and F. oxysporum were 107 CFU/mL (for 10-4+SA) and 106 CFU/mL (for 26D+SA). Besides, in variants with joined B. subtilis (especially strain 10-4) and SA application the tubers were fresher. Also, B. subtilis (10-4, 26D) both alone and in mix with SA decreased the pathogens-induced proline accumulation and lipid peroxidation in tubers indicating on protecting the cells against reactive oxygen species and controlling aging processes. Nevertheless, the mechanisms of B. subtilis (10-4, 26D) actions both alone and in mix with SA on potato under postharvest pathogen's infection are require further detailed investigations to fully use their potential in agricultural and food industry.

This research is supported by the Russian Science Foundation (Grant № 18-76-00031).

Take Away Notes:

- Endophytic *Bacillus subtilis, salicylic acid (SA), postharvest diseases, Phytophtora infestans, Fusarium oxysporum, Solanum tuberosum* L.
- The findings presented in the work expand the knowledge about the regulatory action of *B. subtilis* and its compositions with signaling molecule SA on resistance of potato tubers against postharvest diseases caused by *Phytophthora infestans* and *Fusarium oxysporum* during storage. The results of work could be used for development of new microbial biological products for protection of potato tubers against postharvest diseases during storage and prolong their «marketing» life with maintaining quality and nutritional value.
- Researchers from other faculty could use the presented data to expand their research or teaching. The obtained results

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could provide a practical solution to a problem that could simplify or make a job more efficient.

Biography

Dr. Lastochkina is a senior researcher at the Bashkir Research Institute of Agriculture (BRIA) Ufa Federal Research Centre, Russian Academy of Sciences (UFRC RAS) and Institute of Biochemistry and Genetics (IBG) UFRC RAS, (Ufa, Russia). She received her PhD degree in 2011 at the IBG UFRC RAS. Her research areas include Plants Stress Physiology/Biochemistry, Natural growth regulators (PGPB, Bacillus subtilis, SA, jasmonic acid)-Induced Plants Stress Resistance/Tolerance. Her current work is focused on the physio-biochemical and molecular mechanisms of endophytic B. subtilis-induced plants development and response to pathogens, salinity, and drought. She has published more than 80 research articles.

Volatile organic compounds released by maize following herbivory or insect extract application and communication between plants

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To protect themselves from herbivory, plants have evolved an arsenal of physical and chemical defences and release a variety of volatile organic compounds (VOCs). By releasing these VOCs, a signalling plant can both reduce herbivory, sometimes by more than 90%, and also warn neighbouring plants about an attack. The aim of this study was to assess the influence of herbivory and insect extract application on VOC release by damaged/treated and nearby undamaged/untreated maize plants. We confirmed that European corn borer (*Ostrinia nubilalis*) larvae attack or larvae extract application induced maize VOC release. Greater amounts of (Z)-3-hexenal, (E)-2-hexenal, (Z)-3-hexen-1-ol, (E)-2-hexen-1-ol, β-myrcene, (Z)-3-hexen-1-yl acetate, 1-hexyl acetate, (Z)-ocimene, linalool, benzyl acetate, methyl salicylate, indole, methyl anthranilate, geranyl acetate, β-caryophyllene, (E)-β-farnesene and (Z)-3-hexenal, (Z)- 3-hexen-1-ol, (Z)-3-hexen-1-yl acetate, (Z)-ocimene, linalool, indole, methyl anthranilate, geranyl acetate, β-caryophyllene and (E)-β-farnesene were released as a result of biotic stress after insect attack or insect extract application. The amounts of each VOC released were qualitatively and quantitatively distinct and dependent on time after biotic stress exposure. However, for all biotic stresses, significantly lower VOC induction was measured when leaves were damaged/treated for three days, as compared to seven days. Our work also demonstrated that undamaged/untreated neighbouring plants also release significant amounts of VOCs. This suggests that VOC emission by a damaged/treated plant stimulates VOC induction in nearby undamaged/untreated plants. However, the concentrations of all VOCs released by neighbouring undamaged/untreated maize plants were lower than those from damaged/treated plants and were negatively correlated with distance from a damaged/treated plant. Still, significant VOC induction occurred in undamaged/untreated plants even at 3 m distance from a damaged/infected plant. Our work suggests that maize plant protective defence responses (VOC emission) can be induced via application of European corn borer extracts.

Take Away Notes:

- Protecting crops against insect pest using environmental-friendly practices is a growing concern in Europe. This concern led the European commission to re-evaluate and limit the use of pesticides on all crops, banning a number of existing pesticides that were found to be inefficient, redundant or too harmful for the environment or the end-user. Although insecticides are invaluable tools that have no equivalent in flexibility of use and efficacy, a number of problems have arisen in the past due to their repeated and unfocussed use, selecting insect strains resistant to entire families of insecticide molecules, and contaminating and targeting beneficial insects, wild games and sometimes ending up as in acceptable residue levels in the food offered to the consumer.

Biography

Dr. Dariusz Piesik studied at the UTP University of Science and Technology, Poland and graduated as MS in 1995. He received his Ph.D. degree in 2000 at the same institution. Currently, D. Piesik is an Associate Professor at UTP, Department of Entomology and Molecular Phytopathology. He has published 29 publications (papers in JCR journals and others) and participated in 21 conferences, promoted 3 PhDs, and participated in 5 ERASMUS teaching in a framework of the ERASMUS staff mobility.

Attributes of wheat cultivars for late autumn sowing in genes expression and field estimates

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Due to the growing interest in Central and Eastern Europe on cropping of wheat in optional late autumn terms, called facultative, genetic research and field evaluation were taken on four spring cultivars: Tybalt(NL), Monsun (DE), *Ostka Smolicka* (PL) and Bombona (PL), currently being recommended by breeders. The PPD gene analyze, expression level of dehydrine genes (WCS120 and WDHN13) in cooling test, and qPCR for RNA isolation and analyses of WCS120 and WDHN13 gene expression at the BBCH12 stage of wheat were estimated. Molecular analysis of PPD-D1 gene confirmed the presence of photoperiod sensitive allele ppd-D1b in all tested genotypes. The highest level of NRE WCS120 gene was detected in cultivars Tybalt and Bombona. Two-year field experimental study assessed the growth, development and productivity of facultative and spring crops of studied cultivars. Based on our results from field experiments and result of molecular analysis of alleles of PPD-D1 gene, the tested genotypes can be considered as potentially facultative genotypes.

Take Away Notes:

- The poster will be presented the results of the molecular characteristics and field data concerned wheat.
- Facultative attributes of wheats allow in Europe to grow wheat in various terms of sowing, which is smart due to climate changes in Poland and other middle European countries.

Biography

Anna Wenda-Piesik has completed her DSc at the age of 41 years from UTP University of Science and Technology. In 2002-2003 she was an internship researcher at the Montana State University (MSU) in Bozeman, USA. Currently, her position is Associate Professor, at The Department of Agronomy, UTP in Bydgoszcz, Poland. Scientific interests: integrated cropping with biological and management practices, mostly on wheat, soybean and oilseed rape production. She published 80 original articles, the total IF is at 32,751, and total number of citations is at 229, h- index 9 and has been serving as an editorial board member of repute.

A qPCR-HRM assay (high-resolution melting-curve analysis) to discriminate between pathotypes of *Synchytrium endobioticum*

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Synchytrium endobioticum (Shilb.) Perc. is an obligate biotrophic, soil-borne fungus which causes the potato wart disease. S. endobioticum originated from Andean zone in South America and is currently present almost all over the world. The thick-walled winter sporangia are the dormant structures of the fungus and can survive for more than 40 years in the absence of host even under adverse environmental conditions. Since the discovery of pathotype 2(G1) in Germany, more than 40 pathotypes have been reported in Europe. HRM is a recently developed molecular technique. It is a cost-efficient, closed-tube system that allows high-throughput analysis without any post-PCR processing. PCR amplification and HRM were performed using specific primers of SNP sites (L1, L2, L3, L4, L5, L8 & L9) and DNA extracts of 10 different pathotypes of *S. endobioticum* [1(D1), 2(G1), 2(Ch1), 3(M1), 6(O1), 8(F1), 18(T1), 39(P1), #PL5/2010 & #PL2/20015]. Testing the primers set L1 on all pathotypes showed that HRM discriminates clearly between pathotype-1(D1) and non pathotype-1(D1). The second PCR test (L3) showed that HRM discriminates clearly between pathotype 1(D1)/8(F1)/18(T1) and other pathotypes of S. endobioticum. The third PCR test (L4) showed that HRM discriminates clearly between pathotypes 1(D1)/3(M1) and 2(G1)/6(O1)/ 8(F1)/18(T1) and 39(P1)/ #PL5/2010/#PL2/20015. This study presents the first results on HRM method to discriminate different pathotypes of *S. endobioticum* and confirms results obtained by Bonants et al. (2015) by the use of TaqMan PCR assays. HRM is more cost-effective than other genotyping technologies, such as TaqMan SNP typing, because no additional probes are required.

Take Away Notes:

- The results presented on the poster can be used by other conference participants. Especially in countries where this quarantine fungus occurs?
- HRM technique is much cheaper in comparison to TaqMan method. The results provide practical solution for scientists who for scientists who work with *S. endobioticum*.

Biography

Dr. Jarosław Przetakiewicz graduated from Nicolaus Copernicus University in Toruń, Poland – biology department – in 1998. His M. Sc. degree thesis concerned identification of aminoacides connected with phosphorylation in proteins using immunoprecipitation methods in oats. In 1998 Dr J. Przetakiewicz started to work in Plant Breeding and Acclimatization Institute – National Research Institute. This work fructified Ph.D. degree in 2003. Title of thesis: "Production of tetraploid somatic hybrids of potato (*Solanum tuberosum* L.) from selected diploid lines". From 2004 he is working for Department of Plant Pathology in Laboratory of Quarantine Organisms. His research is connected with improving of detection and pathotype determination of *S. endobioticum* and resistance tests of potato genotypes to different pathotypes of the fungus.

CONTENTS

Determination how tobacco plants sense the zinc level in the apoplast. ?

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Based on the experiments performed on the AtHMA4 – expressing tobacco plants (AtHMA4 encodes protein that exports Zn to the apoplast), it was proposed that apoplast may be regarded as a site of perception of the Zn status in cells. It was presumed that the apoplastic Zn concentration might contribute to the generation of a signal of Zn excess leading to loading of Zn to leaf areas consisting of groups of cells in which the exceptional ability to accumulate Zn is initiated. Up to now the question about the nature of the signal inducing loading Zn into these specific cells remain unanswered.

Among the proteins associated with the cell wall, only the WAKs (Wall-Associated Kinases) have been implicated in a plant response to metals. It is known that the members of WAKs family have extracellular domain binding pectins. From the variety of cell wall components, pectins are among of the molecules that may play a signaling role. Furthermore, the exposure to different metals concentrations changes the level of the methylesteryfication of the cell wall pectins.

The expression analysis of NtWAKs/NtWAKLs genes showed the increase in the transcript level of NtWAK2 in the leaves from high Zn-treated plants in comparison to the control ones. To analyze the differences in pectin localization between control and Zn-treated plants, the immunolocalization of pectin fractions was performed on the leaf cross-sections. Only one epitope of rhamnogalacturonan I was present exclusively in the Zn-exposed tobacco. Analysis showed that the level of rhamnogalacturonan I increased with time of exposure to high Zn concertation. Furthermore, this fraction of pectins was localized preferentially near the veins, and its distributions were correlated with the pattern of high concentrations of Zn in the groups of mesophyll cells localized within the same regions. Performed research suggest that signal inducting responsible for formation of the accumulating cells in the mesophyll of tobacco leaves is generated by rhamnogalacturonan I and transduced into the cell.

Take Away Notes:

- Wall associated kinases 2 are probably involved in perception of zinc level in tobacco leaf cells.
- During the prolonged exposure plants for high zinc concentration in medium, the level of rhamnogalacturonan I in the cell wall is increasing.
- Probably RG I generated a signal about zinc level in apoplast which is most likely received by NtWAK2.

Biography

Mgr. Weremczuk studied biology at the University of Warsaw, Poland and graduated as MS in 2013. She belongs to the research group of Prof. D.M. Antosiewicz at the Faculty of Biology, University of Warsaw. Now she finishes her PhD which is about the formation of Zn-related necrosis from Zn-accumulating cells in tobacco leaves, including apoplast role in this process. During her PhD studies she spends 3 month scholarship at the Newcastle University, UK, in the prof. Willats laboratory.

Polymorphism in SSR-loci associated with E genes in soybean mutant lines perspective for breeding

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[2] Lab. of Cytoplasmic Inheritance, Institute of Genetics and Cytology, Minsk, Belarus
[3] Institute of Feeds and Agriculture of Podillia of NAAS, Vinnitsa, Ukraine

Detection of alleles of E genes that are involved in the control of plant response to photoperiod and determination the time to flowering and maturation, with SSR markers could help in the evaluation of adaptive capacity of soybean cultivars in different growth conditions.

With the aim to create new breeding material of soybean (*Glicine max* (L.) Merrill) the cultivars Femida, Oksana, Podils'ka 416, Zolotysta have been treated by chemical mutagenesis. For this purpose, were used mutagens: D-6, DMSSO-11, DMSSO-12, DMSNPIR-11, DUDMS12, D12DMC-11B that have been provided by V.P. Kukhar Institute of Bioorganic Chemistry and Petrochemistry of the National Academy of Sciences of Ukraine (Kiev, Ukraine). After mutagenic treatment lines were growing in experimental field during 5-7 agronomical seasons in Institute of Feeds and Agriculture of Podillia of NAAS (Vinnitsa, Ukraine) and then there were selected perspective for breeding mutant lines.

The aim of our work was to analyse genetic diversity that have been developed in these mutant lines by using microsatellite (MS) markers: Satt_100, Satt_229, Satt_319, Satt_354, Satt_365, Sat_038 that are linked with genes which determined the sensitivity of soybean plants to photoperiod and time to maturation.

In the genotypes of 10 mutant lines, which are perspective for breeding, we have revealed new alleles of microsatellite loci that were not present in parental lines. Totally we have detected 23 alleles of 6 microsatellite loci for this material. Only in 4 cases from 24 (MS-locus/parental genotype) there were not detected changes in allele size for mutant lines in comparing with genotypes of parental cultivars. But this numbers of alleles were less than 35 alleles that we have detected for 19 soybean cultivars also tested also in this project. Among alleles of mutant lines there were 3 new which are not present among alleles of soybean cultivars.

The results have shown that applied mutagens induce changes in soybean genome and by using these mutagens it is possible effectively increase genetic diversity in loci associated with the genes/loci that determined time of maturity and/or photoperiod sensitivity of soybean. The obtained mutant lines can permit to expand the possibilities of creating soybean varieties with different levels of photoperiodic sensitivity, ripening terms and adaptation ability.

Take Away Notes:

- The mutagens: D-6, DMSSO-11, DMSSO-12, DMSNPIR-11, DUDMS12, D12DMC-11B can be effectively used in chemical mutagenesis of soybean.
- The mutagens: D-6, DMSSO-11, DMSSO-12, DMSNPIR-11, DUDMS12, D12DMC-11B can increase genetic variability in microsatellite loci linked with E – photoperiod sensitivity genes.
- Data from this research could be used by breeders who have the aim to select the most adaptive soybean varieties for geographical latitudes similar to Ukraine conditions since early flowering combined with an extended reproductive stage is preferable for soybean.
- The information about genetic diversity in microsatellite loci that are linked with E genes of Ukrainian cultivars and mutant lines of soybean can be used for comparative genetic investigations.

Biography

Prof. Chebotar is corresponding member of National Academy Agrarian Sciences of Ukraine. In 1988 she graduated Odesa National Mechnikov University (ONU), she was PhD student in Plant Breeding and Genetics Institute (1991-1993) and in 1995 defended PhD thesis at the Institute of Molecular Biology and Genetics National Academy of Sciences of Ukraine (IMBG-NAS). In 2001-2002 she held internships in Genebank of the Institute of Plant Genetics and Crop Plant Research (Germany). In 2004-2006 she joined in research group of Dr. Bernard in INRA (France). In 2009 she defended habilitation work in IMBG-NAS. From 2012 Chebotar is a Head of Department of Genetics and Molecular Biology ONU. She has published more than 200 research articles in SCI (E) journals.

Transcriptomic analysis of Moso bamboo seeds during the germination process by RNA-seq

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For advanced plant, germination is start point for growth and development, where life activity is most intense. Changing law in germination will contribute to controlling the processing. Moso bamboo is a large, woody bamboo with the highest ecological, economic and cultural value of all the bamboo types, the major genes regulating seed germination in Moso bamboo are not clear.

In this study, Moso bamboo seeds at four stages from their emergence to maturation were selected, the changes of phenotype was observed. There are three important stages in Moso bamboo seed germination: □: cell initiation, □: radicle and germ growth; and III: leaf formation. In addition, we compared the identified genes at different seed developmental stages. Based on the subcategories in biological process, these genes were classified to 14 sub-categories, The cell matrix and membrane, cell differentiation, cell proliferation and gene expression regulation, energy conversion of cells, chloroplasts, ribosome, protein, biochemical component related enzymes, response stimulus etc.

Seed germination is an energy-demanding process, and only sufficient energy can ensure the smooth metabolism. There is less ATP in mature dry seeds. As the seeds absorb water and germinate various physiological and biochemical activities are active, and the seeds begin to breathe, a large amount of ATP will be produced internally. ATP is produced during respiration and provides the main energy source for the biological reaction during seed germination. Early germination respiration is the core of substance and energy metabolism. There are different respiratory pathways in Moso bamboo seeds, the study found that when the seed respiration pathway changes from EMP/TCA to PPP, it means that the Moso bamboo seeds changes from dormancy to germination. Respiration intensity in the whole germination process of Moso bamboo experiences a gradual upward trend of high → low → high → low → high.

Take Away Notes:

- By the transcriptome analysis to explore the main regulation factors and respiratory pathway on bamboo seed germination.
- This presentation will improve the production efficiency of cultivation and accelerate the breeding process of new varieties of Moso bamboo.

Biography

Juan Li: studied Ecology in Guangxi University, graduated as MS in 2003. She then joined the Department of Forestry in Chinese Academy of Forestry. She received her PhD degree in 2009 in China Academy of Forestry. After three years postdoctoral fellowship supervised by Prof. Dr. Zhenhua Peng at the International center for bamboo and rattan (ICBR), she obtained the position of an Associate Professor at the ICBR. She has published more than 5 research articles in SCI (E) journals.

Diversity of phototrophs in the Crimean hypersaline and lagoons and their biotechnological potential

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[2] Laboratory of Algology, Komarov Botanical Institute, Saint Petersburg, Russia

Widespread, including in Crimea, hypersaline water bodies are among the most polyextreme habitats on the planet. To live in polyextreme environment, organisms have led to the development of a variety of adaptive mechanisms with a synthesis of unique secondary metabolites. This provides the possibility to use organisms dwelling hypersaline waters in different areas of biotechnology and aquaculture. There are more than 50 hypersaline water bodies including different lakes and Bay Sivash (The Sea of Azov), largest hypersaline lagoon in the world. There are three groups of phototrophs, which use different types of phototrophy: oxygenic photosynthesis (cyanobacteria, microalgae, and plants), anoxygenic photosynthesis (purple and green bacteria) and proton bacteriorhodopsin pump (archaea). The study of phototrophic organisms in hypersaline reservoirs of the Crimea has a long history; nevertheless, many of their taxa are still poorly understood. To date, 110 species of cyanobacteria have been found in them; they are massively growing in plankton and benthos, and 70 species of eukaryotic algae of various orders in plankton. In benthos, only diatoms have been studied - 74 species. Among multicellular phototrophs, 7 species of green filamentous algae and 4-5 species of flowering plants were found. The variety of anoxygenic phototrophs is significantly lower (approximately 14 species). In halobacteria, there is only the widespread in such habitats Haloquadratum walsbyi. Diversity of these groups in the Crimean lakes and lagoons provide a lot of perspectives for their practical use. As an example, among cyanobacteria in the Crimean hypersaline waters, 17 genera are noted, 11 of which include potentially toxigenic species producing cytotoxins, hepatotoxins and neurotoxins. These toxins can be used in the development of new drugs. From the samples collected on the Kerch Peninsula, two strains of Nostoc f. linckia Bornet ex Bornet & Flahault 1886, which are characterized by toxicity, were isolated and investigated. Neurotoxin nostokocarbolin was extracted from Nostoc, and it can be used to create new promising drugs for the treatment of Alzheimer's and Parkinson's diseases.

This study was supported by the Russian Science Foundation (grant 18-16-00001).

Take Away Notes:

- It provides new information, gives new data and ideas on a biotechnological and agri-aquacultural use of phototrophs from the Crimean hypersaline lakes.

Biography

Dr. Anufriieva studied ecology at the Lugansk State University, Ukraine and graduated as MS in 2011. She received her PhD degree in 2014 at Institute of Biology of the Southern seas, Sevastopol, Russia. She is a head of two projects on biology of hypersaline waters and aquaculture development. She has published more than 60 research articles in Russian and English.

Evaluation of incompatibility at germplasm of late sweet cherry cultivars at molecular level

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[2] Hop Research Institute Co., Zatec, Czech Republic

Sweet cherries Prunus avium from Rosaceae family are non-climacteric stone fruit, mainly grown in colder temperate climate countries. Lower temperatures (usually below 8 °C) are necessary to provide chilling requirement for induction of flowers. Sweet cherries belong to a commercially important vegetatively propagated fruit tree species. Late ripening sweet cherry cultivars have a higher commercial importance than sweet cherries ripening early in the season due to bigger fruits and higher quality. From the point of view of human diet, sweet cherry provides a delicious fruit, which is rich in sugars and minerals. It has more calorific value than apple. Sweet cherries are also a significant source of polyphenols with antiradical activity. There is a long tradition of sweet cherry breeding in the Czech Republic in Research and Breeding Institute of Pomology Holovousy Ltd. Sweet cherry is an out-breeding, self-incompatible diploid species in the Rosaceae family with a genome of 2n =16. Their self-incompatibility is determined by a gametophytic self-incompatibility system (GSI), controlled by a multi-allelic S-locus. It is important to select suitable pollen donors for successful fruit production in plantations with different cultivars. Today, it is possible to detect individual alleles of S-locus by PCR molecular markers. In analysis of late sweet cherry varieties, we detected 10 different S-alleles in total 18 combinations of S-locus, belonging to 17 incompatibility groups. S3, S1 and S4 were the most frequent alleles and III (S3S4) and II (S1S3) were the most frequent incompatibility groups. A suitable pollinator must overlap with its flowering with the pollinated variety and should have also a high flower set. Results are useful for the selection of pollen donors for ensuring of sufficient yields in commercial sweet cherry plantations. The study of phenotypic characteristics and further molecular DNA analyses (SSR markers) were carried out simultaneously to describe the genetic variability of cherry collections. It is also crucial for the further improvement of sweet cherry breeding programs. Cherry breeding programs face a significant challenge to develop cultivars incorporating the range of attributes (including pollinizing conditions) preferred by the various components of production chain.

Take Away Notes:

- Due to higher return, cherry is gaining popularity in commercial orchards worldwide. The choice of suitable pollinators for particular varieties of sweet cherry is very important for higher yields in commercial plantations with a limited number of varieties. The molecular characterization carried out in our study revealed high diversity of analysed sweet cherry germplasm. Incompatible varieties of sweet cherry are not capable of fertilization and fruiting. A suitable pollinator must overlap with its flowering with the pollinated variety and should also have a regular high flower set. Beside commercial growers, advanced vocational schools and universities could also use obtained results to expand their teaching or research.

Biography

Frantisek Paprstein studied University of Agriculture in Prague, Czech Republic and graduated as MSc in 1974. He received CSc. degree (equivalent of Ph.D.) at the same university in 1988 (postgraduate study). He executed the duties of statutory representative and deputy director of Research and Breeding Institute of Pomology Holovousy Ltd. between 2001 and 2011. Presently he works as the head of the Department of Fruit Genebanks. He has published more than 80 scientific and research articles in the past ten years.

Hull-splitting is caused by a mutation of the gene Os04g0447100 in rice

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Rice hull, consisted of lemma and palea, is an important organ that helps protect seeds, determines seed shape, and ensures grain filling. We identified the split-hull (sph) mutant in rice through chemical mutagenesis, which exhibits hull-splitting in the interlocking part between lemma and palea and/or the folded part of the lemma during the grain filling stage. Morphological and chemical analysis revealed that reduction in the width of the lemma and lignin content of the hull in the sph mutant might be the cause of hull-splitting. Genetic analysis indicated that the mutant phenotype was controlled by a recessive gene, sph (Os04g0447100), which encodes a type-2 13-lipoxygenase. SPH knockout- and knock-down-transgenic plants displayed the same as in the mutant. The sph mutant showed significantly higher linoleic and linolenic acid (substrates of lipoxygenase) contents in spikelets compared to the wild type probably due to the genetic defect of SPH and subsequent decrease in lipoxygenase activity. In dehulling experiment, the sph mutant showed high dehulling efficiency even by a weak tearing force in a dehulling machine. The results provide a basis for understanding of the functional role of lipoxygenase in structure and maintenance of hulls, and might facilitate breeding of easy-dehulling rice. This study was supported by a grant from the Next-Generation BioGreen21 Program (No. PJ013165) of the Rural Development Administration, Korea.

Take Away Notes:

- A new type spikelet mutant in rice.
- Map-based cloning of mutant traits.
- How to confirm the genes through transgenic and PCR technology.

Biography

Hee-Jong Koh has his expertise in rice genetics and breeding for higher yield and better quality. He developed several mutants on morphological and quality traits, and cloned genes responsible for the mutant phenotypes. He has also studied natural variation in yield-related and quality traits demonstrating selection models for better genotypes in rice breeding programs. Recently, he edited a book "Current technologies in plant molecular breeding" published by Springer Verlag.

Improvement of phosphorus utilization and growth in maize (*Zea mays*) seedlings by synergistic biofertlizer application on eastern Indian Oxisol

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Prevalence of aluminium and ferric cations limits the mobilization of phosphorus (P) in the acidic Oxisol of eastern India. Maize (*Zea mays*) is cultivable in this region due to its symbiotic association with arbuscular mycorrhizal (AM) fungi, which facilitate P uptake by increased root surface area and specialized biochemical mechanisms. Maize seedlings were assessed for P utilization and growth on potted soil in Kharagpur, eastern India, when supplemented with inorganic P (at 100 mg per kg soil) and biofertilizers in a greenhouse environment. Biofertlizers were prepared from native strains of AM fungi and phosphorus soluble microorganisms (PSM) isolated from locally grown maize roots and associated rhizospheric soil respectively. The PSM were screened for P mobilization from inorganic culture medium as well as aqueous soil suspensions. Applications of various combinations of P, AM and PSM revealed that the biofertilizers behaved differently in fertilized and unfertilized soil, and during early and later phases of seedling growth. The plant-AM symbiosis was significantly more beneficial in terms of shoot growth and P utilization at 40 days after sowing (DAS) than at 20 DAS, and in unfertilized over fertilized soil. Benefits incurred by rhizospheric PSM activity generally followed the opposite trends, while interactions between jointly applied AM and PSM produced no benefits at all in unfertilized soil and temporally variable benefits in fertilized soil. We concluded that PSM colonies cannot assimilate mobilized phosphates as rapidly they solubilize it, and so consequently provide an antagonistic pressure on VAM activity in P-depleted soil. Nonetheless, fertilization with inorganic P was significantly more effective on seedling growth and health when supplemented with joint AM and PSM inoculation.

Biography

I am a Research Scholar finishing my final year of PhD at the Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur, India. I completed my M.Tech in Agricultural Systems and Management in the same department, working on plant-soil-microbe interactions for my final year thesis. My doctoral research involves studying the production and functions of secondary metabolites in plants. I have authored three publications in international peer-reviewed journals, one book chapter and one review paper.

CONTENTS

A novel protein interaction between RCI2s and PIP2;1 reducing water transport activity in Camelina under NaCl stress

Hyun-Sung Kim, Hyun-Gyu Lim*, Hyun-Sook Lee, Jung-Ho Shin, Yeon-Ok Kim, Sung-Ju Ahn
Department of Bioenergy Science and Technology, Chonnam National University, Gwangju, Korea

Abiotic stresses are major limiting factors for crop growth and productivity. Plants show various adaptations to overcome or avoid abiotic stresses. Rare cold inducible 2 (RCI2) proteins are localized at the plasma membrane (PM) and are significantly induced by cold, salt, and drought stresses. The RCI2s are believed to enhance abiotic stress tolerance by regulating the membrane potential. Aquaporin PIP2 is a water transport channel protein that facilitates the transport of water, ions, and several solutes across the PM. The activity of PIP2s is regulated by phosphorylation of its N- and C-terminal residues. PIP2s are known to be important for water homeostasis under NaCl and drought stress. In this study, we focused on the functions of RCI2s and their interactions with aquaporin PIP2;1, which is important for cell water regulation under NaCl stress in the bioenergy crop Camelina sativa L. The characteristics of CsRCI2 proteins displayed high homology with RCI2-related proteins from various species. CsRCI2A/B/C/H proteins contained only two transmembrane domains (TMD) but CsRCI2D/E/F/G has both transmembrane domains and a C-terminal tail. Subcellular localization of the CsRCI2s encoded proteins were detected in the PM. The transcription level of CsRCI2A/B/E/F genes were induced by salinity stress at 150 mM NaCl, cold stress at 2°C, and 300 mM mannitol as osmotic stress. Protein accumulation of CsRCI2E and CsRCI2F were increased by NaCl concentrations but showed different accumulation level by intensity and duration of NaCl treatment. A bimolecular fluorescence complementation and co-immunoprecipitation test revealed interaction between CsRCI2E-CsPIP2 and CsRCI2F-CsPIP2. Moreover, co-expression of the four CsRCI2 proteins with CsPIP2;1 in Xenopus laevis oocytes reduced water transport activity and lessened current changes. Furthermore, the abundance of CsPIP2;1 protein was decreased under CsRCI2E and CsRCI2F co-expression. These results suggest that NaCl-induced expression of CsRCI2E and CsRCI2F contributes to the repression of CsPIP2;1, which may decrease Na+ ion transport and affect ion homeostasis.

Take Away Notes:

- Mechanism for abiotic stress tolerance in Camelina.
- Function of RCI2 proteins which related to abiotic stress tolerance.
- A physiological approach to compare abiotic stress tolerance.

Biography

Lim studied bioenergy science and technology at Chonnam National University in Korea and graduated in 2017. He then joined Prof. Ahn's lab at Chonnam National University. He received his master's degree from the same institution in 2019. His field of study is plant physiology, which is to produce crops by improving tolerance to abiotic stress.

Over-expression of OsASR confers drought tolerance in rice

Dipali Srivastava*, M.Sc., Giti Verma, Ph.D., Debasis Chakrabarty, Ph.D.
CSIR- National Botanical Research Institute, India

Rice (*Oryza sativa L.*), a staple food for more than half of the global population; being as a paddy crop is particularly susceptible to water stress which reduces its yield drastically. Thus, developing strategies which would help in developing rice variety that can grow even in water deficit condition can be beneficial for increasing crop yield as well as increasing probability of agriculture in drought prone areas. Abscisic acid stress-ripening proteins (ASR) are a family of plant-specific small hydrophilic proteins encoded by abiotic stress-regulated gene. The expression of OsASR is strongly induced under the application of drought, salt and abscisic acid (ABA). To provide evidence on the biological role of OsASR proteins against drought, we generated transgenic lines of rice overexpressing OsASR. The extent of tolerance to drought stress of these plants correlated well with the level of OsASR expression. Various biochemical and physiological analyses like malondialdehyde content, proline, ROS scavenging enzymes, electrolyte leakage and histochemical analyses for H2O2 and O22- radical showed differential activities during drought tolerance in T3 generation of transgenic lines as compared to wild type (Wt) plants. In addition, transcriptome analysis revealed that OsASR regulate the expression of a wide spectrum of stress-related genes in response to abiotic stresses through an ABA-dependent regulation pathway. In addition, few genes that are possible OsASR specific target genes were identified based on the comparison of the expression profiles in the transgenic line and the Wt plant and validated through qRT-PCR analysis. These results demonstrate, OsASR to be a positive regulator commonly involved in the tolerance to drought stress in rice and its simple manipulation has great potential with regard to plant improvement.

Take Away Notes:

- Our current approach of manipulating OsASR expression in Rice may be developed as a valuable tool for improving the drought tolerance of agronomically important crop plants.
- This research provides useful information that supports biotechnology applications and molecular breeding that leads to improved drought tolerance in various plants.
- In addition, OsAsR can be transformed into other staple food crop for farming in drought prone area of the world.

Biography

Dipali Srivastava is a senior research fellow in Genetics and Molecular Biology Division, working under the supervision of Dr. Debasis Chakrabarty (Sr. Scientist) at CSIR-National Botanical Research Institute, India. She had her M.Sc. degree (Biotechnology) from Department of Biotechnology, CSJM University of Kanpur, India. She also qualified CSIR NET-Lectureship in year 2015. She possesses excellent knowledge and technical experience in the area of Plant molecular biology. With her sound knowledge of scientific writing she earned two international publications. Presently her work is to improve the adaptability of crop to drought conditions, by developing transgenic rice, which shall be able to cope with drought conditions before grain filling in rice.

Development of high yield and stress-tolerant crops via the regulation of splicing patterns of chloroplast genes

Su Jung Park*, **Hunseung Kang**
Department of Plant Biotechnology, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 61186, Korea

Chloroplasts are the most important small organ of plants, play an essential role in adapting to environmental stress as well as plant growth and development. The expression of chloroplast gene is influenced by development and environmental factors after RNA metabolism in chloroplasts, and is mainly regulated at post-processing level. To understand the significance of chloroplast RNA metabolism during stress responses, such as application of DCMU, DBMIB and environmental stresses. We analyzed the splicing patterns of chloroplast introns in cabbage and Arabidopsis under different environmental stress conditions. To determine the importance of splicing of chloroplast introns in stress responses, the cabbage and Arabidopsis chloroplast genes whose intron splicing was affected by environmental stresses were introduced into Arabidopsis, and their functional roles during stress response were determined using the transgenic Arabidopsis plants. The results showed that transgenic plants had increased thermo-tolerance and growth as well as much better seedling growth under normal growth conditions. Taken together, our results suggest that intron splicing of chloroplast transcripts is affected by various environmental factors and that stress-tolerant plants can be developed via the regulation of chloroplast intron splicing.

Take Away Notes:

- Through this presentation, we will be able to identify the function of chloroplast genes in plants and to control the development of crops under environmental stress by controlling the expression of chloroplast genes.
- If the chloroplast gene expression can be adjusted to increase the productivity and stress resistance of plants, this technology can be applied to various kinds of crops, such as grains and bio-energy crops, to develop crops that are resistant to environmental stress or that have increased yields.
- Research on the chloroplast gene regulation and function of crops worldwide has yet to be done, and the results of studying the chloroplasts of plants could provide important information to researchers studying chloroplasts of plants.

Biography

Dr. Park studied horticulture at the Chonnam National University, Korea and graduated as MS in 2003. She then joined the research group of Prof. Kang at the Chonnam National University, and studied about plant molecular biology. She received her PhD degree in 2007 at the same institution. After two years postdoctoral fellowship supervised by Dr. Yun at the Gyeongsang National University. And she is currently working as a research professor at the Lab. of Prof. Kang at Chonnam National University, Korea.

CONTENTS

Microbial endophytes and soil enzymes contribute to the growth and establishment of *Ginkgo biloba* L.

Ashish Dhyani*, Anita Pandey
Center for Environmental Assessment and Climate Change, G. B. Pant National Institute of Himalayan Environment and Sustainable Development Kosi-Katarmal, Almora, Uttarakhand, India 263 643

Ginkgo biloba L. (English name- Maiden hair tree), often referred as the "living fossil", is the only living member of the family ginkgoaceae. While the species has been interesting from its evolutionary view point, it is also well known for its sturdiness, disease resistance properties and long life. Its natural habitats are located in China, Japan and Korea. Some well-established *Ginkgo* trees have also been located in the hilly tracts of Indian Himalayan region (IHR), maximum being in the state of Uttarakhand. It has been in use as food component and as medicine (memory enhancer and anti-vertigo agent) traditionally since ancient times. In America and European countries, *Ginkgo* extracts are prepared at commercial scale. IUCN red list and Botanical survey of India declared this species as "endangered" and "rare", respectively. While the species is extremely slow growing, its regeneration through seeds is also very poor. In this background, the species needs focused efforts for its propagation and conservation.

Root microbiome, microbial endophytes in particular, play crucial role in plant growth. *Ginkgo* has been studied for its root associated microflora and has been reported to be colonized by a number of endophytic microorganisms, both bacteria and fungi. *Pseudomonas sp.* MTCC9476, a bacterial endophyte isolated from the mycorrhizae infected roots of *Ginkgo* was demonstrated for its plant growth promoting and biocontrol properties. The bacterial species, in liquid formulation, is being used in propagation of *Ginkgo* through stem cuttings. Root and rhizhosphere soil samples, collected from approximately 10 year old plants of *Ginkgo* that were raised using stem cuttings and the bacterial formulation and field transferred at a forest nursery (Kalika, Ranikhet, Uttarakhand), are being evaluated in active (summer) and dormant (winter) seasons with respect to plant growth related parameters. Influence of bacterial inoculation on microbial colonization and soil parameters (physico-chemical and soil enzymes) are main components of this presentation.

Microscopy of the root samples revealed higher colonization of dark septate endophytes (DSE) 51.10%, fungal mycelium (FM) 95.00%, microsclerotia (MS) 24.44% and arbuscules (AR) 20.00% in treated plants as compared to the roots of control plants (DSE 25.00%, FM 83.33%, MS 12.50%, AR 8.30%), in dormant season. Soil organic carbon (3.74%) and total nitrogen content (0.25 g/kg) was also higher in treated plants while the total phosphorus was recorded higher (0.13 ppm) in control plants in dormant season. The activity of soil enzymes namely acid phosphatase (176.50pNP μg/g dry soil/ h), alkaline phosphatase (244.46pNP μg/g dry soil/ h), β-glucosidase (127.44 pNP μg/g dry soil/ h) and dehydrogenase (0.49TPF μg/g dry soil/h) were also higher in the treated plants. The pattern of soil physico-chemical and enzyme activity was at par in both active and dormant seasons. The results are indicative of the positive influence of bacterial inoculation on the plant and soil health related parameters. The study has implications in recommending the use of this microbial based ecofriendly technology in propagation and conservation of the endangered or rare plant species.

Take Away Notes:

- The importance of root associated microorganisms and soil enzymes in soil, plant and environment health.
- Application of this microbe based and environment friendly technology in cutting down the use of chemical fertilizers which are harmful for the heath of soil, plant and environment.
- Replication of this technology in similar studies.

Biography

Mr Ashish Dhyani did MSc in Microbiology from S.G.R.R Institute of Technology and Science, Dehradun, Uttarakhand, India in 2013. He then joined the research group of Dr Anita Pandey as Research Fellow in the project entitled "Extremophiles from Himalaya: ecological resilience and biotechnological applications" at G.B. Pant National Institute of Himalayan Environment and Sustainable Development, Kosi- Katarmal, Almora, Uttarakhand, India. Presently, he is working in the project "Establishment and conservation of *Ginkgo biloba* and Taxus wallichiana using microbial technology: Field evaluation" at the same Institute. He is also perusing his PhD in Biotechnology and has published 3 research papers in peer-reviewed Journals.

CONTENTS

Carbon flow mediated by brackish-water algal mats in Indian Sunderbans: A case study for environment-friendly and sustainable source of biodiesel

Prakash Chandra Gorain*, **Ruma Pal**
Phycology Laboratory, Department of Botany, University of Calcutta, Kolkata, West Bengal, India

High nutrient influxes through regional river systems strongly affect the algal populations in the heavily populated Sunderbans brackish-water ecozone. Twelve brackish-water sites in the Indian Sunderbans were surveyed for growth and carbon (C) sequestration performances of algal / cyanobacterial taxa dominating the mat-forming communities at different seasons. The dominant species at the twelve sites included seven genera (*Spirogyra, Rhizoclonium, Ulva, Cladophora, Pithophora, Chaetomorpha*) belonging to Chlorophyta, three genera (*Polysiphonia, Gracilaria, Catenella*) belonging to Rhodophyta and Lyngbya majuscula from cyanobacteria. Environmental variables and biomass productivity parameters monitored at each site and analysed by statistical techniques indicated that nutrient availability, particularly dissolved P concentration and N:P ratio in the water column, as well as with salinity, mainly affected biomass yield and C sequestration of mat-forming genera and net OC input into water column. However, OC contents of the underlying muck proved to be very stable, with small increments following each seasonal bloom of algal mats. High biomass yields (34-3107 g/m2) of the dominant mat components accumulated large stocks of OC, very little of which were found to reach the pedologic pool (muck). Thus the algal mats actually form a large but transient pool of harvestable OC which would ultimately be consumed and emitted back to the atmosphere, but might be alternatively utilized as feedstock for dietary supplements or biofuel production. Availability of important dietary fatty acids in *Spirogyra punctulata, Gracilaria sp., Polysiphonia mollis, Rhizoclonium riparium, R. tortuosum, Pithophora oedogonia* and *Ulva lactuca* was considered as suitability of these taxa for nutraceutical applications. Fatty acid compositions of *L. majuscula, Catenella repens, R. tortuosum* and *Cladophora crystallina* were estimated to be applicable for producing biodiesel usable in sub-tropical climates.

Biography

Prakash Chandra Gorain is currently a PhD scholar in his final year of graduation at the Phycology Laboratory, Department of Botany, University of Calcutta (India). His work involves the analyses of carbon foot-prints of phytoplankton populations in the Sundarbans, and bio-prospection of algal lipids for biodiesel production. He previously finished my M.Tech in Applied Botany at Indian Institute of Technology Kharagpur. He has authored eight publications in international peer-reviewed journals, and one in a national journal.

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DAY 2

E-POSTERS

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Physical mutagenesis application in selection of *Sesamum indicum* L.

Nina Chavdar*, Alexander Rushchuk
Pridnestrovian state university named after T.G. Shevchenko, Tiraspol, Pridnestrovie

Relevance of carrying out researches on selection of tropical culture – (*Sesamum indicum* L.) is caused by warming of climate in general and in Pridnestrovie, in particular, and also wide use of seeds in the food industry and sesame absence in the variety register allowed touse in Pridnestrovie.

Researches were conducted in Tiraspol, located on 46th northern latitude. Therefore, it was necessary to receive short vegetative period forms not more than 145 days first of all.

Physical mutagenesis was used as a selection method because of absence of sesame various initial material.

The collection sample of the Republican botanical garden (Tiraspol) of sesame of unknown origin relating to Asian group (*ssp bicarpellatum Hilt, var. albidum*) has been served as an initial material for receiving mutant posterity. Seeds coloring white with a gray shade, branchiness of stalks from 3 to 6 - 7, in a leaf bosom 1 box.

Mutant material was received in 2012 by seeds irradiation of 60Co radioactive isotope on the «Researcher» gamma-ray irradiation facility (fig. 1) located in Pridnestrovian research institute of agriculture (Tiraspol), using up to 240 Gray doses.


a) b)

Fig. 1 a, b. «Researcher» gamma-ray irradiation facility

Two varieties of sesame Lebed and Mulatka suitable for cultivation in Pridnestrovie were received as a result of research.

The sesame variety Lebed, was created by a physical mutagenesis method with the subsequent selection of the best line. Plants have 130-140 days of the vegetative period duration, 165-175 cm height, 7-8 escapes of the first order, first branch height laying at 10-13 cm, flowers are trimmed, light pink (fig. 2). Productive part of the main escape length is 100-115 cm on which there are from 50 to 76 densely located boxes (fig. 3). 250-400 of boxes are formed on a plant in total, when maturing crack poorly. Boxes length is about of 24-25 mm. Seeds mass from one plant – 25-55 g, (maximum from some plants up to 75 g). Weight of 1000 of seeds – 2,7 – 2,9 g. Seeds are white with a cream shade and have an extended form (fig. 4). The productivity is about 20-22 c/hectare without irrigation.

CONTENTS

Fig. 2. Sesame flower of variety Lebed

Fig. 3. Sesame escape of variety Lebed

a)

b)

Fig. 4 a, b. Sesame seeds of variety Lebed

The sesame variety Mulatka plants height is about 150-160 cm with 5-10 escapes of the first order. First branch height laying at 10-15 cm. Flowers are trimmed, light-violet with small dark-violet spots on an internal surface of four side petals and larger – on a lower lip of a flower (Fig. 5). Productive part of the main escape length is 100-115 cm on which there are from 48 to 60 boxes (Fig. 6). 200-250 of boxes are formed on a plant in total, when maturing crack poorly. Boxes length is about of 25-26 mm (Fig. 7). Seeds mass from one plant – 18-30 g, on some plants is formed up to 45 g. Weight of 1000 of seeds – 2,6-2,8 g. Seeds are light brown color with an extended form (Fig. 8). The productivity is about 17-20 c/hectare without irrigation.

Fig. 7. Sesame boxes of variety Mulatka

Fig. 8. Sesame seeds of variety Mulatka

Take away notes:

- For sesame irradiation doses at which it is possible to receive a high variety of mutant forms with useful signs are defined.
- An initial material for selection is characterized in following plants signs: forms with a length of vegetative period up to 145 days, upright arrangement of escapes, dense arrangement of boxes, plants with an acinaciform boxes with well-developed false partitions which are steady against of seeds fall, different color of seeds, with sterile forms.
- The physical mutagenesis method allows to receive desirable practical results very quickly and especially effective at a limit of initial material variety, for cultures promotion to a nonconventional regions of cultivation for expansion of species areas. Received mutants are of practical interest to expansion of sesame genetic variety in the different directions of selection process. Also, received initial selection material are of interest to physiologists for the purpose of assessment on: drought and salt resistance, to soil reaction and for ecological geneticists for determination of genotypes potential in different climatic zones. In general, received initial selection material will allow to accelerate selection process.

Biography:

Nina Chavdar, graduated from Chisinau agricultural institute named after M.V. Frunze in 1979. From 1980 to 1984 postgraduate study at the Moldavian research institute of the irrigated agriculture and vegetable growing (Tiraspol) where executed researches on a subject: «Manifestation and use of heterosis at hothouse tomato in the conditions of Moldavia». PhD in Agricultural sciences (1986). Till 1993 worked in laboratory of selection of Pridnestrovian scientific research institute of agriculture. Since 1993 till present works at Pridnestrovian state university named after T.G. Shevchenko, Associate Professor of the production technology and processing of agricultural production department, lecturer of genetics and selection of agricultural plants, scientific researches on selection and cultivation of Sesamum indicum L., Silybum marianum (L.) GAERTN., Gyssopium hirsutum L. Leading researcher of the Republican botanical garden (Tiraspol). On materials of researches more than 90 works are published.

CONTENTS

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Biography:

Alexander Rushchuk, Agrarian Dept., Pridnestrovian State Corporative University named after T.G. Shevchenko, Tiraspol, graduated 1996. PhD in Biological sciences (2008, Lomonosov Moscow State University). Associate Professor, head of the production technology and processing of agricultural production department of Pridnestrovian State University, Tiraspol, lecturer (agricultural meteorology, plant growing). Expertise in botany: phytocenological, floristic studies, classification, diversity of steppe vegetation. Training at Turkish Atomic Energy Authority, Sarayköy Nuclear Research And Training Center, Plant Breeding Unit in the field of Induced Mutations And Related Biotechnologies in Plant Breeding (2010). Scientific researcher of Republican research institute of ecology and natural resources, Bendery, «Yagorlic» reservation, Gojany. More than 50 scientific publications.

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Biography

Dr. Yinghua Huang is a Research Geneticist for U.S. Department of Agriculture and serves as the Lead Scientist for the Plant Genetics Program. Before 2002, he served as faculty member for Oklahoma State University for ten years and now remains an Adj. Professor at the university. He serves as a member of editorial boards for several scientific journals. He has published more than 80 research articles. He earned a Ph.D. in Biological Sciences from Michigan Technological University. His scientific background is in plant genetics and molecular biology, and he has considerable research experience in plant biotechnology, genomics, and crop improvement.

Omics approaches to plant genetics and crop improvement

Yinghua Huang
USDA-ARS and Oklahoma State University, USA

Omics sciences represent new disciplines for comprehensive studies of an organism at various molecular levels, and these newly developing omics technologies primarily focus analysis of DNA, mRNA, proteins and metabolites in individuals of life. Thus, the omics sciences have four major components: genomics, transcriptomics, proteomics and metabolomics, and nowadays the integrated omics technologies are revolutionizing the ways we study biology and biological systems. While omic studies in the areas of plant genetics and crop improvement are relatively new, these advancing technologies are the rapidly expanding areas of research and enable a system biology approach toward a better understanding of the sophisticated relationships between genes, proteins and metabolites and the resulted phenotypes. For example, information generated using those technologies allow us to identify genes and related expression products, i.e. proteins and metabolites, that are responsible for host plant defense against harmful insects and diseases and to identify important regulatory networks that are governing innate genetic mechanisms to protect plants from attack by external biotic and abiotic attacks, thus offering valuable information for the development of now crops with rationale design. These powerful omics technologies can complement the traditional crop breeding methods to facilitate crop improvement and efficient development of our food crops that are resistant to various stresses but give higher yield and better nutritional value. These cutting-edge technologies are leading to a true application of molecular knowledges in plant biology and modern sustainable agriculture.

Take Away Notes:

- This report introduces the development of omics technologies and their impacts in studies of plant genetics and crop improvement.
- This presentation will discuss recent progresses and current challenges of omics technologies in relation to their application in plant biology, agricultural, and environmental sciences, which provides valuable insights into the applications of modern omics technologies to real-world problems in the life sciences.
- The audience will acquire the up-to-date knowledge of omics technologies, which will offer them the most efficient, cost-effective tools and environmentally friendly strategy for facilitating crop improvement and ensuring the sustainable agriculture.

Biography

Agronomist engineer and Ph.D in agricultural research, I lead the table grapes team of IMIDA, public institute of agrarian research. We developed a genetic breeding program to obtain new seedless table grapes varieties with the use of biotechnological techniques such as in vitro culture and molecular markers for obtaining hybrids; in the field we use hormonal growth regulators (PGR). Breeder of 17 new varieties of which around 1.000 ha are grown in Spain; the first commercial farms are being planted in Chile, Peru and Australia; and in coming years in South Africa and Brazil; 2 of the varieties have powdery mildew resistance genes, we are now focused on biological agriculture. Speaker at international congresses in Mexico, Chile, Italy, Germany, Brazil, Argentina, Peru and Greece; and poster in Australia, Hong Kong and France.

New table grapes varieties obtained in Spanish breeding program ITUM-IMIDA for the world

Manuel Tornel Martinez

IMIDA & ITUM, Spain

Murcia is the Spanish region that produces and exports the largest amount of table grapes with some European countries consuming a large proportion of the production. 30 years ago the vine growers of our region cultivated local varieties with seeds, then the varietal panorama was transformed with the foreign seedless varieties and since 2013 they are cultivating grapes obtained in our own IMIDA-ITUM breeding program. At present, the partner companies have seventeen new varieties at their disposal that stand out by their crisp texture, of which nine are white, six are red and two are black varieties, and they already cultivate an area that exceeds 900 hectares, equivalent to more than 15% of the regional land devoted to the cultivation of table grapes.

A decade ago, we started a new line of work to obtain disease-tolerant varieties, the result of which is "Itumfifteen" and "Itumseventeen", our registered varieties with genes for tolerance to powdery mildew. Growing them, producers will have less harvest losses and will also save in phytosanitary treatments, consumers will get grapes with less residues, and there will be a considerably smaller environmental impact, all of which aims at achieving a more sustainable type of agriculture.

The development of the new varieties IMIDA-ITUM was initially produced to meet the needs of local farmers, but due to the interest shown by producers from the rest of the world, plant material has been sent to Chile, Peru, Argentina, Brazil, South Africa and Australia.

We need to fine-tune the protocols for introducing plant material from field to in vitro culture of each variety, to make shipments to these countries, in line with the optimization of the in vitro rooting. The pre-selection assisted with molecular markers speeds up the first phase of the breeding program. The cultural techniques in seedless table grapes and management of PGR are tested and developed for each variety.

Take Away Notes:

- With the obtaining of new varieties that have genes of resistance diseases like powdery mildew and mildew, now the producers are focused on biological agriculture.
- The development of the in vitro culture tissues of grape seed sketches improves the results when we use cross seedless varieties, we break statistics.
- The pre-selection assisted with molecular markers speeds up the first phase of the breeding program.
- The cultural techniques in seedless table grapes and management of PGR are totally applicable in other parts of the world.
- Seedless, crunchy texture, extraordinary flavor and color, easy handling and very productive, are the basic characteristics of the grapes demanded by the market, the producer and mainly the consumer.

Biography

Dr.S.Sadasivam completed his Ph.D (Biochemistry) in 1968 at University of Madras, India. He did his Post-Doctoral research at University of Florida and University of California, USA. He worked in various capacities at Tamil Nadu Agricultural University, Coimbatore (1974 – 2003) and Kumaraguru College of Technology, Coimbatore (April 2003 to May'2011).He has Guided 8 students for Ph.D. He has 225 publications in journals and conference presentations. He has published several books and one of them on "Biochemical Methods" is still popular among students studying Biological sciences in India. Another title published in USA "Molecular Basis for Host Plant Resistance to Pests" is used by researchers in this area.

Plant biotechnology: Progress and prospects

Sadasivam Sankaranarayanan

Tamil Nadu Agricultural University, India

Demographic prediction is that by 2050, nine billion people will inhabit this planet and there is an urgent need to plan for food security. Since the beginning of the 20th century various tools have been introduced to increase agricultural productivity. Innovations in biotechnology enabled better interpretation of gene functions for increasing crop productivity through improving resistance to pest and diseases. Biotechnological tools have also been used to improve nutritional values, to produce fresher products and molecular pharming.

Advent of high throughput genomics technologies viz., whole genome sequencing, transcriptome, proteome, metabolome and ionome profiling methods have opened new vistas for development of stress-tolerant varieties. By the end of 2016, >4000 living organisms including >100 major crops have been sequenced and the information are available in NCBI GenBank. Re-sequencing of large number of germplasm in crops viz., rice (3000 genotypes at IRRI, Philippines), Arabidopsis (1001 genomes at SALK Institute, USA) and tomato (150 genome project at Wageningen University, Netherlands) paved way to discover novel alleles of agronomically important genes.

Advanced tools are being developed to produce new plant products with new functions. These tools include synthetic promoters, 'tunable' transcription factors and genome-editing tools like zinc-finger nucleases, transcription activator-like effector nucleases (TALENs) and clustered regularly interspaced short palindromic repeats (CRISPRs). In future, assembly and synthesis of large DNA molecules, plant transformation with linked multigenes and plant artificial chromosomes will be integrated to find solutions to agricultural and environmental constraints. Biotechnology is sure to help to achieve increased productivity to match the population growth.

Take Away Notes:

- Students and young researchers will be exposed to recent applications of biotech tools in crop improvement.
- Audience will be briefed on the progress made through Breeding By Design in developing resilient crop varieties.
- Students and young researchers will gain information on various WGS projects and Genome editing tools.
- Enable private industries to find potential research collaborators.

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DAY 3

SPEAKERS

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Fibrillarin sinteny evolution and viral interactions

Enrique Castano de la Serna[*1]**, Alejandro Pereira Santana**[1]**, Francisco Guillen Chable**[1]**, Stefano Decle Carrasco**[1]**, Andrea Bayona Hernandez**[1]**, Luis Carlos Rodriguez Zapata**[2]
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Fibrillarin known as a RNA methyl transferase that has recently been shown to also methylate Histone H2A. Besides the escential role in the cell, Fibrillarin is also highjack by several virus and it is required for their progression through the floem. Becourse of their relevance and its good level of protein conservation in almost all eukaryotic cells and all archea kingdom we check its evolution. Some plants have had several duplications of their genome and therefore several copies of this protein are present, however our results show the unexpected that their sinteny is maintain showing some interesting genes that have been kept during the different steps in evolution. Here we show its evolution through eukaryotic genomes as well as the changes in sequences that interact with virus.

Take Away Notes:

- Fibrillarin is a essential gene required for methylation and rRNA processing that is required for all protein translation. Changes in this protein have a dramatic impact on cell viability and protein level.
- Here the chromosomal sequences that surround fibrillarin have been analyzed in more than 300 genomes as well as changes that are required for viral progression in plant cells.

Biography

Dr. Enrique Castano de la Serna, receive his Ph.D degree in 1997 from the department of Biochemistry and Biophysics from the University of Rochester, NY, USA. After one year postdoctoral in MCB at Harvard University in Boston, he did 4 Years of Postdoctoral fellow at the Mary Curie Research Institute in the field of transcription. In 2002 he started a position in the department of Biochemistry and Molecular Biology in the Centro de Investigacion Cienfica de Yucatan, Where he is currently a senior professor in Molecular Biology. He has publish 50 Research articles in index journals and has graduated 10 Ph.D students.

A novel approach to enhancing grain yield in acid soils prone to extreme water regimes

Hossein Khabaz-Saberi*, **Zed Rengel**
UWA School of Agriculture and Environmental Science, University of Western Australia, Australia

Toxicities of Al, Mn and Fe in acidic soils (40% of global arable land) are major constraints to growing intolerant crops. The transiently induced high-to-toxic concentrations of Al, Mn and Fe under reduced soil conditions during wet season (waterlogging) hinder root growth, delay maturity and, if coincided with terminal drought, exacerbate the yield loss. Soil acidification is on the rise, and the future climate changes predicted to include intense winter rainfall (inducing reduced soil conditions), followed by high temperature and drought toward crop maturity, accentuate the importance of solving the problem of poor tolerance of most crops and varieties to ion toxicities induced in acidic soils subjected to transient waterlogging.

We have pioneered the idea of improving the wheat grain yield in acidic soils prone to transient waterlogging and terminal drought via enhanced tolerance to combined ion toxicities (Al, Mn and Fe). We have provided evidence that improved tolerance to individual ion toxicities can increase grain yield by 10% in acidic soils prone to transient waterlogging (Khabaz-Saberi and Rengel 2010; Khabaz-Saberi, Barker and Rengel, 2012) and terminal drought (Khabaz-Saberi, Barker and Rengel, 2014) following optimisation of screening techniques for tolerance to ion toxicities in wheat germplasm (Khabaz-Saberi et al. 2010a; Khabaz-Saberi et al. 2010b). Our research has demonstrated that genotypes tolerant to ion toxicities responded better to lime application than intolerant genotypes (Khabaz-Saberi, Barker and Rengel, 2014) and that induced ion toxicities are not confined only to waterlogged acid soils in the high-rainfall zones, but also occur in the low-to-medium rainfall areas during wet seasons. We have produced the required tools, including mapping populations from parents distinct in ion toxicities, for producing molecular markers to be used in marker-assisted selection. Moreover, pyramiding tolerance to multiple toxicities in commercial wheat genotypes will widen their environmental adaptability and result in increased yields under a variety of soil/water conditions.

Take Away Notes:

- The target audience will learn about dynamic soil-water-plant interactions occurring in acidic soils that constraint crop growth in 40% of world arable land, with a particular emphasis on the changes in soil chemistry under waterlogged (reduced) compared with aerated (oxidized) conditions.
- The audience will be able to learn and use our approach of tackling the constraints from early observation of the phenomenon, its validation, substantiation of the importance and provision of the required advanced tools to alleviate similar problem.
- Our genetic approach to solving the problem of poor crop growth on acidic transiently-waterlogged soils (including germplasm screening, mapping population production and trait pyramiding in commercial varieties) will enhance the knowledge of using theoretical genetics knowledge in the real-world situations where the success will translate into huge increases in agricultural profitability and sustainability.
- The output of this research could be used in teaching (soil science, plant nutrition, plant breeding and molecular genetics) to update and revise the current knowledge and approach of tackling the constraint of growing crops in acid soils successfully and profitably.
- Our innovative integrative approach could be employed in research addressing problems associated with environmental adaptability in wheat and other major crops.
- We do also welcome collaborative work toward progression and accomplishment of the current research work which is currently hindered by lack of research funding.

Biography

Dr. Saberi obtained B.Sc. and M.Sc. at University of Pahlavi Shiraz and the Tehran University, received his early career trainings at ICARDA and CIMMYT, and worked with Iranian cereal improvement program for 15 years. He received his PhD at the University of Adelaide (Australia) in 1998. He spent 2 years as a postdoc at Cooperative Research Centre for Molecular Plant Breeding in Adelaide. After that, he worked at Department of Agriculture Western Australia and the University of WA. He recently pioneered the idea of increasing wheat tolerance to ion toxicities (Al, Mn and Fe) to enhance grain yield in acid soils prone to waterlogging and drought.

CONTENTS

Probiotic microorganisms in the rhizosphere of agricultural plants

Nadezhda Verkhovtseva*[1] Marina Lukianova[1], George Osipov[2]
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Microbial metabolites and plant exudates are the main regulatory mechanisms of the relationship between agricultural plants and the community of soil microorganisms. The presentation of the report will present experimental materials on the content of bacteria with probiotic properties in the rhizosphere of corn, potatoes and sugar beet anaerobic gg *Bifidobacterium* and *Lactobacillus* as the most well-known genera with favorable properties for human health. The dependence of their number on the soil type and their properties, such as acidity and organic matter content, will be considered. It is shown that the number of specific bacteria depends on the yield, apparently, on its root exudates. To study the soil microbial community, a method of microbial diagnostics based on gas chromatography – mass spectrometry of fatty acids, hydroxy acids and fatty aldehydes – was used. Mass spectrometry of the microbial markers method (MSMM) allows you to simultaneously determine more than one hundred microbial fatty acids in situ in clinical, biotechnological or environmental samples without prior cultivation and biochemical analytical materials and primers. This allowed us to quantify 35-40 species of bacteria, including anaerobic bacteria in microbial communities of agricultural soils. Anaerobic bacteria g.g. *Bifidobacterium* and *Lactobacillus* did not correlate with the amount of Corg. in the studied soils. Bacteria g. Lactobacillus sp. was identified only in the acidic soils of arable land and bare steam. In separate studies on sandy sod-podzolic sand (humus = 0.8%), lactobacilli (13%) in the NPK + lupine variant prevailed. *Bifidobacteria* were present in quantities of more than 5% on arable land and on the field. Lactobacilli have not been identified in the maize rhizosphere soil. However, in the maize rhizoplane, the amount of lactobacilli reached 2.6%, while bifidobacteria are ten times less. Thus, the number of specific bacteria depended on the culture cultivated in the rotation. High concentrations of *Bifidobacterium* were found in the rhizosphere of potatoes in all studied soils. Mycorrhizal fungi of the genus Gigaspora were also found for all cultivated plants. The possibility of including these types of bacteria in agricultural biological products is discussed.

Take Away Notes:

- The subject matter: What do we know about probiotic bacteria in the soil, which are believed to have an important role in health and fertility of soils? This concept of probiotic bacteria came to environment researches from medical practice.
- The quantity of specific bacteria depends on the crop cultivated in the rotation – from roots' exudates which initiate and modulate dialogue between roots and these soil microbes.
- Probiotic role of *Bifidobacterium* species was the formation of soil nucleus aggregates. Is it possible to include this species in agricultural supplements? How to do it?

Biography

Dr. N.Verkhovtseva studied Agrochemistry at the Lomonosov Moscow State University (MSU), Russia. After graduation, she entered the graduate school of the same university and received her PhD degree in 1975. She then taught at Yaroslavl State University, Yaroslavl, Russia. She then joined the research academic group of Kondrat'eva at the MSU. She received her degree Doctor of Science (microbiology) in 1994 at the same university and the title and position of professor at the Department of Agrochemistry and Plant Biochemistry, Faculty of Soil Science, Moscow State University. She has published more than 140 articles in journals and collections of articles in Russian and foreign journals, SCI (E) 36.

How harvest date affect physiological status of *Miscanthus × giganteus* and *Miscanthus* seed-based hybrids cultivated on heavy metal contaminated arable land?

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Renewable energy and bioeconomy targets are set to increase market demand for lignocellulosic biomass in Europe. Different environments and end uses, i.e. combustion vs. conversion to liquid fuel, will require the introduction of much more diverse energy crop varieties. As there are different conversion technologies the harvest date will vary depending on the selected process. The harvesting of the lignocellulosic biomass for the anaerobic digestion required green plants. This required earlier harvest date and may cause disturbance in the senescence process which might affect the plantation efficiency in the following years. The aim of this study was to assess *Miscanthus × giganteus* (Mxg) and two *Miscanthus* seed-based hybrids (GNT41, GNT34) physiological status in the following year after autumn harvest (October) when compare to the regular harvest time (March). A field trial was established in 2015 on arable land contaminated in the past with Pb, Cd and Zn from nearby metal smelting industry in Southern Poland. The trial design was a complete randomized block including three replicates. At the end of the second growing season half of each plot was harvested green in October (2016), while the other half in March (2017). During the following growing season (2017) gas exchange, chlorophyll content, Nitrogen Balance Index as well as prompt chlorophyll a fluorescence measurements were performed twice at the beginning of July and September. Data obtained from chlorophyll fluorescence were used to calculate JIP-test parameters. A the end of the growing season (October) samples for analysis of N, P, K, Pb, Cd, Zn concentration in above-ground biomass were collected. Additionally, measurements of shoot height shoot die of height and stem number were performed. GNT41 was the most affected variety by the previous year green harvest, what appeared as lower shoot height, delayed senescence as well as the reduction of the photosynthesis intensity (Asat), intrinsic water use efficiency and fluorescence parameters in July. The nitrogen content was the main factor conditioning differences between green and brown harvest, thus impact photosynthetic apparatus. Green harvest in all of the investigated plants was associated with the lower nitrogen concentration and was more pronounced later in the growing season, what was particularly reflected in chlorophyll content and differences among JIP-test parameters. Lower values of the Asat for brown harvested Mxg and GNT41 during September measurements might be associated with the shift of the growing season in time, what could be observed in the delayed senescence in case of those two varieties.

The University of Costa Rica financed this work (801-B7-294).

Take Away Notes:

- Presented work had strong practical implication as it refer to the energy crops cultivated in the field conditions.
- This work may indicate features of plants which denote unsuitability for the autumn harvest.

Biography

Szymon Rusinowski studied Biotechnology at the University of Silesia, Poland and graduated as MS in 2015. Afterwards, he joined the research group of Dr. Marta Pogrzeba at the Institute for Ecology of Industrial Areas, Poland. Since now he participated as contractor in two European projects Phyto2Energy (2014-2018) and MISCOMAR (2015-2019). In 2018 he open doctoral dissertation at the Warsaw University of Life Sciences (SGGW) under Dr. Hazem Kalaji supervision. He has published 7 research articles in JCR journals.

Defense-related reprogramming in *Sorghum bicolor* against infection by *Burkholderia andropogonis*: a metabolomics study

Ian Dubery*, **Charity Mareya, Fidele Tugizimana, Lizelle Piater**
Department or Biochemistry, University of Johannesburg, South Africa

Background: *Burkholderia andropogonis* is the causal agent of bacterial leaf stripe, one of the three major bacterial diseases affecting *Sorghum bicolor*. However, the biochemical aspects of the pathophysiological host responses are not well understood. An untargeted metabolomics approach was designed to understand molecular mechanisms underlying *S. bicolor–B. andropogonis* interactions. At the 4-leaf stage two sorghum cultivars (NS 5511 and NS 5655), differing in disease susceptibility/ resistance, were infected with B. andropogonis, and the metabolic changes monitored over time.

Results: The NS 5511 cultivar displayed delayed signs of wilting and lesion progression compared to the NS 5655 cultivar, indicative of enhanced resistance. The metabolomics results identified statistically significant metabolites as biomarkers associated with the sorghum defence. These include the phytohormones salicylic acid, jasmonic acid and zeatin. Moreover, metabolic reprogramming in an array of chemically diverse metabolites that span a wide range of metabolic pathways was associated with the defense response. Signatory biomarkers included aromatic amino acids, shikimic acid, metabolites from the phenylpropanoid and flavonoid pathways, as well as fatty acids. Enhanced synthesis and accumulation of apigenin and derivatives thereof, was a prominent feature of the altered metabolomes.

Conclusions: The analyses revealed an intricate and dynamic network metabolic pathways and metabolites comprisingthe sorghum defence arsenal towards B. andropogonis in establishing an enhanced defensive capacity in support of resistance and disease suppression.

Take Away Notes:

- Application of metabolomics tools and approaches in Plant Science.
- New knowledge regarding sorghum defense responses.
- Research that other faculty could use to expand their research or teaching.

Biography

Prof. Ian Dubery received his PhD in 1982 and has since published more than 140 research papers in ISI-listed international journals. His interest are plant-microbe interactions, plant defense responses and plant metabolomics. He is a council member of the South African Society for Biochemistry and Molecular Biology (SASBMB) and the director of the Research Centre for Plant Metabolomics at the University of Johannesburg, South Africa.

Studies on effect of herbal extract *Samved Fugall* (CO_2) absorbent on Cotton

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An experiment entitled, "Studies on effect of herbal extract *Samved Fugall* (CO_2) absorbent on Cotton." cv. Bunny Bt BG II at Agricultural Research Station, Dharwad, Karnataka, India was carried out with objectives to study the effect of Samved Fugall on growth, yield and also to quantify the influence of foliar application of fugall on gas exchange and phenology in Bt cotton hybrid. The experiment comprised seven (7) treatments with three (3) replications laid out in Randomised Block Design. The results of experiment revealed that the treatment RD + foliar application of Samved Fugall @ 2ml/lit (60 and 90 DAS) recorded significantly high yield (1084 kg/ha) over control (824 kg/ha) and other treatments. In the same treatment the number of bolls/plant (18.30), plant height (48.20cm) and total number of leaves (40.90) were significantly higher than control and other treatments. In the same way days taken for 50% squaring, days taken to 50% flowering were significantly less in the same treatment than control. The same treatment showed significantly more no. of sympodia (13.80) than control RD (12.40). Foliar application of Samved Fugall @ 2ml/lit (60 and 90 DAS) recorded significantly more photosynthesis rate before spray (at 90 DAS) (18.23). The photosynthesis rate was highest after spray (at 110 DAS) (22.6). Untreated control recorded significantly least photosynthesis rate at all stages. Leaf area index, SPAD values (chlorophyll content) were also significantly more than untreated control.

It appears from the results that foliar application of *Samved Fugall* @ 2ml/lit water at 60 and 90 DAS recorded significantly more yield. This has been supported from the physiological observations like rate of photosynthesis, leaf area index, total number of leaves, plant height and more number of sympodial branches including yield component viz. boll weight and number of bolls/plant.

An optimistic foresight of micro-algal biotechnology

Ruma Pal
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Microalgae are most primitive oxygen evolving photosynthetic organisms appeared 3.2 billion years ago growing in almost all environmental conditions. They are with simplest morphology, without having root, stems or leaves and having naked reproductive structures ranging from unicellular, colonial, simple filamentous form .Algal Biotechnology have had a long history especially in the food industry initially used by people of China (eg. Nostoc Commune) .Microalgae are the inexpensive source of different bioactive compounds like, carotenoids, pigments, proteins and vitamins etc., which are being used recently for the production of nutraceuticals, pharmaceuticals, animal feed additives and cosmetics.

Due to their aquatic habitats algae are widely used in the commercial rearing of many aquatic animals, especially the fishes and penaeid prawn larvae either in live form or as feed ingredients of 'Value added feed'. Due to coastal water pollution and other factors there is a continuous decline in natural fish catch, which has led to an ever increasing focus on aquaculture. Application of different microalgae from Sunderban –the largest Mangrove Forest as value added feed ingredients for colored fishes carp fishes at field level would be discussed.

Algae have their inherent capacity for phytoremediation of toxic chemicals. Over the past few decades a significant

attention has been paid to toxic and precious metal removal employing phycoremediation technique for environmental protection. Different selectivities of various algae towards different metals are generally exploited in precious metal separation process and removal of toxic metals including stable metals and radionuclides .Therefore, Phycoremediation or use of algae as bio-reagent in metal removal process is considered as one of the most suitable methods for environmental management. Use of local strain, Leptolyngbya valderiana in arsenic removal process to be discussed using a designed Biofilter and their mechanism is an interesting study of Algal biotechnology.

Phyco-nanotechnology is another promising field of algal biotechnology, where exploiting algal biomass as bioreagent, several metal nanoparticles like gold, silver,Fe,Cu and Cr and their alloys can be produced in green technology based process and their use in different fields ,like antibacterial, anti-cancerous and in fruit preservation appeared to be very effective.

For any biotechnological program local strain exploitation is more effective, therefore algal diversity study and the cultivation of potential strains at field level would be discussed as prerequisite of Algal biotechnology.

Biography

Dr. Ruma Pal, Professor in Algology, Department of Botany, University of Calcutta, India, did her Masters and Ph.D. from the same University in 1989 and joined as in charge teacher in 2000. She is the 'Fellow of West Bengal Academy of Science and Technology'India. She has an experience of 35yrs in the field of Algal Biotechnology and also explored Algal diversity from different niches. Scope algae in Nano-biotechnology, Bioremediation, Aquaculture, cancer biology, and CO2 sequestration is her field of research. Prof Pal has completed 15 Govt.projects published 125 researches papers, writer of 3 books, 3 patent holders and produced more than 12 Ph.D. students.

Phytoplankton diversity of two different ecological niches in relation to physico-chemical parameters

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The 'Phytoplanktons', floating or drifting organisms of plant origin, constitute the basis of nutrient cycle of aquatic ecosystem. Being primary producers they play an important role in maintaining the equilibrium between living organisms and environmental variables. Cyanobacteria and other eukaryotic planktonic algae like Dinoflagellates may create massive blooms in eutrophic water bodies throughout the globe, causing harmful algal bloom (HAB). HAB critically alter ecosystems through hypoxia/anoxia, food web efficiencies, stimulation of pathogenic bacteria, or other ecological consequences. However, formation of toxic algal blooms in water bodies depends on variations in nutrient and other physico-chemical parameters. In the present investigation, it was aimed to survey two different water bodies of different ecological niches of Eastern India, such as domestic pond at Serampore (22.8893N, 88.38385E) and manmade water body, Rabindra Sarobar Lake(22.5121N, 88.3637E) for nutrient dynamics study in relation to phytoplankton diversity and bloom formation. Correlation between physicochemical parameters like pH, temperature, pond depth, BOD, COD, DO, nitrate, nitrite, ammonia, phosphate, sulphate, alkalinity and the phytoplankton productivity in terms of total chlorophyll content was performed by Pearson's (r2 value) correlation coefficient to detect bloom formation. The most dominant group recorded in the domestic pond (site I) was Chlorophyceae, but in site II cyanobacteria were predominant. Both the sites showed almost similar temperature variations and light intensities at pre-monsoon (March–May), monsoon (June-July), post-monsoon (Aug-Oct) and winter period (Nov-Feb). The pH of water body of site II was almost same throughout the seasons (ranging from 7.8 – 8.0), whereas it varies in different seasons in site I. The BOD and COD values of each pond vary with climatic conditions – being highest during pre-monsoon and lowest during post-monsoon period. The DO and silica levels were comparatively higher in site II, but ammonia, nitrate and phosphate contents were more at site I. Seasonal changes in phytoplankton diversity in relation to chemical parameters of the study sites would be discussed in detail for early detection of bloom.

Take Away Notes:

- This study shades light on changes in phytoplankton population with biotic and abiotic parameters. The audience will gather knowledge about the ecological condition leading to harmful algal bloom. The planktons are the primary producers of aquatic ecosystem. So presence of non-toxic planktons facilitates pisciculture, whereas toxic blooms are harmful for both fishes and humans. This type of study can give prior information about toxic algal bloom formation.
- This study will be helpful for the researchers working in the field of ecology and ecosystem, as well as it will be beneficial for the common people. Audience can gather knowledge about phytoplankton diversity in artificial water bodies like swimming pools and they can be cautious about the deleterious effects of toxic phytoplanktons on human body.
- They can use the research protocol to study the ponds of their locality and can be able to forecast the water quality of ponds based on phytoplankton diversity.

Biography

Mr. Partha Talukdar studied Botany at the University Of Calcutta, India and completed his M.Sc. in 1998. Then he was engaged in several research projects. He Joined Serampore College, India as Assistant Professor in 2004. Now He is the Head of the Department of Botany, Sermpore College and Senior Faculty of Post Graduate section of Serampore College. He has published more than 20 research papers in peer-reviewed international journals. In addition to teaching, he is pursuing his Ph.D. degree from Phycology Lab of Department of Botany, University of Calcutta under the guidance of Prof. Ruma Pal.

Effect of enhanced solar UVB (280-320 nm) radiation morphology, photosynthetic pigment and synthesis bioactive compounds in medicinal plants

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UV-B is the primary environmental factor in tropical region to stimulate growth, development and induction of secondary pigment synthesis in medicinal plants. The studies on UV- in medicinal plants are very less particularly with respect of UVB induced bioactive compound in plants. In the present study, the traditional medicinal plants like Achyranthes, Acalypha and Phyllanthus were subject to UV-B radiation under field condition and assessed the harmful effect on morphology, photosynthetic pigment synthesis and accumulation of bioactive compounds at different ages. There is no significant changes were seen the morphology of the plants. Rather than negative effect the UVB radiation to promote the growth of Phyllathus from early to later stages of the plant. Whereas, in Acalypha and Achyranthes in early stage showed slight inhibition but later stage it recovers from such inhibition and lead to a normal life. The chlorophyll and carotenoid synthesis did not demonstrate any significant impact by UV-B. The phytochemical analysis of dried leaf methanol extracts of individual plant showed the presence of flavonoids, anthocyanin, alkaloids, phytosterol, saponin, tannin and steroids. Further examination of TLC also reveled quantitative and qualitative difference in bioactive compound profile. They were additionally confirmed by few significant chromatographic peaks of GC-MS analyses. This examination inferred that the UVB stress is a more intense factor to increasing concentration of active components in medicinal plants. In future the UVB induced bioactive components is more essential potential herbal drug for human healthcare.

Biography

Dr. N. Shanthi is the Assistant Professor, PG and Research Department of Botany, Pachaiyappa's College, Chennai, India. She has one decade of Post Graduate teaching and Research experience in the field of Stress Physiology. She has completed one research project. She has signed an MOU in 2018 with SynkroMax Biotech Pvt Ltd., Chennai, for research and exchange of faculty and research scholars. She has published 1 books and 25 papers in national and international journals. She is a reviewer for many international journals. She has also presented the paper at the International conference in Malaysia and Singapore. Recently She has received Outstanding Scientist Award for Initiatives, Discoveries, and Developments in the discipline of Botany from Venus International Foundation, Chennai and Distinguish professor awards fromAIMIST University,Kedah,Malaysia.

Phycoremediation of tannery waste using cyanobacteria as bioreagent with special reference to nano chromium formation

Iman Dey* **and Ruma Pal**
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Tannery wastewater carry heavy pollution load due to high organic and inorganic contents, highly colored compounds and toxic metallic substances. Characterization of this water from inlet point showed high level of BOD (1234.33 mg/L), COD (1706.64 mg/L), Total Chromium (56.85 mg/L), TDS (6984mg/L), sulfide (140.8 mg/L) and ammonium (134.5 mg/L). These values were several folds above the standard limits set by ISI (2000). From the present investigation it was found that Cyanoprokaryotes efficiently removed toxic metals on one hand and nutrients on the other hand from tannery wastewater. In this investigation marine Cyanoprokaryote Phormidium valderianum was grown in various dilutions including raw tannery wastewater of leather complex, Eastern India in open tank (4.0 L with depth of 15 cm and the breadth of 25 cm). The cyanoprokaryote was found to be efficient in removing nitrate and phosphate by 90% and 76% respectively from raw wastewater. Dissolved oxygen increased by 10 folds in all dilutions of Tannery Wastewater. Efficiency of ammonia removal (84%) was found to be maximum in case of 50% dilution. The growth performance of exposed biomass was measured in terms of dry weight and Chlorophyll content. Surface topography and distribution of elements adsorbed in algal biomass was analyzed with SEM and EDAX study. The functional groups of the algal biomass before and after treatment were investigated through FTIR spectroscopic study. Atomic Absorption Spectroscopic analysis of treated algal biomass showed significant amount of chromium removal from wastewater and formation of nano chromium was determined using UV-VIS spectra in an in-vitro exposure of algal biomass to potassium dichromate solution. The Scanning and Transmission Electron Microscopy study revealed cluster of rod shaped nano chromium formed by the cyanobacterial biomass. Detail characteristic features of nano chromium would be discussed.

Take Away Notes:

- Efficiency of marine Cyanoprokaryote in removing toxic compounds from tannery wastewater.
- Nano chromium formation by Cyanoprokaryote.
- Characteristics of nano chromium formed by marine cyanoprokaryote.
- Chromium removal capacity of Phormidium.
- Type of functional groups of Phormidium biomass involved in chromium removal.
- Algae based treatment of tannery wastewater in large scale could be a future prospect.
- Chromium nanoparticles can be used in various electronic applications.

Biography

Miss. Iman Dey completed her graduation in Botany in the year of 2014 from Scottish Church College, University of Calcutta and her rank was Fifth. She completed her post-graduation from University of Calcutta in the year of 2016. She then joined Phycology Laboratory of University of Calcutta under guidance of Prof. Ruma Pal.

Importance of plant growth regulators in table grape production

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Use of plant growth regulators have become a very common practice for the grape growers of India for achieving high quality export grape production. To increase export quality grape production proper management of nutrients, canopy and judicious use of plant growth regulators (PGR's) are the ways for grape growers and among these use of PGR's are more responsive and effective to achieve target productivity and quality of grapes and every aspect of plant growth and development is controlled by plant hormones. In addition to naturally occurring hormones, a number of synthetic PGR's like, hydrogen cynamide, forchlorfenuron (CPPU), 6-benzyl amino purine (6-BA), 1-naphthyl acetic acid (NAA), Chlormequat chloride (CCC), gibberellic acid (GA3) etc. are being used in modern viticulture. These growth regulators (PGR's) are generally used in grape for various purposes viz. increasing fruitfulness, inducing bud break apart from increasing rachis elongation for production of well filled bunch, berry setting and also for increase in berry size besides quality improvement & increase in shelf life. With the application of these PGR's there is always risk of residues in grapes particularly the CCC, which is stable compound hence its use is restricted. There is no problem of any kind with the application of other PGR's. Hence in brief it is confirmed that the Indian grapes are free from residues of PGR's.

Take Away Notes:

- The audience will be able to understand the role of PGR's in table grape production.
- Improved production in respect to yield, quality or residue free will increase the net profit of the grower's.
- Able to standardized the dose of plant growth regulator for new promising varieties.
- Able to understand the export scenario of table grapes.

Biography

Dr. S. D. Ramteke received Ph.D (Crop Physiology) from University of Agril. Sciences, Dharwad, India and become a pioneer in "Use of bioregulators in viticulture, stress physiology in grapes" and "studies on physiological disorders in viticulture" has extended his services on food safety and enhanced export of table grapes for 20 years. Dr. Ramteke joined ICAR-NRC Grapes as an ARS in Plant Physiology during 1996 and working on crop physiology, bioregulators, water stresses and canopy management. He is life member of five of scientific societies including ISPP, Annals of Plant Physiology, Indian Journal of Horticultural sciences, Journal of Advance horticulture, NESA, and published more than 80 research papers, 200 popular articles, covering 5 book chapters/reviews, 6 books.

An Investigation on cyanobacteria based nano-iron production and their characterization

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Biogenic production of gold, silver and some other metal nanoparticles have been extensively explored using algae and cyanobacteria. However, these photosynthetic organisms have been less investigated for their nano iron biofabricating potency. Selected strains Leptolyngbya valderiana and Lyngbya sordida were screened for their nano-iron synthesizing capacity by exposing them to 0.01M $FeCl_3$ solution for four days. The biomass as well as the cell-free suspensions has shown a significant change of color from yellowish to brownish as a result of transformation to nano form both in the intracellular and extracellular regimes. The particles were initially characterized using UV-vis spectroscopy, Scanning Electron Microscopy (SEM), Transmission Electron Microscopy (TEM) and Energy Dispersive X-Ray Analysis (EDX) study. In the case of L. sordida and L.valderiana intracellular particle dimensions were 22.92×19.12nm and 47.42×7.7nm, whereas extracellular particle dimensions were 49×10.36nm and 66.37×12.49nm respectively with a spindle-shaped morphology. The particles were zerovalent (Fe0) as found from EDX study. Cellular sections under TEM revealed exact location of the particles in the cells. The extracellularly synthesized particles have shown a relatively larger dry size as inferred from their TEM analyses. The size discrimination between the two species and their intracellular and extracellular compartment was also reflected in hydrodynamic size analysis using Dynamic Light Scattering. The particles were monodisperse having poly dispersity index (PDI) values within 0.2-0.4. The dry sizes, as well as hydrodynamic sizes, showed a species-specific as well as a compartment-specific size distribution pattern. Electron microscopic characterizations have revealed magnetic force of interaction between the particles depicted from their arrangement like typical magnetic dipoles. The property was confirmed when the particles were exposed to a static magnetic field (SMF) exposure. For intracellular particles, 1-2 fold and extracellular particles 4-5 fold increase in hydrodynamic size was observed with also increase in PDI values to 0.4-0.5. The nano-irons were found to be fluorescent as inferred from the fluorimetric analyses. Interestingly a rise in fluorescence was seen after SMF exposure for 10 mins which may be due to a magnetic field induced clustering effect. SQUID-VSM analyses of intracellular nano irons of L. valderiana were carried out for magnetic characterization.

Such a compartment-specific magnetic and fluorescent nanoparticle synthesis is an interesting approach where the microbial biomass is producing 40-50mg particles/g tissue. Another major focus is the scaling up of the process to increase the production of nanoparticles with high medicinal value.

Take Away Notes:

- Cyanobacteria mediated green nanotechnology will be discussed in detail and anyone who will be interested in this work can go ahead with other algae mediated nanoiron synthesis.
- The iron nanoparticles can be investigated further in detail, the uptaking and nucleation of nanoiron can be studied.
- This can be taken as an alternative approach of chemical synthesis of nanoiron. It will pave a new way towards environmentally benign nanoiron production.
- Considering the fluoromagnetic nature of the particles, it can be used to design MRI contrast agent.

Biography

Smt. Sreemanti Banerjee completed both her graduation and post-graduation degrees in the field of Botany from University of Calcutta in the years 2012 and 2014 respectively. She has presently joined the research group under the kind guidance of Prof. Ruma Pal (C.U.) as CSIR-NET –junior research fellow in 2016. Recently she has been promoted to senior research fellow (SRF) with a publication in an international peer-reviewed journal.

Strategies for improving artemisinin content in the engineered *Artemisia annua* plant

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Artemisinin, an endoperoxide-containing sesquiterpene lactone isolated from *Artemisia annua* L., is extensively used in treating malaria. The artemisinin-based combination therapy (ACT) is recommended by World Health Organization (WHO) to combat the drug-resistant malaria. China's pharmacologist Youyou Tu received 2015 Nobel Prize in Physiology or Medicine due to the finding of artemisinin. However, the artemisinin content in A. annua is low (0.01-1% dry weight, DW), and the demand for artemisinin is huge (180-200 tons/year). In addition, although the artemisinin biosynthesis in A. annua is almost elucidated, how artemisinin biosynthesis is regulated is poorly known. Here, we report the development of multi metabolic engineering strategies to increase artemisinin content in A. annua. The strategies include over-expressing artemisinin biosynthetic pathway genes, downregulating the competitive pathway genes, indirect regulation, transcriptional regulation, increasing glandular trichome density and transporting strategy. Using these strategies, we have developed extremely high artemisinin content engineered A. annua lines in which the artemisinin content reached 2-3% (DW), which are in the field trial in Africa. In addition, we have identified and functionally characterized a number of transcription factors which can work alone or form the complex to regulate artemisinin biosynthesis and trichome initiation. These achievements, combined with efforts of the newly established Artemisinin Industrial Alliance comprised of all major Artemisia growers, artemisinin and ACT producers in China, will fundamentally solve the unstable artemisinin supply problem and guarantee the world the constant supply of artemisinin at low price to combat malaria.

Take Away Notes:

- The audience will learn possible strategies for improving valuable specialized metabolites in plants.
- The audience will know the price of artemisinin can be further reduced through technique advance.
- The audience will learn state-of-art techniques for metabolic engineering and metabolic regulation.

Biography

Dr. Kexuan Tang is the distinguished professor at Shanghai Jiao Tong University, China. He got Bachelor degree from Sichuan University in 1985, master degree from Beijing Agricultural University in 1988, and Ph.D degree supervised by Prof. Edward C. Cocking from University of Nottingham, UK in 1996. From 2007 to 2009, he did his postdoctoral research at John Innes Research Centre with Dr. Paul Christou and University of California-Davis with Dr. Pamela Ronald. He was awarded honorary doctorate by Linnaeus University, Sweden in 2012. He has published over 300 papers in SCI journals and has over 200 patents filed or granted.

CONTENTS

Characterization of nano-structured siliceous frustules of *Amphora sp.* and application in nanodevices

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Diatoms are unicellular photosynthesizing algae having unique shells made up of siliceous materials covering the cell, called "Frustule". Chemically the frustules are inert being made up of silicon dioxide–mainly nano patterned silica acting as nanofabrication factories. The objective of the present work was to develop a nano electronic metal-insulator-semiconductor (MIS) device by using biogenic diatom based silica which can be an alternative route to achieve gate dielectric applications. Also, effort was given to optimize the growth recipe of Diatom-SiO_2 ultra thin film by varying growth temperature, time and Au layer thickness. The first step of the work was characterization of Amphora frustule being isolated from east coast of India. The structure analysis, optical and chemical characterization of the frustules have been investigated through UV-Vis, SEM, FESEM, TEM, EDS, FTIR, Confocal laser scanning microscope, spectrofluorimeter and cathodoluminescence studies. Electron microscope images gave a clear picture of the surface topology and intricate morphology of the nano-sized silica framework of the species and its ultra-structural pattern. The maximum absorbance of the frustule was around 230nm as revealed from Uv-Vis spectroscopy. The frustules of Amphora have both photoluminescence and cathodoluminescence property and the maximum absorbance was centered around 460-470nm, whereas confocal microscopic pictures revealed strong autoflourescence property of it when viewed under FITC filter. After proper characterization of the frustule a high-quality crystalline thin film (~22 nm) of biogenic SiO_2 was grown on p-Si (100) substrate by employing the vapor-liquid-solid (VLS) method. The biogenic amorphous silica was used as a source material in VLS growth technique. The formation of crystalline silicon dioxide films was confirmed by X-ray diffraction study and surface morphology being analyzed by FESEM study. Also, the optical properties like absorption coefficient, extension coefficient reflective index were studied by employing spectroscopic ellipsometry. The thickness of the film was also confirmed by ellipsometric measurements. The capacitance-voltage characteristics of Al/biogenic SiO_2 film/p-Si metal-oxide-semiconductor (MIS) capacitor indicated the growth of excellent thin film of diatom-SiO_2 with high effective dielectric constant. The performances of newly formed MIS fabricated device were investigated in detail by measuring effective oxide thickness, hysteresis and frequency dispersion showing good results. Thus, this work provides a cost-effective novel alternative technique to grow high-quality 'Diatom-SiO_2 films' on p-Si substrate which may be used as the reliable gate dielectrics on semiconductor-based MIS devices and circuits.

Take Away Notes:

- Detailed characterization of the Amphora frustules and its potential ability would be discussed in detail.
- Green technology based biogenic silica of diatom origin being applied in the field of electronics to develop a semiconductor-based MIS device has been characterized and studied thoroughly.
- This work provides a cost-effective novel technique to grow high-quality '**Diatom-SiO_2 films**' on p-Si substrate which may be used as an alternative technique for achievement of reliable gate dielectrics on semiconductor-based MIS devices and circuits.

Biography

Mr. Rahul Bose has completed his bachelor's in Microbiology in 2011 from University of Calcutta and completed his Masters in Marine Science in 2013 from the same University. Later he joined the Phycology laboratory of Department of Botany, University of Calcutta as Junior Research Fellow under the Supervision of Professor Ruma Pal. He has published two papers in international peer-reviewed journals.

New strategies in clonal micropropagation of fruit crops

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Traditionally, clonal micropropagation of fruit crops is implemented in 5 stages: introduction to culture, bud proliferation, elongation of shoots, rooting of micrografts, and adaptation of microplants to non-sterile conditions. Many attempts have been made to modernize this well-known scheme, especially its last stages. For example, it was proposed to carry out rooting of microchips not on an agarized nutrient medium, but on a solid substrate of different composition, both under sterile conditions and non-sterile, while solving simultaneously the problem of adaptation. The greatest difficulties arise with woody fruit trees, such as, apple, pear, sweet cherry, plum, sour cherry, because these crops need a period of rest. Adapted microplants of these species can be obtained in large quantities, but special conditions and special techniques are required so that they can be transferred to open ground. These plants, as a rule, have a very inconvenient size for work (stem length is 2-5 cm) and do not survive well after transplantation. For this case, we have developed a technique of triple simulation of the rest period during a calendar year and alternating it with periods of growth. Such work is performed using the greenhouse with a temperature regime of + 18 ... + 22 0C and a refrigerating chamber with a temperature regime of + 1 ... + 6 0C. According to this strategy, without leaving the greenhouse for the calendar year, you can grow plants of sweet cherry, plum, and sour cherry to a height of 100-120 cm.

For berry bushes (raspberries, blackberries, honeysuckle), as well as grapes, combining the elongation and rooting stages proved effective. Microshoots with a length of 0.5-1.0 cm were planted on a nutrient medium with a low concentration of cytokinin. 250 ml flasks were used as cultivation vessels, and micrografts were planted with 10–12 pieces each. Within 1.5 months microplants reached a height of 5-7 cm, at the same time their spontaneous rooting occurred, even in those varieties that were previously difficult to root using auxins.

Mass successful adaptation of grassy plants (strawberries) was obtained using hydroponics and it was based on the natural ability of strawberries to root when in contact with a moist environment. A thin synthetic material, perforated with 3-4 mm diameter holes, was placed above the surface of the nutrient solution, which circulated in automatic mode, washing the roots. The roots of microplants were immersed in the solution through the mounting holes, leaving the plantlets themselves above the solution. Within 1 month the plants formed a strong root system, adapted to normal air humidity and maintained viability at the level of 100% when transplanted into a non-sterile soil substrate.

Take Away Notes:

- This experience will make it possible to take a fresh look at the possibilities and prospects of clonal micropropagation.
- The presented information can be used for the implementation of industrial schemes for obtaining plants by the in vitro method.

Biography

Pr. Kornatskiy studied Agronomy at Kharkov National Agrarian University (Ukraine, 1983). He received a Ph.D. degree in 1991 in the specialty "Fruit Growing". After, for 15 years, he headed the laboratory of tissue culture at the All-Russian Selection and Technological Institute of Horticulture and Nursery. Since 2006 he has been working as an Associate Professor of the agrobiotechnological department of the Agrarian-Technological Institute of RUDN University. Now he supervises biotechnology. He has more than 50 published scientific articles.

Growth, yield and anthocyanin content in black rice (*Oryza sativa* L 'Cempo Ireng') treated with paclobutrazol and methyl jasmonate

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Black rice (*Oryza sativa* L.'Cempo Ireng') is getting popular because of its low glychemic index and anthocyanin content that can functions as an antioxidant. Paclobutrazol is a growth retardant that reduce the plant height but increased assimilate allocation to the sink, whereas methyl jasmonate is a hormone that may regulate the biosynthesis of secondary metabolites in plants. This research was aimed to evaluate the effect of paclobutrazol and methyl jasmonate on growth, yield and anthocyanin content in black rice. Black rice seeds were obtained from local farmer in Bantul, Yogyakarta. Seeds were selected and placed in a plastic tray containing a growth medium then wetted with water (control) or paclobutrazol of 12.5 ppm, 25 ppm or 50 ppm. Seedlings of 2 weeks old were transplanted in a plastic bucket containing a growth medium; two seedlings were planted in each bucket. Seedlings were watered regularly and methyl jasmonate was sprayed to the plants at 4 and 8 weeks following transplantation. The concentration of methyl jasmonate applied were 0 mM (control), 2.5 mM, 5 mM or 7.5 mM. Eight replicates were made for each treatment combination. Parameters observed were plant height, tiller number, percentage of full grain, chlorophyll, oxalic acid content in leaves, and anthocyanin content in black rice caryopsis. The results showed that paclobutrazol reduced plant height, but when combined with methyl jasmonate tiller number and chlorophyll content were increased. Percentage of full caryopsis increased by application of paclobutrazol 12.5 ppm or 25 ppm combined with methyl jasmonate of 2.5 mM or 5 mM. The oxalic acid content increased in plants treated with 5 mM methyl jasmonate whereas seven type of anthocyanins were determined in black rice and three of them were dominant, namely cyanidine 3-O-β-D glucoside, cyanidin 3 O-β-D galactoside and delphinidin 3 O-β-D galactoside. Those anthocyanins were increased significantly in plants treated with paclobutrazol of 25 ppm combined with methyl jasmonate of 7.5 mM. In conclusion the growth, yield and anthocyanin content of black rice can be increased by an appropriate combination of paclobutrazol and methyl jasmonate.

Take Away Notes:

- Through this presentation the audiences will learn about:
- (1) The importance of black rice as a good source of antioxidant
- (2) Plant growth and development manipulation by paclobutrazol application and
- (3) Increasing anthocyanin content in black rice by application of methyl jasmonate
- The audiences could apply this technique not only to alter the growth and anthocyanin content in black rice only, but also in other plants species such as ornamental plants or fruit plants.
- The information in this presentation can be used as knowledge for those who work as a lecturer or researcher to develop other research project concerning plant hormones, growth retardant and / or anthocyanin biosynthesis in plants. For rice farmers the information / technique presented can be allied in the field.

Biography

Dr. Kumala Dewi studied Plant Biology at Botany Department, The University of Tasmania, and Australia and graduated as MSc.St. in 1993 she continued her PhD at the School of Biochemistry and Molecular Biology, Australian National University and graduated as Doctor in 2006. She works as a lecturer at Faculty of Biology, Universitas Gadjah Mada, Yogyakarta, Indonesia since 1995. She won a research scholarship from Fullbright in 2011 and she did a short term research at Department of Biology, University of Washington, Seattle, USA, supervised by prof. Elizabeth van Volkenburg. She has published more than 20 research articles in SCI (E) journals.)

Biodiscovery of secondary metabolites from beneficial microbes for potential application against oil palm pests & diseases using metabolomics approach

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Oil palm is the primary industry leader amongst crop commodities in Malaysia. However, despite the rapid growth of the industry, oil palm remains prone to threats by a variety of pests such as insects, vertebrates and plant diseases. Basal stem rot (BSR), caused by Ganoderma spp., is the most devastating oil palm disease throughout Malaysia. The estimated yield loss due to BSR disease can reach up to RM 2.5 billion a year. Interestingly, despite the immense Ganoderma research studies that have been conducted in the country, we have yet to find a definitive treatment towards controlling the disease. With this view, we need to tackle a different approach and explore new research possibilities. Beneficial microbes have a prolific history in providing us a diversity of clinical and pharmaceutical drugs for human use. With this understanding, we can now venture into a similar approach by exploring the diversity of natural products from microbes through the use of metabolomics. These natural products are the results from the behavioural characteristics of a specific microorganism in response to a specific environmental condition. The specific behavioural characteristics can be stimulated with the induction of specific markers or components from the target pest or fungal pathogen. In this study, we focused on the use of a known prolific secondary metabolite producer, Trichoderma asperellum strain, and its capability to produce a diversity of metabolite profiles based on different sets of culture conditions and analyzes its data via metabolomics platforms. Results have shown that T. asperellum metabolite profiles significantly changed when the culture conditions are stimulated with different isolates of Ganoderma boninense collected from different parts of Malaysia. This observation is crucial to not only discover potential bioactive metabolites that are produced by T. asperellum in response to G. boninense attack, but also potentially to develop a profile algorithm for early G. boninense detection in the field. In summary, using the metabolomics approach, we can potentially discover unlimited knowledge of chemical diversities that can exist in biocontrol microbes in order to successfully develop a natural product that could be active against various pests and diseases. Furthermore, this knowledge can also provide an extensive framework for subsequent studies relating to the development of potential early disease detection diagnostic tool based on metabolite markers that can be useful for the control and management of oil palm diseases, particularly BSR disease.

Take Away Notes:

- Metabolomics is an expanding area in the "omics" field and many biotechnology and systems biology industries have implemented this approach to tackle various issues and problems relating to early disease detection, omics breeding, phenotypic strain studies and development of a biosensor platform. Our study can help bridge this knowledge of applying fundamental omics study into full-scale application into the oil palm industry, by developing the necessary tools to determine the potential of natural products from beneficial microbes.
- This omics approach can assist major industry players and university academics to implement fundamental knowledge into full-scale application in the oil palm plantation.
- It can assist in the early disease detection of Basal Stem Rot in oil palm plantation. We can help detect metabolite markers to provide a practical solution for early disease diagnosis and help simplify the detection method. This is because there is currently no early disease detection tool for this particular disease and no current effective method for cure. This allows the plantation management to make preventive measures and decisions early on before the onset of the disease. This would eventually save millions of dollars from economic damage from Ganoderma disease annually.
- This approach would complement well with the current disease control practices and allows it to be integrated into the Integrated Pest/Disease Management (IPM) procedures. The use of this early detection tool and the discovery of potential compounds from beneficial microbes using this metabolomics method would facilitate a more rapid control measures and complements with the current practice of applying biofertilizers and a tolerant planting materials that are already in practice.

Biography

Dr Ahmad Radhzlan Rosli studied and obtained his PhD in Molecular Plant Pathology at the University of Queensland, Australia in 2015. He then joined the research group of Prof. Peer Schenk and Prof. Robert Capon at the Institute of Molecular Biosciences, Brisbane, Australia for his postdoctoral fellowship. After one year of postdoctoral fellowship, he ventured into the oil palm industry by joining the Advanced Agriecological Research, a R&D company under Boustead Estates Agency and Kuala Lumpur Kepong Berhad as a Research Officer. After 1 year, he then joined FGV Research & Development, a subsidiary R&D company under FGV Holdings Berhad, which is one of the largest crude palm oil (CPO) producers in the world and owns one of the largest oil palm plantations by area, in the world. He currently leads the Plant Pathology R&D Group Crop Protection.

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