



Global Conference on

PLANT SCIENCE *and* MOLECULAR BIOLOGY



GPMB

SEP SEP
11 TO 13

2017

Venue

Eurostars Rey Don Jaime, Av. de les Balears,
2, 46023, Valencia, Spain

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Welcome Message

Dear Congress Visitors,



It is an honor and pleasure to write a welcome note. Biotechnology today makes unprecedented progress, since a few years with new “Gene Editing” methods for faster and more precise plant breeding. This opens new opportunities to adapt modern breeds to climate change, to achieve higher productivity and to introduce intelligent, differentiated methods to work against crop pests. It is not a coincidence that most mass crops in modern agriculture originate from ancestral species with natural monodominant stands. Organic farming, seemingly incompatible with those

trends, opens alternative cropping systems with more respect to natural processes and biodiversity. Sine gene transfer and natural mutation are based on similar processes, it is obvious that both agricultural strategies basically could go together. Organo-Transgenic Agriculture, based on Precision Agriculture will be the future basis for success.

We look forward to seeing you in Valencia, Spain!

Klaus Ammann

Prof. Dr. Klaus Ammann

University of Bern

Switzerland

GPMB 2017

Welcome Message

Dear Attendees, Presenters, Organizing Committee and Distinguished Guests,



Attending the conference “Plant Science 2017” is the best way to be updated on the most recent developments in the world of plant science. Welcome to discuss the latest results and the new technologies. The conference will provide students and scientists with great opportunities to build international networks

We look forward to seeing you in Valencia, Spain!

A handwritten signature in blue ink, appearing to read 'Leif Sundheim'.

Leif Sundheim

Norwegian Institute of Bioeconomy Research
Norway

Welcome Message

Dear Conference Participants,



It is my great honor and pleasure to welcome you to the GPMB 2017, in the beautiful city of Valencia. The 3-day event includes invited and contributed talks, organized in different sessions, as reported in the Conference Program, each coordinated by selected chairs.

The Conference will provide an important platform as well as an opportunity for presentation and discussion of the most recent progressions in all the fields of Plant Sciences, including biology, tissue culture, pathology, physiology and biochemistry, molecular

biology and biotechnology.

I hope that this international Conference may represent a starting point to stimulate the interaction in areas of common interest, towards new research directions and new collaborations for both young and senior scientists. We look forward to a stimulating conference with a great scientific debate and pleasant social interaction. I am sure that GPMB 2017 will fulfill this expectations.

We look forward to seeing you in Valencia, Spain!

Dr. Monica Ruffini Castiglione

University of Pisa

Italy

GPMB 2017

Welcome Message

Dear Colleagues and Friends,



I am delighted and honoured to welcome you to the Global Conference on Plant Science and Molecular Biology, organized by the Magnus, at the Eurostars Rey Don Jaime in Valencia, Spain. The conference will cover but not be limited to areas like Plant Biology, Plant Physiology and Biochemistry, Plant Tissue Culture and Molecular Biology. It will deal with how plants sense, process, integrate and store information related to environmental challenges. I am sure that your expectation on in-depth information with cutting-edge research activities will be

fulfilled. I am grateful to the organizing committee members for their tireless efforts that will certainly make the conference a great success.

We look forward to seeing you in Valencia, Spain!

Samir C. Debnath, Ph.D., P.Ag.

St. John's Research and Development Centre

Agriculture and Agri-Food Canada

St. John's, Newfoundland and Labrador

Canada

GPMB 2017

Keynote Speakers



Klaus Ammann
University of Bern
Switzerland



Cornelia Butler Flora
Kansas State University
USA



Monica Ruffini Castiglione
University of Pisa
Italy



Leif Sundheim
Norwegian Institute of
Bioeconomy Research
Norway



Samir C. Debnath
St. John's Research and
Development Centre
Canada



Goutam Gupta
Los Alamos National
Laboratory, USA



Elena Rakosy-Tican
Babes-Bolyai University
Romania



**Kariyat Ramachandran
Rupesh Ram**
Swiss Federal Institute of
Technology, Switzerland



Ivica Djalovic
Institute of Field and
Vegetable Crops
Serbia

About Magnus Group



Magnus Group (MG) is initiated to meet a need or to pursue collective goals of scientific community, especially in exchanging the ideas which facilitates growth of research and development. We specialize in organizing conferences, meetings and workshops internationally to overcome the problem of good and direct communication between scientists, researchers working in same fields or in interdisciplinary research.

MG promotes open discussions and free exchange of ideas at the research frontiers mainly focusing on science field. Intense discussions and examination based on professional interests will be an added advantage for the scientists and helps them learn most advance aspects of their field.

It proves that these events provide a way for valuable means of disseminating information and ideas that cannot be achieved by usual channels of communications. To encourage an informal community atmosphere usually we select conference venues which are chosen partly for their scenic and often isolated nature. Suggestion from many scientists and their reviews on our conferences reflected us to continue organizing annual conferences globally.

About GPMB 2017

GPMB 2017 will bring together a collection of investigators who are at the forefront of their field, and will provide opportunities for junior scientists and graduate students to interactively present their work and exchange ideas with established senior scientists. This program will include workshops, symposia, poster sessions and special discussions on wide range of session themes on plant sciences.

Don't miss this opportunity to exchange information, engage in stimulating discussions and collaborate with your fellow members from around the world. We assure that our expert speakers will provide you with the most clinically relevant and up-to-date information.



GPMB 2017

DAY 1

Keynote Forum

Global Conference on
**Plant Science and
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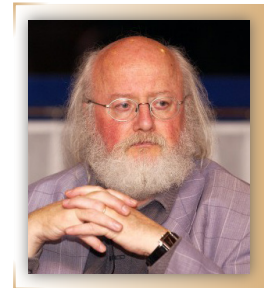
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How science can help to ease up the harsh GMO dispute

Klaus Ammann*, Prof. Dr.

University of Bern, Switzerland



If we want to escape this kind of years long regulatory limbo on GMOs, we have to do more than just to deplore the debate full of artificial (or imagined) contrasts and continue in a rather naïve way the war on facts and pseudo-facts. Here two main arguments:

First: We need to see behind the curtain and focus on the driver elements behind the debate. The industry, together with important farmer organizations worldwide, want to see better results of the new breeds in the field and cannot understand the resistance of consumers – all the more that the future of modern breeds with higher yields and better qualities are just around the corner, ready to be cultivated. The opposition deplores to lose the debate, still sticks to unscientific principles of an imaginary “genomic integrity” and activists fear to lose a major part of their income with the fast growing higher precision of Gene Editing (they still like the black and white picture full of risks for all “artificial” gene transfer methods. The reason: the main driver behind their campaigns is diffuse fear, tribal solidarity and stigmatization, built on questionable interpretations of substantial equivalence and sustainability and plain other false arguments.

Second: Surprisingly, molecular science and unbiased views on agricultural history should be able to ease down the contrasts in this debate here two of many arguments: The process of gene transfer is identical, whether done in natural mutation or modern biotechnology, a view supported in the past many times by Nobel Prize Winner Werner Arber, cited and summarized under keywords such as Genomic Misconception..

And it is fact (after Wood and Lenne 2010) that our main world crops (Rice, Wheat and Sorghum) have been chosen by our ancestors because they already lived in large monodominant stands, an important precondition of efficient food production. As a consequence, we need proposals to merge organic farming with its too strict focus on anti-biotechnology and industrial farming with its too strict perspective on production alone, better to think the unthinkable such as organo-transgenic breeding. Both farming methods could actually go together under well defined circumstances - across ideological and commercial barriers.

Conclusion: The regulatory views should in consequence also be not the black and white view, but instead consider a flexible dynamically scalable regulatory modus, which is more realistic, closer to the existing breeding reality and more acceptable to friends and foes according to Nancy Podevinet al. 2012 and Jeffrey Wolt 2015 et al. 2015 and Agnès Ricroch et al. 2016 - all three papers showing more regulatory details.

Audience Take Away:

- The audience will understand that the GMO dispute should be conducted on an interdisciplinary level including natural and social sciences.
- The audience will be able to judge on a broader basis how modern breeding should be applied, beyond the usual ideologically fixed principles of organic and biotech farming.

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Prof. Emeritus Bern University Switzerland, thesis: vegetation and glacier history, summa cum laude in 1972, lecturing in Biodiversity, Vegetation Ecology, Lichens and Mosses, Biomonitoring of Air Pollution, Plant Biotechnology: Biosafety, Gene Flow and Ecology of Transgenic Crops. Guest Prof. in Delft, Netherlands, Istanbul, Turkey, research in Jamaica, USA: Duke University and Missouri Botanical Garden. Steering committee of www.prii.net. Scientific activities based on 650 reference bibliographies on plant biotechnology and biodiversity, 320 publications in journals, blogs, newspapers, books, 200 slide presentations with literature references. Editor, Co-Editor in journals from Elsevier, Springer and Taylor&Francis. Scientific committees in Switzerland and Europe on biodiversity and biosafety. Fellow of the Royal Society of Biology, external member of the European Academy

<http://www.ask-force.org/web/Curriculum/Links2.pdf>

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The Social Imperative of Soil Microbiology: Understanding Soil/Plant Interactions for a Better Planet

Cornelia Butler Flora*, *PhD.*

*Distinguished Professor, Emeritus, Iowa State University and Research Professor,
Kansas State University, USA*



Farmers in settler societies, such as the United States, viewed soil as the medium that held up the plants, despite advice from indigenous people about caring for the soil, agriculture moved west as eastern and southern soils were “worn out”. With the dust storms of the 1930s, there was concern for soil erosion and soil physics, and with the availability of chemicals to be used as fertilizers after World War II, soil chemistry became a concern – and a profit center for agro-chemical companies. Only relatively recently has soil biology – particularly microbiology – gain attention of researchers and some farmers. Although seed inoculants were used with some legumes to enhance nitrogen fixation, there was little appreciation of role of diverse microbes found in soil organic matter that impacted plant health. There is still no easy and reliable measure of soil microbial biodiversity. This paper traces the implications of how society frames soil and its health, how it is changing, and how that has impacted research and practice.

Audience Take Away:

- Microbial diversity is critical for soil and plant and human health
- Microbial diversity can be best achieved through farming practices, rather than purchased inputs.
- We can only act toward something when we can name it – thus it is critical to name soil microbiology as a key to sustainable agricultural productivity
- The audience will be able to use this as they work with others to expand the understanding of agricultural systems and the importance of diversity through rotations and cover crops

Biography

Cornelia Butler Flora (Ph.D., Cornell University) Charles F. Curtiss Distinguished Professor Emeritus of Sociology, Iowa State University and Research Professor at Kansas State University. She served as Director of the Population Research Laboratory at Kansas State University, Chair of the Technical Committee of the Sustainable Agriculture and Natural Resource Management Collaborative Research Support Program, Head of the Department of Sociology at Virginia Polytechnic Institute and State University, Director of the North Central Regional Center for Rural Development, and a member of the Board of Directors of CONDESAN (Council for the Sustainable Development of the Andean Region), the Northwest Area Foundation, and Winrock, International, past president of the Rural Sociological Society, the Community Development Society, and the Agriculture and Human Values Society, and consultant for international organizations and foundations in Africa, Asia, Latin America, the U.S. and Canada. Her primary research interests are the intersections of human communities and agro-ecosystems, and sustainable intensification in the context of climate change. She has taught courses and done research on rural development in Spain, Uruguay, Costa Rica, Argentina and Peru.

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New scenarios for crop plants: TiO₂ nanoparticles in sludge-amended agricultural soil

Monica Ruffini Castiglione*, Ph.D

Department of Biology, University of Pisa, Italy



Beyond all studies published to date on the effects of nanoparticles (NPs) on living organisms, the overall picture of their possible interactions with crop plants and with food chains are not at all clear.

These emerging contaminants are becoming a worldwide problem, given that nanotechnologies are increasingly gaining ground in all sectors of the economy and innovation, with their consequent unintentional and intentional release into the environment. Poorly estimated is indeed the behavior of nanomaterials (NMs) in the different environmental matrices, especially in agricultural soils. These become a site of possible accumulation of NMs through potentially contaminated surface waters, by the use of plant protection products, and by their amendment with sludge from wastewater treatment plants. The recycle of sludge in agricultural soils is identified as one of the best environmental management practice, due to its increasing amount of production and the supply of organic matter and nutrients to the soil-plant system, but, due to the uncertainty of its contents not thoroughly tested for safety, can result a possible sink of unknown pollutants as well as of NPs. In such complex matrices the bioavailability of the different NMs often is not predictable, due to the tendency of NPs to aggregate, to adsorb/precipitate on solid phase, as well as to be coated by organic molecules.

In order to investigate the environmental impact of TiO₂ NPs we have used two different concentrations of the crystal forms of TiO₂ (applied singularly or in a mixture as anatase and rutile NPs and as bulk material). The effects were evaluated on growth and development of the crop *Pisum sativum* L. at microcosm scale under long term exposure, to possibly mime environmental exposure in sludge amended agricultural soil. We were particularly interested in understanding the response elicited by NPs in tissues/organs, at cellular and organism level, taking into account different aspects. Ultrastructural studies demonstrated that the applied NPs were internalized in root cells and synchrotron studies showed that both titanium crystal forms, especially anatase, were taken up and moved to the vascular tissues. Oxidative stress was evaluated by biochemical approach and in situ histochemical techniques. The amended sludge soil was in itself an element of disturbance for plants. The presence of NPs in the sludge-amended soil pronounced oxidative damages in *P. sativum*, in particular that grown at the lowest NPs concentration. This result was speculatively attributed to a likely easier enter the root of more diluted NPs, having less tendency to form homo- and heteroaggregates in the complex matrix. The most responsiveness treatments seemed those conducted with anatase crystal form, alone or mixed with rutile as well as with the corresponding bulk material. The results of our work pose a reflection on the promising agronomic practices and on the use of nanomaterials and their safety, which must be carefully analyzed, in order to establish right regulation over their use, confinement, and disposal for the environmental protection and living organism health.

Audience Take Away:

- I hope that conference audience, depending on the proper skills, will be able to enter the proposed issues, getting the key messages, especially useful for colleagues working on or approaching to environmental problems related to emerging contaminants and higher plants.
- Our presentation aims, among other things, to show how to proceed with a multidisciplinary approach applied to a complex problem, by means of both traditional and innovative techniques.

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- Due to the complexity of the study system, interdisciplinary competences are needed. In this respect our work may also be of interest for researchers coming from other faculties.
- The presentation of our work poses a reflection on the promising agronomic practices and on the use of nanomaterials and their safety, which must be carefully analyzed for the environmental protection and living organism health

Biography

Monica Ruffini Castiglione is senior researcher and lecturer at Botany Department, University of Pisa. Graduated in Biological Sciences in 1987, she received her PhD degree in 1993 and from 1993 to 2000 different post-doc positions. From 2001 to 2007 staff member and from 2008 researcher position at the Department of Biology, University of Pisa. Her recent areas of interest concern the study of the stress-induced morphogenic responses following exposure to different abiotic stressors in higher plants and their employment in toxicity assessment by different endpoints. She is author and co-author of more than sixty publications in extenso and more than sixty contributions to international and national conferences.

DAY 1

Speakers

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Sessions on: Plant Physiology and Biochemistry | Plant Tissue Culture | Plant Sociology

Session Chairs

Samir C. Debnath

St. John's Research and Development Centre
Canada

Kariyat Ramachandran Rupesh Ram

Swiss Federal Institute of Technology
Switzerland

Session Introduction

Title: Annual ring formation in Scots pine stems as the reaction on seasonal changes in photosynthesis and respiration

Antonova Galina Feodosievna, VN Sukachev Institute of Forest Siberian Branch of Russian Academy of Sciences, Russian Federation

Title: The effect of Tetraneura ulmi L. galling process on the activity of amino acid decarboxylases and the content of biogenic amines in Siberian elm tissues

Cezary Piotr Sempruch, Siedlce University of Natural Sciences and Humanities, Poland

Title: Positive and negative feedback between reactive oxygen species and auxin for adjustment of plant growth under stress conditions

Ivan Paponov, Norwegian Institute of Bioeconomy Research, Norway

Title: Plant intramembrane proteases and beyond...

Malgorzata Adamiec, Adam Mickiewicz University, Institute of Experimental Biology, Poland

Title: Solanum lycopersicum (tomato) possesses multiple lipoyl synthases capable of increasing lipoylation levels in vivo

Michael Handford, Universidad de Chile, Chile

Title: Modulating effect of low and high temperatures on wheat response to cadmium stress

Natalia Repkina, Institute of Biology Karelian Research Centre of the Russian Academy of Sciences, Russia

Title: Salt tolerance in rice: Plant strategies and genetic improvement

Elide Formentin, University of Padova, Italy

Title: Plant i-AAA protease controls the turnover of the essential mitochondrial protein import component

Magdalena Opalinska, University of Wroclaw, Poland

Title: Physiology and metabolism of roots in response to extreme temperatures stress

Moses Kwame Aidoo, Ben-Gurion University of the Negev, Israel

Title: Development of leafy head upon microRNA coordination

Yuke He, Shanghai Institutes for Biological Sciences, China

Title: Differential oxidative and biochemical responses of tomato and maize leaves to Spodoptera exigua herbivory

Sameera Omar Bafeel, King Abdulaziz University, Science college, Saudi Arabia

Title: Manipulation of the starch granule number and morphology in Arabidopsis thaliana

Joerg Fettke, University of Potsdam, Germany

Title: A novel CBF from oil palm that regulates abiotic stress response and the ripening process through modulation of the ethylene signaling pathway

Siti Nor Akmar Abdullah, Universiti Putra Malaysia, Malaysia

Title: An ecological approximation for the study of Arbuscular mycorrhizal fungi (AMF) sporulation in Mediterranean sand dunes

Alberto Guillen Bas, University of Valencia, Spain

Title: Thapsia garganica L. in vitro plants as a new production platform of thapsigargin

Carmen Quinonero Lopez, University of Copenhagen, Denmark

Title: How does indole-3-butyric acid induce adventitious root formation in Arabidopsis thaliana thin cell layers?

Laura Fattorini, Sapienza University of Rome, Italy

Title: Contributions of Plant Tissue Culture to Plant Science

Meltem Bayraktar, Ahi Evran University, Turkey

Title: Comparative evaluation of biochemical changes in tomato (Lycopersicon esculentum Mill.) infected by Alternaria alternata and its toxins (TeA, AOH and AME)

Mukesh Meena, Banaras Hindu University, India

Annual ring formation in Scots pine stems as the reaction on seasonal changes in photosynthesis and respiration

Antonova G.F.^{1*}, Stasova V.V.¹, Suvorova G.G.², Oskolkov V.A.²

¹VN Sukachev Institute of Forest, Siberian Branch of RAS, Russia

²Siberian Institute of Physiology and Biochemistry of Plants, Siberian Branch of RAS, Russia

Annual wood increment formation in Scots pine stems was studied simultaneously with the photosynthetic activity of tree crown and stem respiration, steaming of newly formed and the maintenance of living tissue. The formation of annual wood layer was evaluated as the production of xylem and phloem cells by cambium and as biomass accumulation in separate periods of the season. With this purpose the number of the cells, produced by cambium, and morphological parameters of tracheids were estimated at cross-sections of the cores, knocked out of the trunks through 7-11 days during vegetation. In each of the days of observation period photosynthesis and respiration of the trunk were registered, the data were summarized and divided into the day of this period. Additionally the respiration of growth and maintenance were considered. All calculations were carried out for whole season vegetation and separate periods of the season. Photosynthesis influenced the cambium production of phloem cells mainly in May-June whereas of xylem cells in May-June and August. Temperature positively influenced xylem cell formation, but the level of dependence changed in different season periods. Most active cambium initials were divided in the direction of xylem at a temperature of no higher than 20° C. Phloem cells formation by cambium during vegetation showed a negative relationship with temperature and optimal temperature for that was not higher than 15°C. But in each of the periods the values of optimum changed because of a variation of other external factors. Reduced soil moisture store, lack of rainfall and increasing temperatures in July adversely affected the activity of cambium. Cambium activity didn't show any dependence with the overall cost of respiration throughout the season, but xylem cell production in certain periods had a significant positive correlation with growth respiration and maintenance respiration. Cambium produced the cells of xylem or phloem with different degrees of their relationships with respiratory process.

According to data on tracheid wall cross-section area increment the principal amount of annual ring biomass was accumulated twice in the season – in May-June and in August. In those periods the biomass deposition had very high connection with photosynthesis as the source of substrates for biosynthesis of cell wall components due to favorable temperature and moisture. In July biomass deposition decreased significantly since the temperature higher 23o C suppressed photosynthesis. The connections between biomass deposition and growth respiration as well maintenance respiration were practically rectilinear in May-June. In July because of high temperature the biomass deposition had direct correlation with maintaining respiration whereas the connection with growth respiration was absent. In August due to temperature declining and the intensification of photosynthesis the biomass accumulation was enlarged. Simultaneously growth respiration increased with diminution of maintenance respiration.

The coherence of cambial activity and biomass accumulation in xylem cell walls with weather conditions of separate periods, as well as with photosynthesis, growth respiration and maintenance respiration has been found to be described more adequately by the second order equations. This allows finding out optimal conditions of physiological processes, in which the production of cells by cambium and accumulation of substances in cell walls occurs.

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Antonova Galina Feodosievna, born 31 October, 1936. Graduated from the Siberian Institute of Technology (at the present time – M. F. Reshetnev Siberian State Aerospace University), Faculty of Chemical Technology (1959). Leading Research Scientist for the Laboratory on Physical and Chemical Biology of Timber Plants, Department on Physical and Chemical Biology and Biotechnology of Forest Ecosystems' Components at V.N. Sukachev Institute of Forest, Russian Academy of Sciences, Siberian Branch, Doctor of Biological Sciences (1995). Expert in forest biology, biochemistry and physiology of woody plants. PI and CoPI for research projects, directed to study of biochemical and physiological processes of cell growth and development during wood formation. Member of the Russian Coordinating Council on Contemporary Problems of Wood Science (2004). Author (and co-author) of more than 180 papers, including 3 books. Some of them: "Cell Growth in Coniferous", Novosibirsk, 1999 (in Russian with summary and contents in English), "Physiology of Common Pine", Novosibirsk, 1990 (in Russian with summary and contents in English), "Oxidative Stress in Plants: Causes, Consequences and Tolerance", New Delhi-Bangalore, 2012. Veteran of the Siberian Branch of the Russian Academy of Sciences. For a creative scientific activity of many years, outstanding contribution to the development of science, and in connection with 50-year jubilee of the Siberian Branch of the Russian Academy of Sciences, awarded by the "Silver Sigma" Honorary Sign of the Presidium of the Siberian Branch of the Russian Academy of Sciences (2007), Honorary Notes, Diplomas and Letters of the Presidium of the Russian Academy of Sciences, the Siberian Branch of the Russian Academy of Sciences.

The effect of *Tetraneura ulmi* L. galling process on the activity of amino acid decarboxylases and the content of biogenic amines in Siberian elm tissues

Cezary Sempruch*, Ph.D., Katarzyna Kmiec, Ph.D., Grzegorz Chrzanowski, Ph.D., Pawel Czerniewicz, Ph.D.
Siedlce University of Natural Sciences and Humanities, Poland.

This report describe the changes in the content of plant biogenic amines (putrescine, cadaverine, spermidyne, tryptamine, spermine and histamine) and key enzymes of their biosynthesis: lysine decarboxylase (LDC), tyrosine decarboxylase (TyDC) and ornithine decarboxylase (ODC) in galls and other parts of Siberian elm (*Ulmus pumila* L.) leaves during the galling process induced by the gall-forming aphid *Tetraneura ulmi* (L.). Three stages of gall development were studied: the 1st stage – the initial period of galling -galls were green, about 5 mm in height with one fundatrix larva inside; the 2nd stage – the galls were green and fully grown with fundatrix and her young offspring inside; the 3rd stage involved the time period just before the gall opening. The direction and intensity of the observed changes for particular amines and enzymes were dependent on the stage of gall development and part of the galling leaf. Generally, the amine content tended to increase in gall tissues during the 1st and 2nd period of galling process and decreased in later phase. LDC and ODC activities were markedly enhanced, especially in gall tissues at the initial stage of the galling process. Moreover, the level of the majority of the analysed amines was reduced in damaged and undamaged parts of galling leaves during the initial period of galling process and at the time when the galls were fully developed. The participation of biogenic amines in the gall formation in Siberian elm leaves infested by *T. ulmi* is discussed.

Audience Take Away:

- The study provides new information on the biochemical mechanisms of plant response to insect pests.
- Those documents are the source of new data on the importance of amines for plant biology.
- The results can be useful from the point of view of the application of biochemical mechanisms of plant resistance in integrated methods their protection.
- The information may suggest the possibility of the search for new biopesticides plant among amines and their derivatives.

Biography

Dr. Cezary Sempruch is associate professor in Department of Biochemistry and Molecular Biology in Siedlce University of Natural Sciences and Humanities (UPH), Siedlce, Poland. His research is mainly focused on biochemical basis of insect-plant interactions, and especially on importance of amino acids, biogenic amines and enzymes of its metabolic transformations. He was also studied toxicity of some pesticides against non-target organisms. Dr. Sempruch is member of the board of Hemiterological Section of Polish Entomological Society and member of Polish Biochemical Society. He is author or coauthor of over 90 original papers and 113 reports on scientific conferences.

Positive and negative feedback between reactive oxygen species and auxin for adjustment of plant growth under stress conditions

I. A. Paponov^{*1,2}, T. Khodus¹, V., Budnyk¹, M. Paponov^{1,2}, K. Palme¹

¹Institute of Biology II/Molecular Plant Physiology, Albert-Ludwigs-University of Freiburg, Germany

²NIBIO, Norwegian Institute of Bioeconomy Research, Norway

During the presentation I will discuss about the mechanism of plant adaptation to abiotic stresses. Specifically, I will address to the observation that different abiotic stresses all seem to modulate plant growth in a way that generates a similar plant phenotype – one that helps to attenuate the adverse effects of stress and increases the chances of plant survival. This similarity of plant phenotypes under different stresses has been assumed to reflect a common mechanism of plant adaptation in which reactive oxygen species (ROS) and plant hormone auxin each play important roles. ROS are well known and extensively investigated inhibitors of auxin activity, acting via auxin oxidation, attenuation of signalling and inhibition of auxin transport. However, the mechanisms by which auxin affects ROS are less well understood, which limits our understanding of cross-talk between ROS and auxin. Therefore, in my talk I will focus on mechanism of auxin action on ROS. I will show quantitative determination of ROS production after auxin treatments, which demonstrate that auxin differentially regulates the levels of ROS in roots: it decreases cell wall levels of superoxide and increases hydrogen peroxide levels. Therefore, ROS–auxin cross-talk occurs by the operation of positive and negative feedback loops between ROS and IAA. Positive (double negative) feedback consists of inhibition of auxin activity by ROS and reduction of superoxide levels by auxin. This positive feedback loop includes the regulation of plastid gene expression, including upregulation by superoxide and inhibition by auxin. Negative feedback loops consists of inhibition of auxin action by ROS and stimulation of H₂O₂ production by auxin. General oxidative response genes were highly over-represented among the auxin-induced genes, possibly due to stimulation of H₂O₂ production by auxin and the presence of binding sites in the promoters of auxin responsive genes for transcription factors WRKY and bHLH, which are involved in ROS signalling. Expression analysis of ROS-related genes that respond to auxin showed that peroxidases are the best candidates for the differential production of ROS and the guiding of feedback loops between ROS and auxin.

Conclusions: Differential induction of ROS by auxin and regulation of auxin activity by ROS create a combination of positive and negative feedback loops between ROS and auxin to allow adjustment of plant growth to environmental stress conditions.

Audience Take Away:

- The main topic of discussion – How do plants adapt to stress conditions? – will be of interest to a broad audience.
- The presentation of an analysis of wet lab data and gene regulation data from a publically available database will demonstrate a successful example of the integrative use of one's own and publically available data. This approach allows the selection of the most promising hypotheses to explain plant responses under stress conditions.
- The idea of using positive and negative feedback to understand plant growth adjustment under stress conditions can be applied to investigate ROS-auxin cross-talk, but it is also useful for understanding the interactions between any factors that play important roles in plant growth and development.
- Researchers who focus on the functions of ROS and auxin in plants will benefit from the presentation because new mechanisms of ROS and auxin action will be introduced during the talk. Thus, the talk can initiate the design of new experiments aimed at validating the hypotheses proposed to explain ROS and auxin action.

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Ivan Paponov received his Ph. D. degree from the Moscow Timyrazev Academy in Russia in 1992. Following postdoctoral periods at Moscow Lomonosov University and the University of Hohenheim in Stuttgart, he worked on genotypic aspects of mineral nutrition in higher plants. In 2002, he began research at the University of Freiburg in the field of auxin transport and auxin signalling in which he applied the chemical genetics and bioinformatics tools. He is currently a researcher at the Norwegian Institute of Bioeconomy. His research focus is on plant adaptation to different environments, with emphasis on the molecular responses of plants to light, CO₂ concentration and nitrogen.

Plant intramembrane proteases and beyond...

M. Adamiec*1, Ph.D, L. Misztal1, Ph.D, E. Kosicka1, Msc, R. Luciński1, Ph.D

¹Adam Mickiewicz University, Poland

Proteolysis is considered as a crucial factor determining the proper development of the plant and its efficient functioning in variable environmental conditions. The role of proteases in protein quality control and protein turnover processes is well documented. However, knowledge accumulated in the last several years has revealed another, previously unknown mechanism of proteolytic control – regulated intramembrane proteolysis (RIP). RIP is performed by intramembrane proteases – integral membrane proteins able to hydrolyze a transmembrane helix of their substrates and release them from the membrane. This recently identified class of proteases occurs ubiquitously in all living organisms from Bacteria through Archaea to Eukarya. The first described intramembrane protease was identified in human cells in 1997, and in 2005, in *Arabidopsis thaliana*, the first plant intramembrane protease was identified. To date, four families of intramembrane proteases have been identified in *Arabidopsis thaliana*: site-2 proteases (S2Ps), rhomboids, presenilins and signal peptide peptidases. The knowledge concerning the potential physiological role of plant intramembrane proteases is very limited. Continuously accumulating data indicate, however, that their role in development should not be underestimated. Many studies indicate that intramembrane protease performs crucial functions in providing plant fertility, proper chloroplast biogenesis and photosynthetic process efficiency. In most cases the mechanisms leading from gene mutation to phenotypic changes and development aberrations have not been discovered yet. We demonstrated, that *Egy2* –intramembrane zinc metalloprotease located in chloroplasts – participates in regulation of chloroplast genes, encoding crucial photosystem II proteins: *PsbA*, *PsbD* and *PsbC*. Furthermore, according to our comparative genomic analysis, several inactive rhomboid-like proteins share relatively high sequence identity, highly conserved primary structure motifs and domain architecture what may indicate that they perform an important physiological function. The role of this proteins remains, however, unknown. This makes the plant transmembrane proteases and they relatives extremely interesting field for future research.

This work was supported by the Polish National Science Center based on decision number DEC-2014/15/B/NZ3/00412

Audience Take Away:

- The speech give the audience a chance to expand and systematize knowledge concerning plant intramembrane proteases and their role in plant physiology. It also draw attention to strongly conserved groups of proteins of unknown function. I present results of our latest research concerning *AtEgy2* – *Arabidopsis thaliana* chloroplast intramembrane protease.
- The discussed subject concerns basic research. The intramembrane proteases remain, however, relatively new field of research and knowledge concerning this issue remain very limited. Present research are focused mainly on a model plant – *Arabidopsis thaliana* and the mechanisms leading from gene mutation to phenotypic changes and development aberrations had not been yet discovered. This makes the plant transmembrane proteases an extremely interesting field for future research.

Biography

Małgorzata Adamiec Ph.D. - molecular biologist (Master degree at Faculty of Biology, University of Warsaw), plant physiologist (PhD degree at Faculty of Biology, Adam Mickiewicz University, Poznań) and popularizer of science. Currently an associate professor in Department of Plant Physiology at Faculty of Biology, Adam Mickiewicz University.

Research area: Photosystem II structure and excitation energy transfer; chloroplast proteases and their role in regulation of photosynthetic processes during response to abiotic stresses and in physiological conditions. At present the main researcher in project entitled: "The physiological role of chloroplast intramembrane proteases *AtEgy1-3*"

Solanum lycopersicum (tomato) possesses multiple lipoyl synthases capable of increasing lipoylation levels in vivo

Jorge Araya¹, Simón Miranda¹, María Paz Covarrubias¹, Michael Handford^{*1}, Ph.D.

¹Universidad de Chile, Chile

Lipoic acid (LA) is a functional metabolite with powerful antioxidant capacities present in eukaryotic and prokaryotic organisms. LA is both lipid- and water-soluble, and is the prosthetic group of several key multi-subunit enzyme complexes, including pyruvate dehydrogenase and α -ketoglutarate dehydrogenase of the tricarboxylic acid (TCA) cycle. LA biosynthesis and incorporation into these target proteins (lipoylation) proceeds de novo or via a salvage pathway. During de novo synthesis, octanoyl transferase (LIP2) uses octanoyl groups linked to an acyl carrier protein to transoctanoylate target proteins. Subsequently, lipoyl synthase (LIP1) catalyses the final step by inserting two sulphur atoms into the prosthetic group. Whilst a number of the enzymes have been functionally-characterised in *Arabidopsis thaliana*, the aim of the current work is to identify and evaluate the role of this pathway in a fruit-bearing species. Towards this aim, we identified two proteins in tomato (*Solanum lycopersicum*) with the molecular characteristics of LIP1. We call these proteins SILIP1 and SILIP1p, which possess 78% and 84% amino acid identity with AtLIP1 and AtLIP1p, respectively. Confirming bioinformatic predictions, SILIP1 has a mitochondrial localisation whereas SILIP1p is plastidial, as shown by confocal microscopy. Furthermore, both proteins rescue carbon source requirements and lipoylation levels of an *Escherichia coli* lipoyl synthase mutant (*lipA*), and thus act as lipoyl synthases in this heterologous system. Additionally, stable over-expression of these genes in tomato produces transcriptional alterations in genes encoding proteins involved in LA metabolism, and target proteins of the TCA cycle, which in turn correlate with developmental differences and increased levels of lipoylation measured in several over-expressing lines.

Audience Take Away:

- The importance of lipoic acid for the plant, and in human health will be explained
- The identification and characterisation of several enzymes from tomato that are key in the synthesis of lipoic acid will be described
- The utility of over-expression techniques in bacteria and plants required for functional characterisation will be highlighted

Biography

Michael Handford is an Associate Professor in the Biology Department of the Faculty of Sciences in the Universidad de Chile. Since completing his PhD and postdoctoral fellowships in the University of Cambridge, he has focused his research on various aspects of plant metabolism, such as cell wall synthesis, and more recently on the metabolic changes that plants undergo in order to withstand abiotic stress conditions, including antioxidant and sugar alcohol metabolism. He also carries out multiple teaching and administrative commitments in the University, and for Chilean organisations.

Modulating effect of low and high temperatures on wheat response to cadmium stress

Natalia Repkina*¹, Ph.D., Vera Talanova, D.Sc.,

¹Institute of Biology of Karelian Research Centre Russian Academy of Sciences (IB KarRC RAS), Russia

The comparative study of wheat plants response to cadmium (Cd) impact in combination with normal (22°C), low (4°C) and high (37°C) temperatures was performed. The similarities and differences of wheat plants responses to these stresses were observed. In particular, plant growth was more reduced under combination of cadmium with low and high temperatures than at 22 ° C. According to the results of electrolyte leakage, MDA content, Cd accumulation, it was found that in combination of cadmium with low or high temperature, the temperatures have dominant effect, and reaction of plants was similar with the response to separate effect of cold or heat. Moreover, the response of plants to cadmium in combination with high temperature has been faster and more pronounced than at normal and low temperatures.

It is well known, that the low-molecular-weight protectors, including proline play one of the key role in plants tolerance to stress. Proline as an osmoprotector is very efficient for plant adaptation to unfavorable temperatures influence. With this context, the role of proline as well as the expression of WP5CS gene, encoding pyrroline-5-carboxylate synthetase were studied in wheat at cadmium influence in combination with normal (22°C), low (4°C) and high (37°C) temperatures. It was found that at cadmium impact at normal temperature the proline content slightly increased. Whereas accumulation of proline dramatically increased in wheat leaves under cadmium treatment in presence low (4°C) and high (37°C) temperatures. It should be noted that at combination of cadmium and heat the proline content was almost twice as much at cadmium and its combination with cold influence. Probably, in this case a significant increase in the accumulation of proline caused of the protein degradation and did not concern its protective role. This is proved by protein content data. Also the proline content correlated with the changes in WP5CS gene expression in wheat.

Summarizing all results, we can conclude that the low and high temperatures in combination with cadmium modulate the reaction of plants to cadmium impact. Particularly, low temperature prevents cadmium accumulation and plants can adapt to this stress. On the other hand high temperature leads to higher cadmium accumulation and as a result caused to damage effect on plants.

Audience Take Away:

- The obtained results expand the existing knowledge of plant tolerance to cadmium and mechanisms of cross adaptation.
- The presented results can be used in the development of technologies aimed at increasing the plant's tolerance to cadmium in different climatic regions.
- This presents the possibility of developing methods for increasing plant resistance to cadmium by physical factors, without the use of chemical agents.
- The present data broadens the state-of-art knowledge about adaptation of plants to abiotic stress. Moreover our results can help to design new experimental approaches for investigate the cross adaptation of plants to different stressors. This data can be used for the teachers, who read the lectures about plant adaptation to stress as well as a part of Plant Physiology course. Also obtained data can be interesting for biotechnologists because it can discover a new way for control the plant tolerance to heavy metals using for this the temperature influence.

Biography

Natalia Repkina graduate from Petrozavodsk State University in 2010 and holds a Ph.D. in the Laboratory of Plant Ecophysiology at the Institute of Biology of Karelian Research Centre Russian Academy of Sciences (IB KarRC RAS) (defense date 02.04.2014). In present time she occupies a position of research scientist in the Laboratory of Plant Ecophysiology at the IB KarRC RAS. She is author and co-author of more than 60 publications. Natalia Repkina is a member of Russian Society of Plant Physiologists and The Federation of European Societies of Plant Biology (FESPB).

Salt tolerance in rice: Plant strategies and genetic improvement.

Elide Formentin*¹ PhD., Cristina Sudiro¹, PhD., Elisabetta Barizza¹, Giorgio Perin¹, PhD., Samantha Riccadonna², PhD., Elena Baldoni³, PhD., Enrico Lavezzo¹, PhD., Piergiorgio Stevanato¹, PhD., Michela Zottini¹, PhD., Fiorella Lo Schiavo¹

¹University of Padova, Italy

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Salinity tolerance is a complex trait and, despite many efforts to obtain rice plants resistant to salt, few results have been achieved and a deeper understanding of the tolerance mechanisms is needed. By studying two Italian rice varieties with contrasting salt response, we demonstrated the involvement of both cell and whole-plant mechanisms in salt tolerance.

In cultured cells, the tolerant variety showed higher activity levels of antioxidant enzymes in control conditions and a more consistent increase in these activities after salt treatment. Several genes regulated by salt stress involved in ROS signalling and detoxification showed rapid upregulation in tolerant cells. The tolerant variety also exhibited rapid upregulation of K⁺ transporter genes and ion homeostasis recovery during the stress. In plants, the tolerant variety responded more effectively to osmotic and ionic stress. In roots, an increase in levels of H₂O₂ was observed as early as 5 minutes after treatment. Consequently, the expression of genes involved in perception, signal transduction and response to salt were induced at earlier times when compared to susceptible plant roots. Transcriptomic analyses supported the set-up of an adaptive program consisting of allocating sodium preferentially to roots, restricting it to the oldest leaves and activating regulatory mechanisms of photosynthesis in new leaves. As a consequence, plants resumed growth even under prolonged salt stress. Overall, our findings show that a tight control on ROS is fundamental in triggering a coordinated response resulting in adaptation instead of senescence in salt treated rice plants.

Audience Take Away:

- Comprehension of salt tolerance as a complex trait
- Characteristics of contrasting genotypes to be used in addressing salt response
- Differences in cell and whole plant responses
- Application to the field

Biography

Elide Formentin has an extensive and documented experience in Plant Molecular and Cell Biology, Bioinformatics and Biochemistry. She is involved in various studies on the physiology of plant stress (salt and oxidative) response, both at single cell and whole plant level, in model organisms (*Arabidopsis*, carrot) and important crop plants (rice, wheat, grape). Thanks to her experience in different laboratories, she owns a multidisciplinary expertise: RNA profiling by NGS techniques, bioinformatics analysis of -omics data, plants and protoplasts transformation, confocal microscopy, signal molecules analysis by imaging and biochemistry, organellar ion channels characterization.

Plant i-AAA protease controls the turnover of the essential mitochondrial protein import component.

Magdalena Opalinska^{*1}, PhD., Katarzyna Parys¹, MSc, Monika Murcha², PhD., Hanna Jańska¹, PhD.

¹University of Wrocław, Poland

²The University of Western Australia, Western Australia

Mitochondria are life-essential, multifunctional organelles that are the main sites of ATP production in cell. The bulk of mitochondrial proteins are involved in diverse metabolic pathways, such as the biosynthesis of cofactors like iron-sulphur clusters, and the metabolism of sugars, amino acids, and lipids. Due to the essential functions of these organelles, mitochondrial content, quality, and dynamics are tightly controlled. Mitochondrial integrity depends on balancing levels of different subunits of protein complexes. Selective removal of excess subunits by ATP – dependent proteolysis is one of the mechanisms employed by mitochondria in order to maintain protein homeostasis. This study focuses on a molecular function of plant mitochondrial inner membrane-embedded i – AAA protease, FTSH4. Lack of FTSH4 causes severe morphological and developmental abnormalities in plants grown under stress conditions. This is accompanied by decreased levels and activities of specific respiratory complexes, anomalies in mitochondrial morphology, and increased oxidative stress. However, the molecular mechanism that directly links the observed phenotypes of *ftsh4* plants with the FTSH4 protease is still missing. We found that FTSH4 protease controls levels of the essential protein import component, Tim17-2, at the mitochondria. Tim17-2 is a core component of TIM23 translocase through which majority of mitochondrial preproteins are transported into the organelle. Plants that are lacking functional FTSH4 protease are characterized by significantly enhanced capacity of preprotein import through the TIM23 - dependent pathway. Together with the observation that FTSH4 prevents accumulation of Tim17-2, our data point towards a role of this i - AAA protease in the regulation of mitochondrial preprotein transport in plants. This work is supported by grant FUGA 2015/16/S/NZ3/00364 from National Science Centre awarded to Magdalena Opalińska. Conference costs were supported by Wrocław Centre of Biotechnology program “The Leading National Research Centre (KNOW) for years 2014-2018.

Audience Take Away:

- First bona fide substrates of the plant mitochondrial i-AAA protease
- Interesting molecular mechanism of the regulation of preprotein influx into mitochondria
- Useful in Plant Science biochemical and cell biology techniques

Biography

Magdalena Opalinska has completed her MS in biotechnology at the University of Wrocław, Poland. In 2012 she obtained PhD from the University of Groningen, Netherlands. Her PhD work was focused on peroxisome quality control and involvement of peroxisomes in antibiotics production by filamentous fungi. In 2012 she moved to University of Freiburg, Germany, where her work focused on molecular mechanisms of mitochondria biogenesis. In 2015 she obtained FUGA Fellowship from Polish National Science Centre to study molecular function of plant mitochondrial i-AAA protease at the Faculty of Biotechnology University of Wrocław, Poland.

Physiology and metabolism of roots in response to extreme temperatures stress

Moses Kwame Aidoo^{1*}, MSc., Tal Sherman ², Ph.D., Naftali Lazarovitch¹, Ph.D., Aaron Fait¹, Ph.D., Shimon Rachmilevitch, Ph.D¹

¹The French Associates Institute for Agriculture and Biotechnology of Drylands, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Israel.

²Zeraim Gadera, Syngenta, Israel.

L Roots play important role in regulating whole-plant carbon and water relations in response to extreme soil temperatures. Soil temperature is generally lower than that of the air and seasonal fluctuations can occur with depth depending on soil and other factors. These factors can strongly influence shoot and root growth, which can cause various stresses to physiology, metabolic, processes below/and aboveground and survival of whole plant. The mechanisms involved with root tolerance to extreme temperatures are far less investigated. The goal of this study was to investigate adaptive and acclimative, physiology and metabolic properties and mechanisms of bell pepper cultivars in response to extreme soil temperatures. Aeroponic low root zone temperatures (7, 14, 17, and 27 °C), winter and summer field conditions, were used for the evaluation of physiology and then GC-MS and elemental analyzer platforms used for the investigation of carbon-nitrogen central metabolism of four bell pepper cultivars will be discussed.

Audience Take Away:

Tolerance to extreme root zone temperature by bell pepper cultivars manifested in:

- Efficient regulation of photosynthesis and stomatal conductance,
- Effective utilization and assimilation of carbon and nitrogen,
- Induction of stress-related metabolites and potential root and shoot growth.

Biography

Currently, PhD. research student (which am completing November, 2017) combines a multidisciplinary research, including ecophysiology, metabolic profiling and soil physics, working on the effects of extreme temperature on crops. A main focus of this research is the root system and its interaction with the aboveground. My research revealed novel findings on tolerance mechanisms of both monocots and dicots. The multidisciplinary nature of my research enables the development of novel solutions for extreme temperatures which is one of the most yield-limiting factors in agronomy.

Development of leafy head upon microRNA coordination

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²Graduate School of the Chinese Academy of Sciences, China

Leafy head and bulb are a type of agricultural products composed of incurved leaves. Many crops with these products undergo a leaf curvature transition from downward to inward upon aging. In a previous study, we used flat and upwardly-curved leaves of Chinese cabbage (*Brassica campestris* ssp. *pekinensis*) to clone the BcpLEAFY HEADS (BcpLH) gene. Here we report that BcpLH controls a composite trait of heading through microRNAs. In the transgenic plants of Chinese cabbage, BcpLH antisense lowers BcpLH protein contents, causing the earliness of leaf incurvature and heading with a round-to-oval head shape transition; and its Arabidopsis ortholog HYL1 inhibits BcpLH activity, resulting in the lateness of heading, due to the incorrect cleavage sites in a subset of primary miRNAs that are competent to bind BcpLH and the altered interrelationship between miRNA pathways that interact genetically. Using QTL mapping of head traits within a population of 150 recombinant inbred lines (RILs) of *B. rapa*, we investigated the relationship between expression levels of miRNA-targeted BrpTCP4 genes and head shape. Herein, we demonstrate that a cylindrical head shape is associated with relatively low BrpTCP4-1 expression, whereas a round head shape is associated with high BrpTCP4-1 expression. In the round-type Chinese cabbage, miR319 accumulation and BrpTCP4-1 expression decrease from the apical to central regions of leaves. Overexpression of Brp-MIR319a2 reduced the expression levels of BrpTCP4 and resulted in an even distribution of BrpTCP4 transcripts within all leaf regions. Changes in temporal and spatial patterns of BrpTCP4 expression appear to be associated with excess growth of both apical and interveinal regions, straightened leaf tips, and a transition from the round to the cylindrical head shape. These results suggest that the miR319a-targeted BrpTCP gene regulates the round shape of leafy head via differential cell division arrest in leaf regions. Therefore, manipulation of miR319a and BrpTCP4 genes are potentially important tools for use in the genetic improvement of head shape in these crops. Our findings suggest that plant coordinates miRNAs for interplay between aging and morphological transitions.

Biography

March of 1978-December of 1981: studied in Vegetable Section of Horticulture Department, Northwestern Agricultural University and the thesis for Bachelor Degree was "Effect of ethylene on maturing of tomato fruits". January of 1982-December of 1984: studied for Master Degree in Vegetable Section of Horticulture Department, Northwestern Agricultural University and the degree thesis was "Physiology of virus disease resistance in Chinese cabbage". October of 1987-November of 1988: studied as visiting scholar in Institute for Horticultural Plant Breeding, Wageningen, The Netherlands, and majored on genetic transformation of Brassica crops with *Agrobacterium rhizogenes*, distant crosses of Brassica crops. June of 1990: got Ph.D. degree in Cytology Section of Biology Department, Lanzhou University, and the thesis was "Genetic transformation of *Agrobacterium rhizogenes* and resistance to the transformants in Brassica crops"

Work experiences: January of 1985-December of 1987: worked as a lecture in Horticulture Department, Northwestern Agricultural University and studied on genetics and breeding, and tissue culture of Crucifer vegetable crops. December of 1991-December of 1993: worked as a postdoctor in National Laboratory of Plant Molecular Genetics, Shanghai Institute of Plant Physiology, The Chinese Academy of Sciences, and majored on transfer and expression of exogenous auxin genes in Brassica crops. December of 1993-now: work in Shanghai Institute of Plant Physiology and Ecology, The Chinese Academy of Sciences.

Differential oxidative and biochemical responses of tomato and maize leaves to *Spodoptera exigua* herbivory

Induction of the activities of antioxidant enzymes as a possible mechanism for *Spodoptera exigua* herbivory resistance in maize rather than tomato leaves

Sameera Omar Bafeel*, Manal El zohari, Wafa Alzahrani
King Abdulaziz University, Science college, Saudi Arabia

Herbivory by chewing insects causes an oxidative burst, characterized by the production of hydrogen peroxide giving rise to both local and systemic responses. Hydrogen peroxide is well known signaling molecule that can activate the antioxidant system to enhance the plant defense response. In his study, we investigated the relationship between antioxidant responses in tomato and maize after *Spodoptera exigua* attack and the plant resistance. As an indication for plant resistance, fresh and dry biomass of tomato and maize shoot was determined. All data were collected after 2 hours, 2 days and 7 days following infestation. The results indicated that, shoot fresh and dry weight of tomato significantly decreased lower than control (uninfected plants) under all studied feeding times. On the other hand, maize leaves fresh and dry biomass did not decrease than controls at 2 hours and 2 days after infestation. The infestation significantly increases H₂O₂ and ascorbic acid concentration in maize leaves at 2 hours and 2 days after infestation while no change recorded in tomato leaves compared to their corresponding controls. Free phenols content significantly increased in infected only in tomato leaves more than control. The infestation significantly enhances the activities of SOD, CAT and APX in maize leaves but had no significant effect on SOD and CAT activity in tomato plant; only APX activity enhanced. In maize, the highest enzymatic activity recorded after 2 days of infestation. The highest APX activity was observed at 7 days after infestation in tomato. Taken together we could conclude that antioxidant system in maize induced and enhance plant defense to *Spodoptera exigua* infestation.

Biography

Sameera O. Bafeel is a Professor of plant physiology at King Abdulaziz University in Saudi Arabia. She received her Ph.D. in Plant Physiology at Agriculture and Plant Science Department, Mississippi State University (MSU, USA) 2005. Her research interests are Environmental Stress of plant (biotic and abiotic stress)

Manipulation of the starch granule number and morphology in *Arabidopsis thaliana*

JoergFettke*

Molecular Plant Physiology, University of Potsdam, Germany

Starch plays an important role in the plant life cycle. Furthermore, starch is an important source for industrial applications. However, the process of starch granule formation is so far obscure. Neither the physic-chemical mechanisms of starch granule formation nor all necessary proteins/enzymes have been identified. Our results clearly illustrate that starch synthase 4 (AtSS4) and the plastidialphosphorylase (AtPHS1) are differently involved in starch granule formation and do not act in series. Besides these two enzymes, also proteins related to starch granule degradation have an impact on the starch granule formation, especially on the granule surface properties and morphology. We discuss the generation of starch granules and the formation of specific starch granule morphologies, as the alteration of starch granules has a significant impact on applications.

Biography

2003 - Diploma Degree in Biology, area Plant Physiology (with honors)

2006 - Ph.D. (Dr.rer. nat.) in Molecular Plant Physiology (summa cum laude)

2008- 2013 - Leader of 'Centre of Mass Spectrometry of Biopolymers' at the University Potsdam, Germany

2011 - Habilitation (Dr.habil.) in Molecular Plant Physiology

2012 – PD (associated Prof) for Molecular Plant Physiology (University of Potsdam, Germany)

2012-2015 Visiting Professor for Plant Biochemistry at Warsaw University of Life Sciences, Poland

10.2011- 12.2013 - Chair 'Plant Physiology' at the University of Potsdam, Germany

Since 2014 - Leader of the 'Biopolymer Analytics' group at the University of Potsdam, Germany

2017 – Prof for Molecular Plant Physiology (University of Potsdam, Germany)

A novel CBF from oil palm that regulates abiotic stress response and the ripening process through modulation of the ethylene signaling pathway

Siti Nor Akmar Abdullah^{*1}, Ph.D., Mortaza Ebrahimi², Ph.D., Parameswari Namasivayam¹, Ph.D.

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A novel C-repeat binding factor (CBF) encoding an AP2-domain protein isolated from oil palm fruit (EgCBF3) demonstrated the highest expression level in the mesocarp at the ripening stage. In the mesocarp tissue, expression of EgCBF3 was upregulated by abiotic stresses including cold, drought and salt stresses as well as phytohormones (ethylene and ABA) treatments. EgCBF3 was shown to bind to DRE/CRT promoter element through in vitro electrophoretic mobility shift assay (EMSA) and in vivo yeast-one hybrid assay. Transient expression of EgCBF3 in tomato fruits influenced the expression profile of the ethylene and abscisic acid biosynthesis-related and ripening-related genes indicating that EgCBF3 can mediate abiotic stress response in ripening fruits and may function as a regulator of ripening process-related genes. The effects of ectopic expression of EgCBF3 in transgenic tomato were also studied. The EgCBF3 tomatoes demonstrated altered phenotypes compared to the wild type tomatoes. These include delayed leaf senescence and flowering, increased chlorophyll content and abnormal flowering. The EgCBF3 tomatoes demonstrated enhanced abiotic stress tolerance under in vitro conditions. In addition, the expression levels of ethylene biosynthesis-related genes were altered in the EgCBF3 tomato leaves and roots compared to that in the wild type tomato plant. Altered expression of eight antifreeze protein genes was also observed. Together, the results of this study suggest possible role of EgCBF3 in regulating abiotic stress response and the ripening process through modulation of the ethylene signaling pathway

Audience Take Away:

- Structure and function of a novel C-repeat binding factor isolated from the oil palm
- Evidence for its role in fruit ripening mediated by ethylene signaling pathway
- Evidence for its role in abiotic stress response
- Potential candidate gene for genetic improvement through molecular marker development and genetic manipulation

Biography

Prof. Datin Dr. Siti Nor Akmar Abdullah is currently the Director of the Institute of Plantation Studies and a Professor in Plant Molecular Biology at the Faculty of Agriculture, Universiti Putra Malaysia. Her current research focuses on functional genomics, genetic manipulation and biomarker technology for yield and oil quality improvement, efficient nutrient uptake and disease monitoring in oil palm. She has published extensively in journals of international repute with five patents granted related to genetic engineering tools and molecular disease diagnosis. She has delivered talks in Australia, China, India and Indonesia and served as a reviewer for many peer-reviewed journals.

An ecological approximation for the study of Arbuscular mycorrhizal fungi (AMF) sporulation in Mediterranean sand dunes.

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¹University of Valencia, Spain

²Technical University of Loja, Ecuador

The Arbuscular mycorrhizal fungi (AMF) belong to the phylum Glomeromycota. These fungi form an important symbiotic association with most plant species, in such a way that the plant receives inorganic nutrients from the fungus and the fungus obtains sugars from the plant. This interaction is very important for ecosystems with low nutrients availability, as it is the case of the sand dunes on the Mediterranean Coast. The main goal of our study was to determine AMF distribution and the optimal conditions for their sporulation. To this end, samples of the rhizosphere of 4 structuring plants (*Elymus farctus* (Viv.) Runemark ex Melderis, *Ammophila arenaria* (L.) Link, *Echinophora spinosa* L. and *Otanthus maritimus* (L.) Hoffmanns. & Link) were collected in 2 sand dunes habitats (2110 and 2120, according the directive 92/43/CEE) as well as in their ecotone. Samplings were taken in 6 geographical locations along the coast and in each season for two years (2014-2015; 2015-2016). The mentioned habitats are characterized by a high soil mobility, low vegetable coverage and exposition to sea flood; all these environmental factors decreasing intensity from the habitat 2110 up to 2120. The preliminary statistical analysis using presence/absence data showed that the probability of finding AMF spores differed according to locality, habitat (lower probability at the habitat closest to the sea), and sampling season (higher sporulation in spring). However, no significant effects of plant species were found on the probability of finding AMF spores. Focusing on AMF species composition, Redundancy Analysis showed a significant ordination model, with the forward selection of particular localities, plant species, habitats and sampling seasons, which notably affected which AMF taxon was found in each sample. Further analysis of soil composition would help understanding if the effects of the studied categorical variables could be related to particular differences in soil traits such as humidity or nutrient availability.

Audience Take Away:

- The sand dunes restoration is a problem in many sites around the world. To know how the spores of the AMF change along the time and the space can be a conservation strategy to protect sandy areas that still remain in good conditions and to have a reservoir of AMF that can be use for restoration of other places. In addition, to know what AMF species sporulate in the field can be a good way to use the beaches to obtain fungi, replicate them in the laboratory and to try these fungi in different conditions to improve the agriculture production.
- If the audience is interested in the ecological restoration, they will be able to replicate the same methodology in other ecosystems or in the same ecosystem but in other locations. Is this research that other faculty could use to expand their research or teaching? Yes, this investigation can offer the possibility of the expand other research, including the factor AMF sporulation in your study. Does this provide a practical solution to a problem that could simplify or make a designer's job more efficient? Provide an efficient design for the sand dunes restoration. Will it improve the accuracy of a design, or provide new information to assist in a design problem? This investigation provides new information for design a problem. For example, it provides information for collect spores of AMF of the field. This is a practical solution for sand dunes restoration and for using the AMF in the agriculture. List all other benefits.

Biography

I got my Biology degree on 2013 and my master's degree on 2014. I am 26 years old and nowadays I am focused in my Ph.D. The topic of my doctorate is "Spatial-temporal variations in the composition and the abundance of AMF in vegetable taxa of interest for the sand dunes restoration". In the year 2015 I won the grant "Atracció de Talent" of the University of Valencia. Since then I am working on it and teaching practical classes on Biology at the University of Valencia. I have attended to several Congress about my Ph.D. topic and, finally, now I am staying for 3 months at the International Bank of Glomeromycota (BEG, Dijon, France) under the surveillance of Dr. Dirk Redecker. The University of Valencia is supporting my stay.

ThapsigarganicaL. in vitro plants as a new production platform of thapsigargin

Carmen Quiñonero López^{*1}, PhD., Patricia Corral², PhD, Franck Michoux², PhD, HenrikToft Simonsen¹

¹University of Copenhagen and Technical University of Denmark, Denmark

²Evonik, Germany

Thapsigargin is a sesquiterpene lactone isolated from *ThapsigarganicaL.*, a Mediterranean plant. Thapsigargin is a potent inhibitor of the sarco/endoplasmic reticulum Ca²⁺-ATPase (SERCA) pump, increasing the cytoplasmic levels of free Ca²⁺ and inducing apoptosis. This mechanism was used to develop a Thapsigargin-based cancer drug, currently in Phase IIB clinical trials by Inspyr Therapeutics. Our current work is focused on the development of sustainable production platforms of this plant based on in vitro tissue culture. In vitro novel biomass from leaf explants, shoot regeneration and rooting was achieved. Thapsigargin production in shoot cultures growing in temporary immersion bioreactors (TIBs) have been enhanced using abiotic stress treatments. In vitro shoots are able to produce 0.34% and 2.1% dry weight of Thapsigargin and Nortrilobolide respectively, comparable with leaves and stems of wild *T. garganica* plants containing between 0.1 - 0.5% of Thapsigargin and below detectable levels of Nortrilobolide. In addition, in vitro shoots were used to study the regulatory role of the two only discovered genes, TgTPS2 and TgCYP76AE2, involved in the Thapsigargin biosynthesis through Real Time-PCR.

Audience Take Away:

- The audience could use my research as an example about how in vitro tissue culture can be used for a sustainable production source of interesting secondary metabolites.
- The research gives an approach for the production of thapsigargin; sesquiterpene lactones used as anticancer treatment currently in Phase IIB of clinical trials.
- In addition, the research shows how in vitro tissue culture can be used for the study of gene expression in metabolic pathways.

Biography

I, Carmen Quiñonero López am a third year Industrial Marie Curie fellowship at University of Copenhagen and the Technical University of Denmark, under the main supervision of HenrikToftSimonsen. The first part of my research has been conducted at the company AlkionBiopharma in France under the supervision of Franck Michoux. At present, the second part is being performed at the Technical University of Denmark. I plan to graduate in October 2017. My main Phd research concern is in vitro production of secondary metabolites of interest in plant tissue cultures.

How does indole-3-butyric acid induce adventitious root formation in *Arabidopsis thaliana* thin cell layers?

Laura Fattorini^{*1}, Angela Velocchia¹, Federica Della Rovere¹, Simone D'Angeli¹, Giuseppina Falasca¹, Maria Maddalena Altamura¹
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Adventitious roots (ARs) are post-embryonic roots essential for plant survival and vegetative propagation via cuttings. In different types of explants, the auxin indole-3-acetic acid (IAA), and its natural precursor indole-3-butyric acid (IBA), when applied exogenously, are the main inducers of AR formation. In many cases, exogenous IBA is more effective in inducing ARs than exogenous IAA, but the reason needs investigation. *Arabidopsis thaliana* thin cell layers (TCLs) consist of stem inflorescence tissues external to the vascular system. Previous researches demonstrated that in TCLs excised from *A. thaliana* and tobacco exogenous IBA induces ARs when combined with kinetin (Falasca et al., Plant Cell Rep, 2004; Fattorini et al., Planta, 2009). However, in dark-grown *A. thaliana* seedlings IBA is able alone to induce AR formation (Velocchia et al., J Exp Bot, 2016). In cuttings as in planta, the endogenous IAA/IBA contents are determinant for the AR process, and differences in response to exogenous IAA/IBA may depend on differences in endogenous contents. It is unknown whether *A. thaliana* TCLs contain endogenous IAA/IBA at culture onset. Results showed that IAA and IBA were at undetectable levels at culture onset, and this was an optimal premise to investigate AR formation under the total control of exogenous auxin, revealing possible differences between IAA and IBA. The AR response of TCLs from various ecotypes, transgenic lines and knockout mutants showed that IBA was an AR inducer better than IAA. IBA positively affected IAA cellular influx, mediated by AUXIN RESISTANT1 (AUX1) and LIKE AUXIN RESISTANT3 (LAX3), and efflux, due to PIN-FORMED1 (PIN1), and expression of ANTHRANILATE SYNTHASE-alpha1 (ASA1), a gene of the tryptophan-dependent IAA biosynthesis. Results support that ASA1 and ANTHRANILATE SYNTHASE-beta1 (ASB1), the other subunit of the enzyme, are required for AR formation in the presence of exogenous IBA. The AR response of IBA-treated TCLs from ech2ibr10 mutant, blocked into IBA-to-IAA conversion, was strongly reduced, showing that IBA action is indirect, i.e. IBA acts mainly by conversion into IAA. Nitric oxide (NO), a downstream signal of IAA, but also a by-product of the conversion process, was early detected in IAA- and IBA-treated TCLs, but at higher levels in the latter ones. Altogether results showed that exogenous IBA induced AR formation in TCLs by conversion into IAA involving NO, IAA transport, and ASA1/ASB1-mediated IAA biosynthesis.

Audience Take Away:

- This presentation may be useful in understanding the mechanisms through which the auxin indole-3-butyric acid (IBA) controls the formation of adventitious roots in cuttings (and also in planta, being the natural precursor of indole-3-acetic acid).
- New informations on the mechanisms of hormone action on root formation may be object of teaching, in order to improve the knowledge of plant development.
- The results may be useful to for planning experiments to overcome the rooting recalcitrance of species of economic value.

Biography

Laura Fattorini was graduated in Natural Sciences at Sapienza University of Rome on 2006. She attended the Ph.D School in Botanical Sciences in the Department of Environmental Biology of the same University and, after three years, obtained the Doctoral Degree. During the following years she worked as PostDoc and her current position is RTDB Researcher. Her research experience focusses on hormonal and genetic control of root development and xylogenesis in plants and thin cell layers (TCLs), of *Arabidopsis thaliana* in particular. Besides, she investigated the effects of cadmium and arsenic on root development, quiescent centre activity and auxin transport and the effects of the endomycorrhizal symbiosis on cadmium and arsenic accumulation in adult plants of *Nicotianatabacum*. She is co-author of 18 publications on scientific journals/book and 36 communications in national and international congresses.

Global Conference on Plant Science and Molecular Biology

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Valencia, Spain

Contributions of plant tissue culture to plant science

Meltem Bayraktar*

AhiEvrans University, Turkey

One of the most important characteristics of plant cells is totipotency. Because of this characteristic, every plant cell possesses the genetic ability to regenerate an entire plant. Plant tissue culture is based on the totipotential characteristic of plant cells. It is the science of growing plant cells, tissues or organs aseptically cultured on agar or in liquid medium under controllable physical and chemical conditions. From its first discovery in the early 1900's to today, a considerable progress has been made in plant tissue culture and a lot of plant tissue culture techniques like meristem, anther, isolated microspore, ovule, ovary, protoplast, cell culture techniques etc. have been developed. These techniques are used for different purposes in various areas of plant science. In this presentation, plant tissue culture techniques and their contributions to plant science will be discussed.

Audience Take Away:

- This presentation contains information about many areas of plant science and thus it appeals to a wide range of audiences.
- Researchers who do not have enough information on this area will increase their knowledge and they will be able to connect with their own area.

Biography

Meltem BAYRAKTAR got her bachelors' degree in Biology in 2000 and then her master degree in Biotechnology in 2004 at Ege University in İzmir/Turkey. She completed her PhD programme in Biotechnology Department of Ege University by specializing on Plant Tissue Culture and now conducts her research activities as an Assistant Professor of Genetic and Bioengineering Department at AhiEvrans University in Turkey. She has studies on micropropagation of fruit and forest trees, ornamental, medicinal and endangered plants; large-scale propagation in bioreactors; disease-free plant production; secondary metabolite production via plant tissue cultures. She has future interest in the production of plant secondary metabolites in bioreactors using plant cell, tissue and organ cultures, in addition to her interest in in vitro selection studies.

Comparative evaluation of biochemical changes in tomato (*Lycopersicon esculentum* Mill.) infected by *Alternaria alternata* and its toxins (TeA, AOH and AME)

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The present study investigates the phytotoxic effect of metabolites produced by phytopathogenic fungi *Alternaria alternata*. We have evaluated the physiological response associated with defence signalling network and the biochemical and molecular changes relevant to three potent phytotoxins including tenuazonic acid, alternariol, and alternariol monomethyl ether. The necrotic lesions produced by pathogen were found to be as similar as those infiltrated with these toxins in tomato plants. The biochemical changes due to toxins induced cell death are characterized by increased H₂O₂ production, increased activity of defence related antioxidative enzymes such as SOD, APx, CAT and GR in order to maintain the level of H₂O₂ produced due to these toxins. APx, CAT and GR were increased for first 48 hours and then decreased furthermore whereas the SOD activity was found to be higher for the first 24 hours and then decreased successively. The isoenzymatic profile of SOD and CAT were found to be higher in pathogen treated plants compared to control. The cellular damages due to phytotoxic effect include lipid peroxidation as evidenced by increased MDA content and reduced chlorophyll content. The assessments of cell death were measured by Evans blue dye and the DAB staining predicts the possible sites of H₂O₂ accumulation as remarkable from reddish brown coloration of tissues ultimately leading to cell death and DNA damages. Thus, a fine tuning occurs for the defense related antioxidative enzymes against detoxification of key ROS molecules and are effectively regulated in tomato plant against pathogen treated and metabolites challenged oxidative stress.

Key words: *Alternaria alternata*, pathogen, phytotoxic metabolites, toxins, Polymerase chain reaction (PCR)

During the presentation we will discuss about the Pathogenic fungus *Alternaria alternata* and its toxins. We will discuss about the isolation, identification and purification of *Alternaria alternata* pathogen. We will discuss about the *Alternaria* toxins their isolation, purification and characterization by different liquid chromatography techniques. We will also discuss the effects of these toxins on the tomato plants and comparative evaluation of physiological and biochemical changes induced by the phytopathogenic *Alternaria alternata* during pathogenesis in tomato plants.

Audience Take Away:

- The study confirms the role of *Alternaria* mycotoxins has phytotoxic effects. The toxin induced biochemical changes evaluates its potency and contribution in disease development.
- The physiological and biochemical defense response as evidenced by increased activities of defense enzymes and generation of ROS molecules is an important indication of the role of these key molecules in plant-pathogen interactions.
- Some mycotoxins are host selective and play an important role in fungal virulence and therefore, in disease development. Further studies on these phytotoxins could resolve the better understanding of host-pathogen interactions and could be used as an antibiotic against noxious pathogens.
- Currently, these phytotoxins are used as probes for rapid screening of plant clones or the progenies from crosses for disease resistance.

Biography

The author (Mukesh Meena) did Ph.D. from Department of Botany, Institute of Science, Banaras Hindu University, Varanasi, India. My Ph.D. title was "Physiological and biochemical changes induced in tomato by *Alternaria alternata* and its phytotoxic metabolites" and completed under the supervision of Prof. R. S. Upadhyay, BHU. I am well versed with culture techniques and taxonomy of fungi. I am also well versed with various analytical tools relevant to mycopathological research.

Sessions on: Plant Biotechnology | Medicinal and Aromatic Plant Sciences

Session Chairs

Elena Rakosy-Tican
Babes-Bolyai University,
Romania

Sergio Molinari
IPSP-CNR
Italy

Session Introduction

Title: Biotechnologies for ex situ Conservation of botanical important Plant Species and molecular Techniques used for investigating in vitro genetic Stability

Victoria Cristea, Babes-Bolyai University Cluj-Napoca, Romania

Title: Transforming the future of agriculture through synthetic photorespiratory bypass

Selcuk Aslan, Max Planck Institute of Molecular Plant Physiology, Germany

Title: Identification of transcriptional regulators of cereal grain development and quality

Sofia Kourmpetli, Cranfield Soil and AgriFood Institute, UK

Title: RNA spray fights fungus

Aline Koch, Justus-Liebig University, Germany

Title: Overcoming the challenges of determining genetic diversity in closely related genotypes that have undergone a genetic bottleneck

Seanna Hewitt, Washington State University, USA

Title: Sequencing of 260 Citrus Varieties: Linking Genotypes to Phenotypes

Javier Terol Alcayde, Centro de Genomica, IVIA, Spain

Title: Plant sex: How hot is too hot? Reproductive screening for heat tolerance in cotton

Susan Yvonne Jaconis, CSIRO Agriculture, Australia

Title: Improving the efficiency of wheat and triticale endogenesis: The starch story

Magdalena Szechynska-Hebda, Institute of Plant Physiology, Polish Academy of Sciences, Australia

Title: There is far more to underutilised cereals than meets the eye

Acga Cheng, University of Malaya, Malaysia

Title: Fragrant plants used as air fresheners in private households

Henrik Toft Simonsen, Technical University of Denmark, Denmark

Title: Integrated analysis of phenome, genome and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase

Yeyun Xin, China National Hybrid Rice Research and Development Center, China

Title: Targeting chloroplast bicarbonate transporters BicA and SbtA to chloroplasts of Nicotiana for enhanced CO₂ fixation

Sandhya Mehrotra, Birla Institute of Technology and Science Pilani, India

Title: Using genomic repeat abundance and cytogenomic approaches to infer phylogenetic relationships in *Caesalpinia sensu lato* (Fabaceae)

Gustavo Souza, Federal University of Pernambuco Bioscience Center, Brazil

Title: Tightly controlled expression of bHLH142 is essential for timely tapetal programmed cell death and pollen development in rice

Rachel Swee-Suak Ko, Academia Sinica, ABRC/BCST, Taiwan, Province of China

Title: Increasing of secondary metabolites against malaria by mutagenesis

Kikakedimau Nakweti Rufin, Regional Center of Nuclear Studies of Kinshasa, Democratic Republic of the Congo

Title: Secretory structures of the leaves of *Hibiscus sabdariffa* Linn. (Malvaceae)

Yougasphree Naidoo, School of Life Sciences, South africa

Title: Medicinal plants and indigenous knowledge for well-being of local people in some areas of Southern Ethiopia

Mathewos Agize Ante, College of Natural and Computational Sciences, Wolaita Sodo University, Ethiopia

Title: Meta-Analysis of Economic Indicators in Developing Genetically Modified (GM) Cotton

Julian Witjaksono, The Assessment Institute for Agricultural Technology of Southeast Sulawesi, Indonesia

Biotechnologies for ex situ conservation of botanical important plant species and molecular techniques used for investigating in vitro genetic stability

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Nowadays, ex situ biodiversity conservation is a very important complementary approach of in situ conservation. Ex situ preservation is based on (i) classical methods (field collection, Botanical Gardens, Arboreta, Seeds banks) and on (ii) modern methods using biotechnologies (in vitro tissue culture and collection, medium and long-term preservation, artificial seeds, etc.). The Global Strategy for Biodiversity Conservation (2011-2020) claims that “at least 75 % of threatened plant species to be preserved in ex situ collections, preferably in the country of origin, and at least 20 per cent to be available for recovery and restoration programs”(target 8). In Romania, 14.5% of the vascular plant taxa are threatened (Dihoru and Negrean, 2009). The ex situ important botanically taxa conserved by our team are: *Lychnis nivalis*, *Moehringia jankae*, *Silene dinarica*, *Dianthus callizonus*, *D. giganteus* subsp. *banaticus*, *D. glacialis* subsp. *gelidus*, *D. henteri*, *D. nardiformis*, *D. pratensis* subsp. *racovitzae*, *D. spiculifolius*, *D. trifasciculatus* subsp. *parviflorus* and *D. tenuifolius*. These taxa were sampled from their natural habitats. All these taxa were successfully introduced in vitro and there are maintained during 3 to 9 years in ex situ collections. The in vitro experiments aimed to obtain an optimum multiplication and rhizogenesis rate. The rooted or unrooted vitroplants were ex situ acclimatized – in laboratory, in greenhouse and then outdoor, on a rocky area in the Botanical Garden.

Molecular analyses of the plant material to assess the somaclonal variability were carried out in more stages: at the moment of sampling, after in vitro preservation with or without slow growth, after cryopreservation. As methods for the evaluation of the modern preservation technologies we used molecular markers as SSR and ISSR. Molecular markers revealed genetic stability of preserved plants. In vitro culture induced several low differences between plants, thus ISSR markers are more valuable for analysis of the genetic stability of preserved plant. SSR markers are not so polymorphic in comparison with ISSR markers, thus SSR patterns were the same in plants preserved by different methods. SSR markers are valuable tools for analysis of genetic structure of the populations.

Audience Take Away:

- The audience – young and experimented researcher could adapt the ex situ conservation experimental protocols presented by us for other important plant species, especially for that which are botanically important in their region.
- Molecular markers used in this study could be easily used for analysis of other taxa, especially ISSR that use universal primers. In some instances SSR primers could also be used for genetic characterization of different related taxa, from the same family or genus.
- Our results could be used as the basis of the development of proper ex situ conservation programs for endangered, rare or endemic plants.
- Plants preserved by different methods could be used for repopulation of natural habitats if necessary.
- Experimental design used in our studies could also be used as teaching activities for students.

Biography

Cristea Victoria, Senior Researcher, coordinator of the Phytogeographical Department of Alexandru Borza Botanical Garden. Professional experience: plant biotechnology - in vitro multiplication and conservation, biodiversity conservation, somaclonal variability, phytogeography, plant physiology. 1 book and 1 book chapter; 2 national patents. 18 ISI indexed papers, 10 quoted ISI papers, 40 IDB papers, 25 papers in other journals.

Transforming the future of agriculture through synthetic photorespiratory bypass

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For a new green revolution to feed the continually increasing population, agriculture productivity has to be significantly improved. Photorespiration represents a big challenge in this respect, since it dissipates energy and leads to the futile loss of CO₂, thereby limiting plant growth yield. Earlier attempts of engineering photorespiration resulted in only limited improvement, mainly because they still lead to the counterproductive release of CO₂.

We designed synthetic photorespiration bypass routes that avoid CO₂ release altogether. One of these promising routes is tartronyl-CoA pathway, in which carbon dioxide is fixed rather than released. This pathway, having only a minimal overlap with non-photorespiratory endogenous metabolism, is expected to support up to 70% higher carbon fixation rate under varying light intensities and different intercellular carbon dioxide concentrations (corresponding to different levels of stomata opening).

The tartronyl-CoA pathway contains several novel reactions: glycolate is activated to glycolyl-CoA, carboxylated to tartronyl-CoA, and reduced twice to give glycerate, which can re-enter the Calvin Cycle via phosphorylation. To catalyze the novel reactions, which no known enzyme can support, promiscuous activities of enzymes catalyzing similar reactions were identified, enhanced via rational design, and tested in vitro.

Before implementing the synthetic pathway within photosynthetic organisms, we aim to confirm and enhance its in vivo activity. For this aim we use *E. coli*, an ideal host for pathway evolution as it can be easily engineered, has a short doubling time, and can be cultivated continuously for a long period. We established a set of *E. coli* deletion strains, each requiring a different magnitude of flux via the synthetic pathway for growth. Specifically, we dissected glycolysis into three segments, such that glycerate, the pathway's product, serves as the sole precursor for one, two, or three of the segments. Hence, each of our selection strains imposes a different level of selection pressure on pathway activity. After optimizing pathway activity within a low-selection strain, it is introduced to a higher-selection strain and optimized again; this process proceeds until high pathway activity is established. The optimized pathway will then be transferred to cyanobacteria and higher plants to test their effect of photosynthesis rate and yield.

Audience Take Away:

- Synthetic photorespiration pathways that do not release carbon dioxide could significantly enhance photosynthetic rate and yield.
- Photorespiration can be engineered to fix carbon rather than release it.
- Enzyme engineering is vital for establishing the most promising synthetic pathways.
- *E. coli* provides an excellent tool for pathway evolution in vivo, before its introduction into photosynthetic organisms.
- Carefully designed selection schemes can serve to gradually evolve higher pathway activity

Biography

I received my B.Sc. degree in biology at the University of Gaziantep (Turkey), studying molecular identification of pathogens of chickpea. I completed my master's degree at Linköping University (Sweden), where I investigated the adaptation of landrace barley to day-length and frost-conditions. I obtained my PhD in Molecular Cell Biology from SLU in Uppsala, Sweden. During my PhD, I demonstrated a novel strategy of utilizing intermediates of the de novo fatty acid biosynthesis pathway in vegetative tissue for the production of wax esters in tobacco plants. I further engineered rice endosperm to reallocate carbon flux. Presently, as a postdoctoral researcher at Max Planck Institute, I engineer synthetic photorespiration pathways, using the model bacterium *E. coli* as a testbed, with the aim to implement the novel routes in photosynthetic organisms.

Identification of transcriptional regulators of cereal grain development and quality

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Temperate cereals, such as wheat, barley and rye, are of great importance for human consumption and animal feed. Even though breeders have been constantly improving the yield potential and quality traits of these major crops, our understanding of the genetic regulatory networks that control key aspects of grain development and quality is still limited. Brachypodium distachyon, as a sister to the core pooids that include the above mentioned cereals, represents a good model for the study of grain development and evolution. Using a comparative developmental and transcriptomic approach, we aim to gain an insight into the transcriptional regulation of key stages in grain development and how they might affect the final grain quality.

We have sequenced the transcriptome of several developmental stages of the Brachypodium grain, from pre-anthesis ovaries, to mature grain. A germination stage was also included in our analysis, in order to capture the transcriptomic changes that occur during this dynamic process. Finally, a young seedling sample was sequenced alongside, to serve as a vegetative control, but also to shed more light into the plants' early life after grain germination. Our comprehensive transcriptomic analysis, represents a new valuable resource for the investigation of gene expression patterns throughout grain development and germination. Used in a comparative context, it can contribute to the identification of novel gene functions and new transcriptional regulators of grain quality traits in cereal crops.

Audience Take Away:

- This is a newly developed resource that can be utilized by researchers working on cereal crops to identify potential targets of future research and breeding programmes.
- The talk will also highlight the potential of using model plants to understand more genetically complex crops, such as wheat

Biography

Sofia Kourmpetli is a lecturer at Cranfield University, UK, and the director of an MSc course in Future Food Sustainability. Her current research focused on grain development and the genetic control of grain quality traits in cereal crops. She is particularly interested in investigating the genetic regulatory networks that link fundamental developmental biology with metabolic processes in the grain, with the aim of gaining a better understanding of the complex mechanisms that control grain quality and identify targets for potential crop improvement.

RNA spray fights fungus

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Meeting the increasing food and energy demands of a growing population will require (the development of) developing ground-breaking strategies that promote sustainable plant production. RNA interference has emerged as a powerful genetic tool for scientific research. The demonstration that agricultural pests, such as insects and nematodes, are killed by exogenously supplied RNA targeting their essential genes has raised the possibility that plant predation can be controlled by lethal RNA signals. Host-induced gene silencing has shown great potential for controlling pest and diseases in crop plants (Koch et al. 2013, Koch and Kogel 2014, Abdellatef et al. 2015). However, while delivery of inhibitory noncoding double-stranded (ds)RNA by transgenic expression is a promising concept, it requires the generation of transgenic crop plants which may cause substantial delay for application strategies depending on the transformability and genetic stability of the crop plant species. Using the agronomically important barley - *Fusarium graminearum* pathosystem, we alternatively demonstrate that a spray application of a long noncoding dsRNA (791 nt CYP3-dsRNA), which targets the three fungal cytochrome P450 lanosterol C-14 α -demethylases, required for biosynthesis of fungal ergosterol, inhibits fungal growth in the directly sprayed (local) as well as the non-sprayed (distal) parts of detached leaves (Koch et al. 2016). Unexpectedly, efficient spray-induced control of fungal infections in the distal tissue involved passage of CYP3-dsRNA via the plant vascular system and processing into small interfering (si) RNAs by fungal DICER-LIKE 1 (FgDCL-1) after uptake by the pathogen. We discuss important consequences of this new finding on future RNA-based disease control strategies. Given the ease of design, high specificity, and applicability to diverse pathogens, the use of target-specific dsRNA as an anti-fungal agent offers unprecedented potential as a new plant protection strategy, thereby opening novel avenues for improving crop yields in an environmentally friendly and sustainable manner.

Overcoming the challenges of determining genetic diversity in closely related genotypes that have undergone a genetic bottleneck

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Identification of genetic polymorphisms and subsequent development of molecular markers is important for marker assisted breeding of superior varieties of economically important species. Sweet cherry (*Prunus avium* L.) is an economically important, non-climacteric tree fruit crop in the Rosaceae family and has undergone a genetic bottleneck due to breeding—This has resulted in limited genetic diversity in the sweet cherry germplasm that is utilized for breeding new varieties. Therefore, it is critical to recognize the best platforms for identifying genome-wide polymorphisms that can help identify and consequently preserve the diversity in a genetically constrained species. For the identification of polymorphisms in five closely related genotypes of sweet cherry, a gel-based approach (TRAP), modified reduced representation sequencing (TRAPseq), a 6k cherry SNParray, and whole genome sequencing (WGS) approaches were evaluated in the identification of genome-wide polymorphisms in sweet cherry cultivars. All platforms facilitated detection of polymorphisms among the genotypes with variable efficiency. In assessing multiple SNP detection platforms, that study has demonstrated that a combination of appropriate approaches is necessary for efficient polymorphism identification, especially between closely related cultivars of a species. The information generated in this study provides a valuable resource for future genetic and genomic studies in sweet cherry, and the insights gained from the evaluation of multiple approaches can be utilized for other closely related species with limited genetic diversity in the germplasm.

Audience Take Away:

- The information gained from these genotyping approaches, whether they are used independently or in conjunction with one another, will assist in future breeding decisions and facilitate efficient crop improvement when there is a lack of diversity in the germplasm.
- The audience will gain insight into a variety of methods of genome-wide polymorphism detection; this is particularly important for crop breeders, as higher resolution methods of polymorphism detection will allow for improved variety production and selection.
- As preservation of genetic diversity has become increasingly important, this information will add to the toolset which can be used to help preserve diversity via understanding relationships between closely related genotypes of a species.
- The manuscript containing the methods and results discussed in the presentation has been accepted for publication, so this information will be available to anyone who wishes to use it as a resource in their research and/or work.

Biography

Seanna is PhD student in the Molecular Plant Sciences Program at Washington State University (USA). In the lab of Dr. Amit Dhingra, she studies biochemistry, physiology, and genomics of fruit ripening, looking at both fundamental and applied aspects of this complex process. The ultimate goal of her research is to reduce food waste associated with unpredictable ripening of fruit. In addition to her thesis research, Seanna recently completed an internship at BioBam Bioinformatics, in Valencia, where she advanced her knowledge of bioinformatics and computational biology.

Sequencing of 260 citrus varieties: Linking Genotypes to Phenotypes

Javier Terol^{*1}, Victoria Ibanez¹, Ph.D., Carles Borreda¹, Estela Perez¹, Jose Carbonell², Ph.D., Ximo Dopazo², Francisco Tadeo¹, Mauel Talon¹

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Elucidation of genomic sequences is an essential and necessary first step to identify genetic variants associated with agronomic traits of interest. The Citrusseq Consortium, a joint effort developed by public institutions and private companies has sequenced the genomes of 260 citrus varieties with the Illumina platform at high average coverage. Paired end genomic DNA libraries of 100 (2x) bp reads and with an average insert size of 500 bp were constructed. The haploid genome of *Citrus clementina* was used as reference genome. More than 260 *Citrus* genomes including rootstocks and species of mandarins, oranges, lemons, grapefruits and limes were sequenced. The consortium also generated a web portal that allows searching and sequence comparisons among approximately 8 million of gene variants and 45 billion of base pairs. The stored information can help unravel fundamental aspects of biological and evolutionary interest such as the origin of citrus. From the commercial standpoint this information may help to authenticate varieties, to improve marker-assisted breeding and to identify genes of major agronomic interest.

Audience Take Away:

- Feedback about crop improvement using genomic tools will be provided
- This work offers a practical solution that simplifies the generation of new citrus varieties, saving time and resources during the process
- We have developed a technology for varietal certification based on genomic analysis that can be transferred to other crops.

Biography

I've been involved in plant genomics since 1997, when I participated in the sequencing of the genome of the model plant *Arabidopsis thaliana*, the first plant genome obtained. Since 2003 I've been working at the Genomics Centre at the IVIA, developing genomic tools for the generation of new citrus varieties. Our team at the IVIA had a leading role in the sequencing of the genome of *C. clementina*, which has become the reference genome for the *Citrus* genus. I'm involved now in GBS and GWAs studies, in order to obtain markers suitable for their use in the generation of new citrus varieties.

Plant sex: How hot is too hot? Reproductive screening for heat tolerance in cotton

Susan Yvonne Jaconis^{*1}, Ph.D., Warren Conaty¹, Ph.D.
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Lacking voluntary locomotion, plants are highly susceptible to the stresses of their immediate surroundings. In particular, abiotic factors such as high temperature and low moisture can have adverse effects on cotton (*Gossypium* spp.) including negative effects on plant growth, development, and subsequently yield. There is a general lack of studies focusing on cotton reproductive characteristics as an early indicator of stress tolerance despite the direct impact on boll (fruit) production. Because plant sexual reproduction and especially pollen is highly sensitive to the environment, the aim of this study was to investigate floral pollen tube germination and growth as well as boll development under both temperature and water stress. In this study, we grew cotton cultivar Sicot 746 B3F in both irrigated and non-irrigated (rainfed) systems. To impose a heat stress, open top chambers were used in both irrigation conditions. Flowers at zero days post anthesis were collected from these treatments for in vivo microscopic analysis to quantify the germination percentage and tube length of successfully deposited pollen on floral stigmas. In addition, open flowers were tagged for boll analysis of seed number and size, lint percentage, and fibre quality at the end of the growing season. We hypothesized that elevated temperature and water stress as individual stressors would decrease the percent germination and tube length of pollen into the floral style of cotton plants and that seed set would be negatively impacted. It was expected that applying both heat and water stress simultaneously would have a cumulative negative effect on these early reproductive traits. This research will be used to understand the physiology and floral biology of cotton under stressful environmental conditions, which will help develop early screening tools in cotton breeding.

Audience Take Away:

- A greater understanding of the abiotic stressors affecting Australian cotton
- A method of in vivo pollen examination which has applications in many floral reproductive studies and teaching
- The significance of pollen as an independent unit exposed to its surrounding environment.
- An understanding of how physiology and reproductive biology has potential use in breeding programs.

Biography

Susan Yvonne Jaconis is a postdoctoral fellow at the CSIRO Agriculture and Food business unit of Australia. She works with an abiotic stress team on a joint venture between plant physiology and cotton breeding at the Australian Cotton Research Institute. Her Bachelor of Science is in Plant Biology with a minor in Environmental Toxicology from North Carolina State University (2010). She received her PhD from the University of Cincinnati in Biological Sciences with her research focusing on air pollution and plant physiology (2015).

Improving the efficiency of wheat and triticale androgenesis: The starch story.

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Androgenesis is an important tool for plant genetics and breeding, since androgenic embryos can germinate into completely homozygous doubled haploid plants. The stress-induced reprogramming of microspores precedes the induction of androgenesis. Most of the genes identified to be differentially expressed during stress treatment to induce androgenesis are involved with stress hormones, cellular protection from stress, proteolysis and sucrose–starch metabolism. Our findings provide ultrastructural and molecular evidence to support the hypothesis that the repression of starch biosynthesis may play an important role in blocking gametophytic development during androgenesis induction in wheat and triticale. Further, our studies aimed to identify structural changes in proplastids at different stages of androgenesis that prevent chloroplasts formation and results in albinism of androgenesis-derived plants. The expression pattern of selected genes related to sucrose–starch metabolism directly corresponds to internal changes in the plastids. These changes are limited to accumulation of starch grains, typical for plastids that continue to function in the same manner as during normal formation of pollen. Finally, we found that light-emitting diode (LED) irradiation at some particular wavelength could reduce the ratio of albino to green seedlings. The illumination system provides light in the spectral region that is involved in photosynthesis and in the photomorphogenic responses, therefore the probable regulatory mechanisms adjusted by LED were identified. The work was supported by PBS3/A9/37/2015 project operating within the Applied Research Programme of the □ National Centre for Research and Development.

Audience Take Away:

- Androgenesis is highly useful for plant breeding, as well as in a wide range of biological research. However, for widespread use this process must be efficient. Despite several decades of research on the phenomenon of androgenesis, many processes involved are obscure. We will clarify some of them.
- Albinism often occurs in androgenesis-derived plants, including wheat and triticale. The direct cause of albinism is the inability of proplastids to transform into chloroplasts; the biological mechanism has not been elucidated. We will present some evidences helpful to understand the albinism.
- Some practical and methodological aspects of the androgenesis will be discussed.

Biography

Doctor in the Biological and Agricultural Sciences. Employment: The FranciszekGorski Institute of Plant Physiology, Polish Academy of Sciences in Krakow, Poland. Second affiliation: Department of Plant Genetics, Breeding and Biotechnology, Warsaw University of Life Sciences. 2006-2008 Forskare (Assistant Professor) at Department of Botany Stockholm University (Sweden). 2015-2016 postdoc position at the University of Konstanz. Scientific interest: Androgenesis, chloroplast to nucleus retrograde signaling, systemic acquired acclimation and systemic acquired resistance.

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There is far more to underutilised cereals than meets the eye

Acga Cheng*

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A warmer world can have both positive and negative impacts on agriculture. Nonetheless, many recent studies have, unfortunately, point to the latter. The prevalent changes in climate have instigated a causal effect on the consistency of food productions in a world where population and food demands continue to escalate. These occurrences are expected to trigger a major influx of price hikes in basic commodities, which could, subsequently, lead to an imminent food crisis. Although the inception of the Green Revolution a half-century ago has drastically improved the productivity of several major staples, preeminently the big three cereals; wheat (*Triticum aestivum*), maize (*Zea mays*), and rice (*Oryza sativa*), it has unexceptionally also done some harm to the environment by virtue of pollution and erosion. While there is no single recipe for achieving food security, laying the first stone on having a more diversified food sources and agricultural systems could be the foundation of addressing this issue. Recently, unlocking the potential of underutilised cereals has been considered as one of the primary strategies for climate resilient agriculture. A concerted global effort is crucial in keeping the momentum going, especially when the possibilities are endless with the recent advances in agricultural biotechnology. This paper will present a sound evidence-based knowledge on the genetics and biology of three trending underutilised cereal crops; namely amaranth (*Amaranthus hypochondriacus*), quinoa (*Chenopodium quinoa*), and teff (*Eragrostis tef*). This paper will also discuss the specific climate resilient traits possessed by each of these cereal crops; painting a vivid picture of the promising potential of these cereals as the next big three which could, perhaps, save a hotter and hungrier world.

The genetics and biology of three current trending underutilised cereal crops; namely amaranth, quinoa and teff will be discussed. The specific climate resilient traits possessed by each of these cereal crops will also be discussed, providing an in-depth understanding of their growth and development under extreme conditions.

Audience Take Away:

- The audience will be able to learn more about the three new cereal crops for the future
- The presentation will provide an in-depth understanding of morpho-physiological responses of the selected underutilised cereals to different environmental conditions, which would serve as a cornerstone in providing a deeper insight into their growth patterns
- The presentation offers a dynamic platform to spread the consciousness of food and nutrition security

Biography

Acga Cheng received her PhD from the National University of Malaysia, and has recently become a Fellow of the Higher Education Academy. Her research interests lie in the area of molecular biology and plant genetics. She is currently a Senior Lecturer at the University of Malaya, Malaysia. In recent years, she has focused on the development of a handful of potential underutilised crops, notably teff, which has been hailed as one of the most promising crops for the future. The ultimate aim of her current research is to improve global food and nutrition security.

Fragrant plants used as air fresheners in private households

Henrik Toft Simonsen*

PhD, DTU Bioengineering, Technical University of Denmark and Mosspiration Biotech IVS, Denmark

Direct assembly of multiple linear DNA fragments via homologous recombination, a phenomenon known as in vivo assembly was recently introduced as a technology for transformation of the moss *Physcomitrella patens*. This technology has enable us to establish several sesquiterpenoid-producing lines in this green cell factory. We have demonstrated that we in moss can produce up to 200 mg/L amorphadiene (the precursor for Artemisinin) and that we can achieve a production of 0.21 mg/g dry weight of Artemisinin within just a few days of cultivation. Similarly we have established lines that produce several fragrances of patchoulol, santalene, bisabolol, α -humulene and valencene at the levels between 0.2 – 1.8 mg/g dry weight. Altogether, this show that the moss is a very good cell factory for the production of terpenoids and in particularly sesquiterpenoids. This has allowed us to establish a fragrant moss line.

Our research also demonstrates that employing the same strategies as for yeast, such as upregulation of HMGR and overexpression of FPPS enhances the overall yield of terpenoids.

These proof-of-principle experiments have paved the way for more complex and increasingly flexible approaches for large-scale metabolic engineering in plant biotechnology. First was the successful integration of five active genes for Artemisinin, but the focus is now for truly freshening fragrances for private households.

Audience Take Away:

- A fast and stable production and bioengineering tools will be presented.
- A new producer of fragrances is presented.
- The presentation also show how basic research can lead to a small start-up based on a novel product line.

Biography

Henrik Toft Simonsen obtained his PhD degree for the Danish University of Pharmaceutical Sciences in 2002, following a post doc at University of Cambridge he took up a post doc at University of Copenhagen in 2006. Here he established his research group and became an Associate Professor in 2008. In 2016, he moved to the Technical University of Denmark with his research group. HTS founded the company Mosspiration Biotech together with Hansol Bae in 2016. HTS has published more than 50 papers and 5 patents.

Integrated analysis of phenome, genome and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase

Longping Yuan¹, Prof., YeyunXin^{*1}, PhD., Zhiyuan Huang¹, Master, Qiming Lv¹, PhD., Xiqin Fu¹, PhD., Bingran Zhao¹, PhD., Lihuang Zhu², Prof., Dayong Li², PhD., Xiaofeng Cao², PhD., Caiyan Chen³, PhD., Donghai Mao³, PhD., Shuhui Song⁴, PhD.

¹State Key Laboratory of Hybrid Rice, Hunan Hybrid Rice Research Center, China

²State Key Laboratory of Plant Genomics and National Center for Plant Gene Research, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China.

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⁴BIG Data Center, Beijing Institute of Genomics, Chinese Academy of Sciences, China

Hybrid rice is the dominant form of rice planted in China, and its use has extended worldwide since the 1970s. It offered great yield advantage and has contributed greatly to the world's food security. However, the molecular mechanism underlying heterosis remained a mystery. In this study we integrated genetics and omics analyses to determine the candidate genes for yield heterosis in a model two-line rice hybrid system, Liang-you-pei 9 (LYP9) and its parents. Phenomic study revealed that the better parent heterosis (BPH) of yield in hybrid is not ascribed to BPH of all yield components but specific to the BPH of spikelet number per panicle (SPP) and paternal parent heterosis (PPH) of effective panicle number (EPN). Genetic analyses then identified multiple quantitative trait loci (QTLs) for these two components. Moreover, a number of differentially expressed genes and alleles in the hybrid were mapped by transcriptome profiling to the QTL regions as possible candidate genes. In parallel, a major QTL for yield heterosis, rice heterosis 8 (RH8), was found to be the DTH8/Ghd8/LHD1 gene. Based on the shared allelic heterozygosity of RH8 in many hybrid rice cultivars, a common mechanism for yield heterosis in the present commercial hybrid rice is proposed.

Audience Take Away:

- Heterosis (hybrid vigor) is an interesting topic for both breeders and biologists. However, although heterosis has been applied successfully to increase crop yields, the molecular mechanisms involved remain obscure. Here we integrated phenomics analysis with genome resequencing, transcriptional profiling, and QTL mapping to identify the genes (QTLs) responsible for the yield-related trait components.
- Our research highlights the importance of integrative methods to uncover the molecular mechanism of heterosis. In order to understand the mechanisms underlying heterosis in rice, we have undertaken sequential research steps towards identifying the genes responsible for yield heterosis in Liang-you-pei 9 (LYP9), which is a model two-line super-hybrid rice from the cross of Peiai64S (PA64S) × 93-11, and was ranked the #1 hybrid rice cultivar in China from 2002 to 2007. We first sequenced the genome of the paternal variety 93-11, and then profiled and compared the transcriptomes of LYP9 and its two parents at various life stages. Subsequently, we released the whole genome sequence of the other parental line, PA64S, and developed a recombinant inbred line (RIL) population consisting of 219 RILs derived from LYP9 and a backcross population (RILBC1) derived from crossing each RIL with the female parent PA64S. In this study, we integrated phenome analyses, QTL mapping by genome resequencing, and transcriptome profiling to identify genes that drive yield heterosis in LYP9s. As a result, the multiple quantitative trait loci (QTLs) cumulatively drive yield heterosis in hybrid rice by regulating two grain-yield component traits in which the RH8 (rice heterosis 8) gene plays a major role was found.
- We encourage the other faculty use the results we obtained in our study to expand their research or teaching.

Biography

Yeyun Xin (PhD), female, was born in September, 1966. Dr. Xin is a research professor at Hunan Hybrid Rice Research Center. She has been working in the field of hybrid rice research for 20 years. Her research orientation is hybrid rice molecular technology. As a team backbone in one of the six major research orientations including rice heterosis mechanism, the PI project of State Key Laboratory of Hybrid Rice, Dr. Xin has been engaging in the research on the mechanism and utilization of heterosis in rice since the establishment of State Key Laboratory of Hybrid Rice in 2011.

Targeting chloroplast bicarbonate transporters BicA and SbtA to chloroplasts of *Nicotiana* for enhanced CO₂ fixation

PanchsheelaNogia¹, M.Sc, Vandana Tomar¹, M.Sc, GurpreetKaurSidhu¹, M.Sc, Rajesh Mehrotra¹, Ph.D, Sandhya Mehrotra^{*1}, Ph.D,
¹Birla Institute of Technology and Science, Pilani, India

In C3 plants, the photorespiratory process that occurs because of the oxygenase activity of the primary CO₂ capturing enzyme Ribulose 1,5bisphosphate Carboxylase/Oxygenase (RubisCO) renders majority of our crop plants poor in terms of productivity. A persistent lower CO₂ concentration due to diffusive resistance at the chloroplast results in reduced RubisCO carboxylation and increased oxygenation, thereby enhancing the expenditure of metabolic energy to recycle carbon and nitrogen via photorespiration. This situation is worsened again by increases in temperature due to a drop in the affinity of RubisCO for CO₂ and an increase in the oxygenase reaction, a situation that is quite important in the context of climate change. Inspirations are hence drawn from lower organisms which possess carbon concentration mechanisms (CCM) to turbo-charge RubisCOs CO₂ supply. It has been proposed that the installation of CCMs into chloroplasts will improve photosynthetic yield and water use efficiency and reduce losses due to heat stress in C3 plants. In this context, one strategy involves transfer of cyanobacterial bicarbonate transporters such as BicA and SbtA to inner envelope membrane of the chloroplast. In our attempt to attain this objective, chimeric genetic elements containing transit peptide (TP) elements from *Arabidopsis thaliana* and two cyanobacterial bicarbonate genes BicA and SbtA (TP6/12+bicA gene and TP3/4+sbtA gene) were prepared and fused upstream of the gus and gfp reporter genes into a plant expression vector pRI 101-AN and pCAMBIA1302 respectively. All the recombinant constructs were transformed into *Agrobacterium tumefaciens* GV3101. pRI constructs were further used to transform *Nicotianatabacum* plants via co-culture of *Agrobacterium* cells with plant leaves/callus and the protein expression was analysed by histochemical GUS assay. Upon obtaining a positive GUS assay, we determined the subcellular location of the targeted proteins by confocal microscopy. To this end, all the pCAMBIA constructs were transiently transformed into *Nicotianabenthiana* leaves by agroinfiltration. Four days post agroinfiltration, protoplast samples were prepared from transformed leaves and GFP expression was analyzed under confocal microscope. We found chloroplastic location for TP4+SbtA. In the case of TP12+BicA construct, protein expression was majorly detected in either cytosol or in golgi or in endoplasmic reticulum with extremely low fluorescence. For determining the exact location of expressed proteins, the results obtained are being confirmed by western blotting. The constructs depicting correct localization and significant levels of expression would be further used to generate stable transgenic plants and their growth rate and photosynthetic performance would be evaluated.

Audience Take Away:

- The role of RubisCO's ambiguous substrate specificity on productivity of C3 plants.
- That several organisms possess carbon concentration mechanisms (CCM) to curtail the above mentioned loss.
- That these CCMs could be incorporated into C3 plants to increase their productivity.
- From this presentation, the audience will take home the information on the current state of art of the ongoing research on RubisCO and carbon concentration and the worldwide attempts to tackle this issue. The subject matter finds its place in the central theme of textbook plant biology and biotechnology and hence will update the audience for both research and teaching. The agricultural productivity and the factors affecting them will always remain a matter of concern for public and scientists alike. Any successful attempt at this research topic will definitely provide a practical solution to the problem of food security in the changing climatic scenario. This biotechnological intervention to incorporate into our crop plants what they lost during the course of evolution is proposed to alter the scenario of crop productivity and their water use efficiency especially with rising global temperature. In addition the research will benefit the cause of CO₂ sequestration hence benefit the environmental cause as well.

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Biography

Sandhya Mehrotra earned her Ph.D from National Botanical Research Institute, Lucknow, India in 2003. She then joined as a post doctoral fellow at Nara Institute of Technology and Science, Nara, Japan where she studied carbon metabolic pathways in lower organisms. She joined Birla Institute of Technology and Sciences, Pilani, Rajasthan, India in November 2008 and has been serving as a faculty member in the Department of Biological Sciences since then. Her research mainly focuses on carbon fixation, RubisCO and related genes, transcription control and designer promoters and lipase mediated biofuel production. She has more than 30 publications in journals of repute and serves as editor and reviewer of several journals from time to time.

Using genomic repeat abundance and cytogenomic approaches to infer phylogenetic relationships in *Caesalpiniasensulato* (Fabaceae)

Gustavo Souza*

Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil

Brazil is a mega-diverse country and has one of the richest floras in the world with about 32,360 species of vascular plants, of which 18,082 are endemics. Among the taxa well represented in its flora, the Leguminosae family (Fabaceae), the third largest family of flowering plants, stands out. Botanically, this family is characterized as trees, herbs, bushes or vines, with mainly alternating phyllotaxy, usually compound leaves and fruit of the legume type. In Brazil, 210 genera and 2,694 species, of which 1,458 are endemic and 190 considered rare, are registered. The family has a great economic importance for food, forage, horticulture, timber and medicine. The systematics of Leguminosae has advanced in recent years due to a better understanding of their evolutionary relationships. Doyle et al. (1997) have first indicated the monophyly of the Mimosoideae and Papilionoideae subfamilies and the paraphyletism of Caesalpinoideae. This complex relationship was confirmed in later studies, suggesting that the traditional classification of Leguminosae in three subfamilies needs to be reviewed. In Caesalpinoideae, the genus *Caesalpiniasensulato* (s.l.) stands out for being pantropical and consists of about 150 species that vary in habit (trees, shrubs and lianas) and are preferably distributed in arid environments such as the Seasonally Dry Tropical Forests. *Caesalpinias.l.* has a complex taxonomy, with different proposals for the separation into smaller genera. Lewis (2005) proposed the division of the group into seven genera: *Coulteria*Kunth, *Erythrostemon*Klotzsch, *Guilandina* L., *Libidibia*Schlt, *Mezoneuron*Desf, *Poincianella* Britton & Rose and *Tara* Molina. Of these only five were confirmed as monophyletic clades in later molecular phylogeny studies. Furthermore, this phylogenetic analysis revealed three well-supported clades (*C. trothae*, *C. erianthera*, and *C. trichocarpa* clades), which can be treated as new genera. However, more detailed taxonomic revisions are needed. An example of this was the circumscription of the genus *Arquita* Gagnon, G. P. Lewis & C.E. Hughes, recently proposed based on molecular phylogenetic analysis, formed by two species of the Andean region. These species are difficult to distinguish morphologically from nearby genera what led *Arquita* to be described as a “cryptic” genus. Therefore, additional approaches, such as cytogenetic analyses, may reveal synapomorphies to help in a better delimitation of these groups. *Caesalpinias.l.* is karyotypically characterized by its numerical stability ($2n = 24$), with small chromosome size and similar morphology. Nevertheless, in plant groups with numerically stable karyotype, detailed analysis using chromosome banding and fluorescence in situ hybridization (FISH) have allowed a better understanding of karyotypic evolution. A recent cytogenetic analysis revealed that the South American species of *Caesalpinia* have high heterochromatic diversity, with variable number of CMA+/DAPI- bands on the proximal and/or distal regions in the analyzed species. Moreover, a correlation between the pattern of heterochromatin and the geographical distribution of species was observed, suggesting that amplification of repetitive sequences may have some environmental influence. With the current facility of obtaining and analyzing a large number sequences, next generation sequencing (NGS) has become an useful tool in characterizing plant genomes. Thus, even genomes of non-model species are now possible to explore, enabling the discovery of repetitive sequences and their use in phylogenomic/phylogenetic approaches. Among these methods, the use of the platform RepeatExplorer provides a high potential tool in the discovery of repetitive sequences and comparative analysis of genomes. Thus, data from genomic sequences of different species of *Caesalpinia* will enable the identification of repetitive sequences that constitute the heterochromatin of the different species of the genus. The comparative bioinformatic analysis will also enable a comparison of the similarity between repetitive fractions of species from different clades, allowing better understand the genomic evolution of the group. The repetitive fraction of the genome, often overlooked was recently reinterpreted, with the demonstration of its use for phylogenetic analysis. This project aims to generate citomolecular and genomic data to support the investigation of evolutionary relationships in *Caesalpinias.l.*, especially the evolution of heterochromatin. For this, we will examine in more detail by NGS the genomes of eight species, covering the major clades of the genus. It is intended also to incorporate phylogenomic approaches, generating cladograms based on abundance and similarity of repetitive genome sequences. The generated topologies will be compared with conventional phylogenies newly available for *Caesalpinia*. Finally, these data aim to test the new classification system of *Caesalpinias.l.*,

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I have a graduation in Biology from the State University of Southwest of Bahia, Brazil (2006), a Master's degree (2008) and a PhD (2012) in Plant Biology from the Federal University of Pernambuco. Currently I'm Professor at the Federal University of Pernambuco, Brazil, and linked to the Department of Botany and Post-Graduate Program in Plant Biology - PPGBV. I have experience in Plant Genetics and Evolution in two main lines of research. In the Line of Plant Molecular Cytogenetics, it carries out studies of cytotaxonomy and chromosome evolution of native and cultivated species. In the line of Molecular Systematics, it operates in the areas of phylogeny and phylogeography, as well as in cytophylogeny - integration of karyotype data to molecular phylogenies using Phylogenetic Comparative Methods.

Tightly controlled expression of bHLH142 is essential for timely tapetal programmed cell death and pollen development in rice

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¹Academia Sinica Biotechnology Center in Southern Taiwan, Taiwan

²Agricultural Biotechnology Research Center, Academia Sinica, Taiwan

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⁴School of Biological Sciences, Washington State University, USA

Male sterility is important for hybrid seed production. We previously showed that knockout of bHLH142 in rice (*Oryza sativa*) causes pollen sterility by interrupting tapetal programmed cell death (PCD) and bHLH142 coordinates with TDR to modulate the expression of EAT1. In this study, we demonstrated that overexpression of bHLH142 (OE142) under the control of ubiquitin promoter also leads to male sterility in rice by triggering the premature onset of PCD. Protein of bHLH142 was found to accumulate specifically in the OE142 anthers. Overexpression of bHLH142 induced early expression of several key regulatory transcription factors in pollen development. In particular, the upregulation of EAT1 at the early stage of pollen development promoted premature PCD in the OE142 anthers, while its downregulation at the late stage impaired pollen development by suppressing genes involved in pollen wall biosynthesis, ROS scavenging and PCD. Collectively, these events led to male sterility in OE142. Analyses of related mutants further revealed the hierarchy of the pollen development regulatory gene network. Thus, the findings of this study contribute to our understanding of the central role played by bHLH142 in the regulatory network leading to pollen development in rice and how alteration in its expression affects pollen development. Exploitation of the novel functionality of bHLH142 may confer a big advantage to hybrid seed production.

Audience Take Away:

- Transcription factor bHLH142 plays an important role in rice pollen development regulatory network. Tightly and timely expression of bHLH142 is essential to ensure normal pollen development.
- Potential of genetic engineering male sterility rice line by overexpression or silencing of bHLH142.
- bHLH142 is an anther-specific expression. It is desirable from the perspective of GMO food biosafety because anther-specific expression will avoid any unintended expression in other tissues, especially in the edible part of the seed.

Biography

Rachel S-S Kodevototes herself in functional genomics studies in rice and orchid. She identified a key bHLH transcription factor in rice that is essential in rice pollen development. She is interested to carry out detail study on the molecular mechanism underlying pollen development, aiming to improve agriculture application of male sterility line for hybrid rice yield improvement.

Increasing of secondary metabolites against malaria by mutagenesis

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Malaria is one of the most important health problems in tropical and subtropical regions. The estimated clinical cases for WHO were 216 million in 2010, approximately disease, mainly children under 5. A major obstacle to malaria control is the emergency and spread of antimalarial resistance drugs, and urgent efforts are necessary to identify new classes of antimalarial drugs.

Plants produce more than thousands of different compounds through the secondary metabolism pathways. Secondary metabolites are often the keystone in the interactions between plants and their environment. The properties of these molecules are used in traditional medicine (80% of the World's population, especially in the developing world), but also in modern allopathic medicine through the use of purified or derived components obtained from chemical hemi-synthesis. Plants have been used medicinally throughout history, and the two best conventional antimalarial drugs, artemisinin from *Artemisia annua* and quinine from *Cinchona* sp, are both derived from traditional medicines.

Phyllanthusodontadenius present in all the coastal countries of West Africa to southern Africa. In Rwanda, the stem part extract is used to treat diarrhea and cholera. The alcohol crude extracts of leaves and stems have used to calm diarrhea induced castor oil in mice. It has been widely used in treating a number of traditional ailments and has demonstrated in vitro antibacterial actions against some bacteria, as well as in vivo and in vitro anti-malaria properties.

Metabolic engineering approach is one of pathways in the production of secondary metabolites with economic interest value. To that, metabolic engineering approach consists to modify the plant physiology to make it produce a molecule of economic interest. Experimentally, induced mutations provide an important source for variability. It is known that various chemicals have several effects on living organisms. Chemical mutagen generally produce induced mutations which lead to base pair substitution especially GC:AT resulting in aminoacid changes, which change the function of proteins but do not abolish their functions as deletions or frame shift mutations mostly. These chemomutagens induce a broad variation of morphological and yield structure parameters in comparison to normal plants.

Sodium azide (NaN₃) is a mutagen and it has proved to be one of the most powerful mutagens in crop plants. It is a common bactericide, pesticide and industrial nitrogen gas generator if known to be highly mutagenic in several organisms, including plants and animals. In order to understand that NaN₃ is mutagenic mechanism used for the improvement economic characters to many studies in crop plants.

In our works, NaN₃ was used as mutagen for increasing secondary metabolites with antimalarial effects in *P. odontadenius* aerial parts.

Results obtained on antimalarial activities showed that the best activities were 1.09±0.13 µg/ml (5 mM of NaN₃) to 1.04 ±0.02 µg/ml (10 mM of NaN₃) at the first generation (M1) and 3.26±0.05 µg/ml (7.5 Mm of NaN₃) to 4.52±0.12 µg/ml (10 mM of NaN₃) at the second generation (M2). These results coincided with the chemo-sensitivity of NaN₃ on seeds germination (LD30 = 4.76 mM and LD50 = 10.99 mM).

This work will be continuous for the stabilization of plant mutated and the characterization of plant mutations.

Audience Take Away:

- The audience will be use sodium azide for crop improvement or the same plant *Phyllanthusodontadenius* or others medicinal plants for secondary metabolites amplification.

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- The audience could use these techniques for their research. Others Professor or researchers could use for developing their teaching or research. This research provides a practice solution for malaria disease and provides new information to assist in a design problem. We worked on increasing secondary metabolites against malaria (*Plasmodium falciparum*) but sodium azide is a mutagenic agent for the improvement some crop plants.

Biography

Dr. KIKAKEDIMAU NAKWETI, Rufin (PhD)

Professor/Researcher

Plant Breeder and Genetics, Biochemist and Physiologist

CGEA/CREN-K, ISP/KENGE & UNIKIN

2015: PhD in Biology, Plant Molecular Biology, University of Kinshasa/DRC.

Dissertation topique: « Exploration des techniques d'amélioration de *Phyllanthus* en métabolites secondaires contre le paludisme: Mutagenèse et transgénèse de *Phyllanthus odontadenius* Müll. Arg. »

2007: DEA in Biology, Biotechnology, University of Kinshasa/DRC.

2000: License in Biology, Molecular Biology (Biotechnology), University of Kinshasa/DRC.

1997: Graduate record in Biology, University of Kinshasa/DRC.

Publications: In international journals: 13

Publications in the last 3 years: 6

Fellowship and Training course IAEA/FAO, Workshop (IRD and others): 7 (2005 to 2016)

Secretory structures of the leaves of *Hibiscus sabdariffa* Linn. (Malvaceae)

K. Raghu1, Y. Naidoo*¹

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Plant secretory structures are known for their role as phytochemical factories, and this character has been exploited by mankind for many centuries. More recently, however, medicinal plants have received considerable scientific interest, for the investigation of chemical principles in the drug discovery process. *Hibiscus sabdariffa* is an ancient medicinal herb of African origin that was used by the Chinese for the treatment of various cardiovascular ailments. Leaves of this species have recently been investigated for their anticancer and antihyperlipidemic properties. The present research employed various advanced microscopy techniques to determine and characterise the sites of phytochemical synthesis as well as to evaluate the main compound classes found within the leaves. Leaves appeared dark green with deep red margins and possessed glandular trichomes on both the abaxial and adaxial regions. The glandular capitate trichomes appeared to be clavate comprising of a multicellular club-shaped head and a 2-3 celled stalk. The frequency of trichomes differed with varying stages of leaf maturity with older leaves showing fewer numbers per unit area than emergent leaves. However, the abaxial surface was more abundantly covered than the adaxial surface. Histochemical evaluations on fresh leaf sections of *H. sabdariffa* showed the presence of numerous chemical compounds within trichome head cells. These included phenolics, alkaloids, acidic polysaccharides, acidic lipids and lipid oils which were prevalent in different regions of the trichome. Whereas phenolic and alkaloid compounds, as well as the flavone and flavanone compound groups were detected in methanol, hexane and chloroform crude extracts. Trichome ultrastructure revealed the existence of a subcuticular chamber on the ventral surface of the trichome, different to those observed in similar capitate trichomes. Secretion produced in the head cells were seen being deposited into the subcuticular chamber after traversing the periplasmic space and the cell wall. They appeared as electron-dense amorphous deposits. A second type of secretory structure was observed within the mesophyll and epidermis of *H. sabdariffa* leaves. Mucilage idioblasts were seen frequently among the adaxial epidermal cells. Their external appearance was characterised by a thickened cuticle surrounded by radially arranged epidermal cells. Mucilage idioblasts and mucilage secreting ducts are a distinguishing characteristic of the genus, and are described here in detail. Antibiotic resistance and the evolution of proliferative diseases necessitates the exploration for alternative and novel drug therapies. Research on the synthesis and activities of pharmacologically relevant compounds are important in furthering the advancement of drug development.

Audience Take Away:

- The incidence of secretory trichomes on a popular medicinal vegetable, *Hibiscus sabdariffa*, may confer certain pharmacological benefits to the consumer.
- These foliar trichomes are ultrastructurally complex and phytochemically diverse.
- Mucilage producing structures are also the sites of phytochemical synthesis and may produce putative biologically active compounds

Biography

Professor Yougasphree Naidoo is a researcher at the University of KwaZulu-Natal in South Africa. Her research interests include the specialised salt glands of marsh grasses and mangroves, secretory structures (trichomes, oil cells, mucilage cells) in medicinal plant species and the phytochemistry and ethnopharmacology of selected southern African medicinal plants.

Medicinal plants and indigenous knowledge for well-being of local people in some areas of Southern Ethiopia

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The traditional management, conservation and sustainable use of plant biodiversity in and around home gardens and the indigenous botanical knowledge in Loma and Gena Bosa districts (weredas) of Dawuro Zone, Southern Ethiopia has played an important role in conservation, sustainable utilization of plant biodiversity and in adaptation to the changes in climatic conditions of the environment as well as in primary health care. The information was gathered through semi-structured interview conducted with 112 medicinal plant practitioners, 32 spices vendors and 100 home garden owners whose ages ranged between 18 to 121 years. Samples of 100 home gardens (HGs) were considered and data on plant species of home garden were collected from 300 plots of 5m x 10m each in right, left and hind sites of home. The data were analyzed using SPSS computer software. The procedure for preference ranking and Shannon diversity index were also applied. A total of 178 medicinal plants distributed in 64 families were documented in this study. The most frequently used plant part was leaf while the growth form with the highest number (43.82%) of representatives among the plants encountered in this study were herbs. About 57.9% medicinal plants were collected from wild while 24.1% were cultivated and 18.5% were both cultivated and collected from wild. A total of 62 human and 27 veterinary diseases were documented in the study. However, only 58% of the traditional healers exercised their indigenous knowledge on treating both human and livestock diseases, while 41.96% practiced treatment of only human diseases. Very small dosage of preparations from some medicinal plants were given even as a drop for children and not allowed for pregnant women - with side effects of nausea, vomiting and diarrhea at therapeutic dosage. There is the practice of relating plant parts, colour, shape, habitat and distance with disease to be treated. Some medicinal and other multipurpose plants were under pressure due to agricultural expansion, firewood collection and selective harvesting for timber and construction materials. The medicinal plant resources and the associated knowledge of herbal medicine need to be used in a sustainable way and developed for more effective use in the future.

Key words: Ethnobotany, Indigenous knowledge, Medicinal Plants, Traditional healers

Audience Take Away:

- Medicinal plants diversity and their Uses: The information they get may help them to access the plant they lost/do not have to get opportunity for further study, to have collaborative work to conserve, train, extend and worldwide sense of utilization.
- Medicinal plants and indigenous knowledge: They might learn how far indigenous knowledge is become the base for modern medicine (the way they used for preparations, route of administration, application, and types of disease treated, contra-indication and side effects issues), giving care for patients (age, sex, conditions like pregnancy), used to conserve diversity of plants, to seek for opportunity for treating unforeseen/epidemic diseases. The presentation of indigenous knowledge in a manner accessible to others, such that they can see its relevance to their work, means avoiding jargon-loaded and obscure accounts, indigenous knowledge needs to be communicated to others so that they can appreciate their relevance.
- Acquisition and transfer of indigenous knowledge: May help the policy makers to design to participate indigenous people from assessment of problem through planning to implementation of projects, An important issue to consider regarding the future is to overcome the misleading 'science' versus 'local knowledge distinction'; set design to train indigenous people/knowledgeable persons, help to avoid expensive mistakes and modernize system; plan to fund assessment on indigenous knowledge before such a heritage of the world is lost/ the death of elders with the wealth of knowledge.
- Threats to medicinal plant availability and indigenous knowledge: The policy makers, administrators, researchers, and interested bodies may give attention to conserve, give directions, and provide alternative

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ways to tackle/reduce the risks of biodiversity.

- Management practices related to medicinal plants: Take lesson in managing resources and incorporating indigenous knowledge in development agendum. Benefit may arise for local area in different aspects.
- When relevant information is tapped, the respectful relationships are built with indigenous peoples; the sustainable management of their resources can enhance national and global action on climate change, food security, and socio-economic conditions as well as significantly contribute to conservation, sustainable use and the equitable sharing of benefits arising from biodiversity.

Biography

Mathewos Agize Ante, Date of birth- 17 June 1968

Educational background: B Sc. Degree and M Sc. Degree in Biology (Dryland Biodiversity) at Addis Ababa University and now I am at Assistant Prof. Level since 13 December, 2016 Senate Approval of Wolaita Sodo University, Ethiopia.

Work experience: Teaching biology for 17 years at high school (preparatory) level ;Worked for four years as expert of Biodiversity conservation and Environment protection under Natural Resources Management and Environment Protection Section in Dawuro Zone Agriculture Sector; four years' experience of working as lecturer, researcher and community service provider at university.

Community service (Awareness creation training) given on "Basic principles and skills on primary health care, dosage form development and plant biodiversity conservation for traditional medicine practitioners in Dawuro Zone, SNNPR". ; awareness creation training on "Integrated Natural Resources Management focusing on Biodiversity Conservation and Management" in the Kechi Research and Community Service Center in Dawuro zone.

Research and Publications: Seven publications; Six presentations of research works and Participation in workshops, seminars and conferences and Three editorial works.

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Meta-analysis of economic indicators in developing Genetically Modified (GM) Cotton

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Today's transgenic cotton are rapidly adopted by farmers around the world. Rising the area of growing GM cotton mostly derived from the yield and income gain. Both transgenic cotton and its counterpart in terms of profit gain are affected by yield, seed cost, pesticide cost, management and labor cost. This study is a meta-analysis as a synthesis of current research by searching literature both peer-reviewed and non peer-reviewed. This meta-analysis based on more than 40 individual studies across the countries of cotton performance which came from the data survey and field trials. The database set has been selected from both transgenic and conventional cotton in order to compare in terms of economic indicators. In this study would be assumed that economic indicators vary from region to region around the world or may have changed over time. This paper will discuss the delivery of this technology has no doubt that increasing yield, reducing the pesticide cost and raising income gain was the main factors for cotton growers to decide planting transgenic seed. Moreover, information from the individual studies that went into the meta-analysis, and an estimate of the overall results. This will also allow to discuss a visual assessment of the amount of variation between the results of this studies both GM cotton and its counterpart. The visual assessment is adapted from systematic review and meta-data analysis which examined economic indicators of GM cotton compared with non GM cotton. This paper also will discuss the benefits of the use GM cotton based on this study shows that, for example in China, GM seed has been adopted widely and rapidly by the farmers due to the yield gain and income gain as the main factors influencing cotton growing area.

Audience Take Away:

- Considering that the use of GM cotton now are the crucial factor based on the cotton demand of rising the world population
- How to boost the cotton production without destroying the environment or ecosystem. This study based on the individual studies performed that the reducing chemical spray is the main factors of using GM cotton
- The positive impact of the implementation of GM seed across the countries should be considered by not only the decision maker but also researcher and any stakeholders particularly in developing countries. For instance, GM seed is the prominent factor, however it is able to be counterbalanced when the crop can deliver higher yield. Increasing yield can raise the income. The expenditure cost of the post harvesters might be raised but it can offset the cost reduction of chemical spray.

Biography

Julian Witjaksono He has been working as a researcher since 2000 at The Assessment Institute for Agricultural Technology of Southeast Sulawesi with the subject of Environmental Economy. His research interest focus on Agro-economy biotechnology, farming system and policy analysis. He got his bachelor in socio economy agriculture from Haluoleo University in 1995 and graduated master degree in environmental management from Bogor Agricultural University in 2000. He studied his Ph.D in environmental sciences at Chinese Academy of Agricultural Sciences and graduated in 2014. His works have been published and presented through articles, national and international journals, meeting or conference in national and international forums. Approximately, he had collected the research paper more than 50 papers since he has been a researcher in 2005. As a researcher he always motivated to enhance his skills and knowledge through the training that have been funded by international organization, viz. Netherland Fellowship Program (NFP) in 2014, China Scholarship Council (CSC) in 2011, and Norman Bourlag Fellowship Program as the research fellow at the International Research Center for Tropical Agricultural (CIAT) in Columbia which funded by United States Department of Agriculture (USDA) in 2014. His research works have been funded by Australian Center for International Agricultural Research (ACIAR), Indonesia Ministry of Science and Technology, Indonesia Agency for Agricultural Research and Development, Farmer Empowerment Through Agricultural Technology and Information (FEATI) project, Sustainable Management of Agricultural Research and Technology Dissemination (SMARTD) project.

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Effects of CO₂ enrichment, high photosynthetic photon flux density and ammonium supply on growth and development of *Nicotiana benthamiana* used as a transient expression system for influenza virus hemagglutinin

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Plants are now proven production hosts for biopharmaceuticals and extensive research has been done over the last decade to develop molecular tools for recombinant protein yield improvement. Despite major advances, little is known about the effects of basic environmental parameters on plant biomass production prior to protein expression. In this study, we investigated three important environmental factors, atmospheric CO₂ concentration, photosynthetic photon flux density (PPFD) and different ratios of ammonium supply, on growth and development of the plant protein expression host *Nicotiana benthamiana* transiently transformed to express influenza virus hemagglutinin in the form of virus-like particles (HA-VLPs), in leaf tissue. High PPFD, CO₂ enrichment and high ammonium supply increased leaf fresh weight during plant growth phase, before *Agrobacterium* infiltration for protein expression. High PPFD and CO₂ enrichment also increased fresh weight at harvest (following the 6-day protein expression phase), but a high ammonium supply had the opposite effect. On a leaf fresh weight basis, high ammonium supply increased the content of both total soluble protein (TSP) and large Rubisco (RbcL) subunit, but had no effect on HA-VLP content. High PPFD had no effect on TSP and RbcL but decreased HA-VLP content, compared to CO₂ enrichment having no effect on TSP, RbcL and HA-VLP contents. On a plant basis, high ammonium supply increased RbcL content, decreased HA-VLP accumulation level under low PPFD and had no effect on TSP content. High PPFD significantly increased TSP and RbcL contents but decreased HA-VLP content at normal ammonium supply. CO₂ enrichment had a slight positive effect on TSP and RbcL contents but no effect on HA-VLP accumulation level. In addition, the increase in TSP content under high PPFD (significant) and CO₂ enrichment (tendency) correlated with the increase in RbcL. HA yield was not positively affected under those conditions.

Audience Take Away:

- Plants present several advantages over conventional expression platforms to produce recombinant proteins, including low-cost and convenience of use for large-scale cultivation setups, minimal risk of contamination with human pathogens or toxins, protein post-translational modifications comparable to those found in humans, and the potential for edible biopharmaceuticals production.
- Despite obvious advantages, obtaining maximum recombinant protein yields still requires investigation of the effects of basic cultural factors on plant growth and protein expression, and the building of a knowledge base to provide advice for large-scale production.
- Increasing recombinant protein yields implicates to balance leaf production and recombinant protein expression, i.e. not only increasing leaf biomass but also maximizing, or at least not compromising, recombinant protein content per leaf fresh weight.

Biography

Lingling Shang, originally from China, moved to Quebec City, Canada in 2013. She got a bachelor degree in Shandong Agriculture University in Shandong Province, China in 2010, and a master degree in China Agriculture University in Beijing, China in 2012. She worked at Syngenta Inc. as a trainee for one year, and then started Ph.D. studies at Laval University in 2013, with the personal objective of improving her skills and becoming an expert in plant science. The main focus of her work is to increase recombinant protein yields in plant expression platforms by the optimization of environmental factors in controlled environments.

Linking plant demography, ecological dynamics and population genetics across space and time

Alotaibi N. Nahaa^{1*}, Dr Bull C. James, Dr Luca Borger

¹Swansea University, United Kingdom

Connectivity between populations is vital to the survival of extinction-prone plants, including those at risk from local environmental change, as well as pests and pathogens, with globally important implications for applied plant ecology. The metapopulation concept has become the dominant paradigm for exploring the role of connectivity in this context. However, many metapopulation models incorporate very little detail about the underlying dispersal mechanisms (demography), and measures of connectivity based on contemporary dynamics and population genetics.

Seagrass is a group of flowering plants that live in shallow sheltered areas along the UK coastline where they form dense green meadows under the sea. It is one of the most significant sources of coastal primary production and it provides a critical habitat for juvenile reef fish and commercial fisheries. During the course of a long-term study of metapopulation dynamics in the seagrass, *Zostera marina*, around the Isles of Scilly, UK, we quantified demographic heterogeneity, population trends and spatial correlations within and between sampling sites. Here, we compare estimates of population connectivity inferred from these ecological dynamics with estimates of connectivity derived from a published panel of fifteen polymorphic microsatellites DNA markers. We test hypotheses on how long term declines in local seagrass populations are predicted to result in restricted genetic diversity and departure from Hardy-Weinberg equilibrium. We also explore whether spatial connectivity between local sites mitigates against population genetic changes at the broader spatial scale.

This project will aim to combine detailed measurements on individual plants with eco-evolutionary modelling and the latest population genetic and genomic approaches, to better understand the link between demography, dynamics and diversity. The over-arching goal of this study is to gain an understanding of the spatial population genetics of eelgrass, *Zostera marina*.

Audience Take Away:

- Understanding of population genetic structure and evolution of population and they can use it with their work.
- How can use microsatellite as a marker in determining genetic diversity.
- They will able to investigate the genetic background using a set of appropriate microsatellite markers.
- They can apply the study to other species.
- This research that other faculty could use to expand their research or teaching.
- Providing a practical solution to a problem as in decline of plants and the reasons.

Biography

I am studying a PhD in the Department of Biosciences, Swansea University, UK. PhD project is looking at spatial structure in population genetics in UK seagrass, *Zostera marina*. Supervised by Dr James Bull and Dr Luca Borger in the Department of Biosciences, Swansea University, UK. I have gotten Masters of Science degree in plant ecology from Princess Nora bint Abdulrahman University, Riyadh, Saudi Arabia. In 2011, I have been working in Princess Nora bint Abdulrahman University, Riyadh, Saudi Arabia. Masters project was looking at The effect of Autotoxicity and Intraspecific competition on the plantation and seedling growth in *Ziziphus nummularia*. I am interested in many research areas such as: Population Genetics structure, Competition and Allelopathy in plant community. I have contributed and participated in several businesses as a volunteer. I have many experiences and courses.

The movement of *Chlamydomonas reinhardtii* in response to light is mediated by abscisic acid

Layla Alhijab*, Heather Macdonald, Ian Wilson, Michael Ladomery
University of the West of England, U.K.

The phytohormone abscisic acid (ABA) regulates plant responses to various abiotic stresses and diurnal rhythms that alter their water status. Sequencing of the *Chlamydomonas reinhardtii* genome has shown that this flagellate, motile, freshwater, photosynthetic green alga is also capable of synthesising and responding to ABA. Algae were sampled at different time points over 24h in a cyclic 16h photoperiod and were treated with or without 50 μ M ABA in either the light or dark and their position in the water column was monitored by measuring the A750 at different depths. The actual position attained by the algae in the water column correlated with the time at which they were sampled in the cycle, but in general, ABA induced upward movement of the algae.

Plants possess a number of glycine rich RNA-binding proteins (GRPs) that appear to be involved in stress responses that are regulated by ABA. *Chlamydomonas* appears to possess only a single GRP gene which appears to encode a flagellum-associated protein, which we have termed CrGRP1, which may be involved in regulating its movement. Expression of CrGRP1 was assessed during the algal movement experiments described above and appeared to decline to the greatest extent when ABA induced the greatest upward movement of the algae.

The suggestion is that ABA regulates the movement of *Chlamydomonas* in the water column in order to position itself to optimise photosynthesis and that CrGRP1 negatively regulates the ABA-induced upward movement of the algae, presumably by binding mRNAs required for this response.

Abscisic acid (ABA)- glycine rich RNA-binding proteins (GRPs)- *Chlamydomonas reinhardtii*

Biography

I got my Biology degree on 2005 and my master's degree on 2012. I am 33 years old and nowadays I am focused in my Ph.D. The topic of my doctorate is "The movement of *Chlamydomonas reinhardtii* in response to light is mediated by abscisic acid". I have attended to several Congress about my Ph.D. topic and, finally, now I am at final year of my PhD under the surveillance of DrMichaelLadomery, Ian Wilson and Heather Macdonald at the Faculty of Health and Applied Sciences, University of the West of England, Coldharbour Lane, Frenchay, Bristol BS16 1QY, U.K

Stability of resistance to Fusarium head blight and Fusarium toxin accumulation in winter wheat lines over different environments

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Fusarium head blight (FHB) resistance of advanced winter wheat breeding lines was evaluated for three year in two locations (six environments). Lines were selected from breeding programs of Polish breeding companies based on their increased FHB resistance. They did not contain any FHB resistance genes from exotic resistance sources e.g. Sumai 3. Lines were sown in field experiments located in Cerekwica, Western Poland, and in Radzików, Central Poland. Three *Fusarium culmorum* isolates - two of DON-chemotype and one of NIV-chemotype - producing deoxynivalenol (DON), nivalenol (NIV) and zearalenone (ZEN) were applied for inoculum production. Wheat heads were inoculated at flowering stage with a mixture of conidial suspensions of the isolates, using the same mixture at both localities. Severity of head infection by *F. culmorum* was assessed (combined type I and II of FHB resistance). After the harvest, the frequency of Fusarium-damaged kernels (FDK) was visually assessed (type III of resistance). Wheat grain was analyzed for concentration of Fusarium mycotoxins (type V of resistance) and ergosterol (ERG) which is marker of fungal biomass amount in kernel (type III of resistance). Zearalenone was quantified using AgraQuant®ZON test kit. Trichothecenes of group B (DON and derivatives and NIV) were quantified using gas chromatography technique. Ergosterol amount was measured using HPLC technique.

In all six environments, we found significant differences between lines in all studied types of resistance. Lines showing moderate resistance to FHB and toxin accumulation were identified. Their reaction was stable over different environments. We found significant correlations between different years and locations for the most of variables; however, correlation coefficients varied depending on weather conditions.

Variables describing different types of FHB resistance correlated significantly. The highest coefficients were found for correlations: FDK vs trichothecenes B concentration and ERG vs trichothecenes B concentration. The lowest were coefficients for correlation between ZEN concentration and the other variables.

Audience Take Away:

- It is possible to identify winter wheat lines with stable FHB resistance (including mycotoxin accumulation in grain) without introduced resistance genes from exotic sources
- Most of the resistant lines possessed high yielding potential only slightly lower than the best (susceptible) lines
- In studied population of winter wheat phenotypic markers (head infection, kernel damage) were good predictors of mycotoxin (trichothecenes) concentration in grain, which does not work in other cereals e.g. triticale.

Biography

Master of Sciences degree in the field of Plant Pathology, at the Agricultural University in Warsaw. MSc thesis title: "Fusarium head blight of wheat, rye and triticale". Doctor of Philosophy degree in the field of Agricultural Sciences, at the Plant Breeding and Acclimatization Institute in Radzikow. PhD thesis title: "Importance of primary inoculum sources for epidemics of *Septoria nodorum* blotch of triticale." Research work in Department of Plant Pathology on fungal diseases of cereals: *Septoria nodorum* blotch and Fusarium head blight. Leading of research programs on Fusarium head blight of wheat, durum and triticale and creating of initial material for breeding of disease resistant wheat. Leading of laboratory working on diseases of cereals (Fusarium head blight of wheat, durum and triticale; Fusarium ear rot of maize), fungal metabolites analysis (mycotoxins, ergosterol, endotoxins) and faba bean diseases.

Identifying and characterising putative aldose 6-phosphate reductases in *Arabidopsis thaliana*

Pamela Cabedo¹, Barbara Rojas¹, Karina Olivos¹, Michael Handford^{*1}, Ph.D.

¹Universidad de Chile, Chile

In Rosaceae (apple, stone fruits) and Plantaginaceae (plantain) species, sugar alcohols like sorbitol are phloem-translocated and allow more efficient use of carbon, act as compatible solutes in abiotic stress (cold, drought, salt) and facilitate boron mobilisation. The key regulatory step in the synthesis of this acyclic polyol is catalysed by aldose-6-phosphate-reductase (A6PR) in source organs, which reduces glucose-6-phosphate. The resulting sorbitol-6-phosphate is then hydrolysed to form sorbitol, via sorbitol-6-phosphatase. In sink organs like roots and fruits, sorbitol is oxidised by NAD⁺-dependent sorbitol dehydrogenase (SDH) to fructose. Curiously, A6PR- and SDH-like enzyme activity is found in families that synthesise and transport sucrose, and in *Arabidopsis* (a sucrose-translocating Brassicaceae), we have identified two proteins with the structural features and >65% amino acid identity with known plant A6PRs; we call these AtA6PR1 and AtA6PR2. Unlike in Rosaceae, we demonstrate that AtA6PR1 and AtA6PR2 are ubiquitously-, but differentially-expressed in different *Arabidopsis* organs. By transient transformation of tobacco, we show that GFP-fusion proteins of both reductases are localised in the cytosol. Potential mutant lines have been genotyped, and along with studies of the relative expression of both genes in wild-type plants grown under different abiotic stresses (cold, saline), we are determining their physiological role in this non-sorbitol translocating species. Additionally, when AtA6PR1 is over-expressed in wild-type and *sdh*- mutant *Arabidopsis* lines, the starch content increases. Currently, similar experiments are underway with AtA6PR2 with the overall aim of analysing the effects that a potential mis-balance in sorbitol metabolism has on the plant. Progress in the biochemical characterisation of these proteins will also be presented. Funding: Fondecyt 1140527.

Audience Take Away:

- The importance of sugar alcohols, especially sorbitol, for the plant will be explained
- The identification and characterisation of several enzymes from *Arabidopsis* that are key in the synthesis and degradation of sorbitol will be described

Biography

Michael Handford is an Associate Professor in the Biology Department of the Faculty of Sciences in the Universidad de Chile. Since completing his PhD and postdoctoral fellowships in the University of Cambridge, he has focused his research on various aspects of plant metabolism, such as cell wall synthesis, and more recently on the metabolic changes that plants undergo in order to withstand abiotic stress conditions, including antioxidant and sugar alcohol metabolism. He also carries out multiple teaching and administrative commitments in the University, and for Chilean organisations.

The p24 protein of Citrus leprosis virus C (CiLV C) is a multi-pass transmembrane protein exposing N cytoplasmic-C lumen topology.

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Citrus leprosis, caused by Citrus leprosis virus C (CiLV C), is considered one of the major viral diseases of citrus in Brazil. Currently, the Brazilian state of São Paulo is the largest producer of orange juice and an estimated annual cost around US\$ 80 million is used to control this disease. Given the importance of the disease, many efforts have been made to unravel the pathosystem and to develop effective control methods of citrus leprosis. However, detailed understanding of the molecular processes involved in the manifestation of the citrus leprosis is still needed. For instance, until present there is no information about the functionality of the viral ORFs. In this context, the present work presents functional studies of the CiLV C p24 protein through studies of the association of p24 with the plant membrane network. To this end, *in silico* analyses were performed and predicted that p24 protein is a membrane protein with multi-pass transmembrane domains. Moreover, chemical treatment with Na₂CO₃ and Urea, after membrane fractionation from *Nicotiana benthamiana* leaf cells agroinfiltrated with p24 construct, revealed that the p24 protein is an integral membrane protein, confirming the prediction. Additionally, the Bimolecular Fluorescence Complementation (BiFC) assay was performed to understand into which membranous subcellular compartment the p24 N- or C-terminal is exposed. BiFC relies on the capacity of two non-fluorescent fragments of the Yellow Fluorescent Protein (YFP), i.e. its N-terminus (N-YFP) and C-terminus (C-YFP), to interact with each other when they are over expressed in the same subcellular compartment. The C-YFP fragment was targeted either to the cytosol (C-YFP_{cyt}) or to the endoplasmic reticulum (ER) lumen (C-YFP_{ER}), and it was co-agroinfiltrated in tobacco leaves with the counterpart N-YFP fragment fused either to the N- or C-terminus of the p24 protein. Reconstitution of the fluorescence was observed when the p24, carrying N-YFP fused at the C-terminus was co-expressed with the C-YFP_{ER} and also when p24 N-terminus fused to the N-YFP was co-expressed with C-YFP_{cyt} indicating that in plant cells, the N-terminal region of p24 is exposed to the cytoplasm whereas C-terminal domain faces the ER luminal side. Taken together these results suggest that the p24 is a multi-pass membrane protein with putative transmembrane domains exposing an Ncytoplasm-Clumen topology.

Key words: Citrus leprosis virus C, membrane fractionation, Bimolecular Fluorescence Complementation (BiFC), viral transmembrane protein, membrane protein topology

Effects of artificial coelux® light on plants growth

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The visible light is an important environmental factor for promoting plants growth and development. Plant pigment molecules, such as chlorophyll and carotenoids, absorb light mainly in the wavelength range of 650-700 nm (red light) and 460-480 nm (blue light) of the electromagnetic spectrum. There are many technologies able to reproduce artificially light for both space lighting and indoor plants production. CoeLux® is a brand new interesting and innovative “green technology” that reproduces the natural light and visual appearance of the sun and the sky through nanostructured materials, LED lighting and optical systems, which create a distance sensation between sky and sun. Unlike other artificial lighting systems, CoeLux® is able to reproduce the effect of Rayleigh scattering, which occurs when light cross earth’s atmosphere and interact with gaseous substances. Although the lighting effects on ornamental and/or agronomic plants are widely studied, the influence of CoeLux® lighting system on plants growth is still unknown. Therefore, the present work aims to assess the short-term effects of this new lighting system on plant morpho-physiological aspects. The experiment was performed at the CoeLux® showroom, located in ComoNEXt science and technology park (Lomazzo, CO - Italy) in a room characterized by 45 HC CoeLux® light type. Two common ornamental plants species, Anthurium and Spathiphyllum, were placed in different position points characterized by a different PAR (Photosynthetically Active Radiation) value. For each position point, plants were grown for 16 days (16/8 hours light/dark) and successively moved to the next position point, which was characterized by a higher PAR value. Photosynthetic efficiency in dark-adapted (F_v/F_m), photosystem II yield in light reaction (Φ_{PSII}) and stomatal conductance (gs) were measured every 24 hours, 48 hours, 4 days, 8 days and 16 days. Moreover, an image of the plants was acquired at the beginning and at the end of the growth period. Later, the image analysis (Image J open access software) allowed measuring the leaf area index. For each position point similar photosynthetic activity and stomatal conductance were detected between Anthurium and Spathiphyllum. In particular, for both first and second position points, plants showed a compensation point characterized by corresponding rate of respiration and photosynthetic activity. Thus, from the visual analysis, there was not leaf area increment. From the third to the fifth position point, although a decrease of leaf area index was detected, both biomass and flowers were produced. The expansion of leaves was not detected by the image analysis due to a phototropic response of leaves. Indeed, while stalks extended leaves moved orienting downwards to the wall light reflection. In conclusion, further analysis with different plant species are in progress. In particular, ornamental (Anthurium and Spathiphyllum), aromatic (Malva sylvestris, Ocimum basilicum, Coriandrum sativum), agronomic (Olea europaea, Solanum lycopersicum) and forestry (Quercus ilex) plant species are under investigation.

Audience Take Away:

- The present work gives important insight on how this two ornamental species, commonly used in domestic environment, can be grown indoor sites characterized by low light intensity.
- In addition to the general knowledge, will be interesting the detection of an optimal photosynthetic activity in particular conditions of lighting, for example the exposure of plants to a photosynthetically active radiation of about 2 PAR.
- This study is a first step to enhance knowledge about lightening uncomfortable environments and has a great potential to expand research and teaching in a multidisciplinary way.

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Biography

Dr. Polzella Antonella is a PhD student at University of Molise. In November 2012, she obtained a Bachelor's degree in Biological Sciences at University of Sannio (BN - Italy). In April 2015, she obtained a Master's degree in Molecular and Cellular Biology at University of Molise. Her Ph.D.'s research activity started in November 2015. She has joined the Laboratory of Environmental and Applied Botany at University of Insubria and, she is currently involved in a series of experiments aiming to study the morpho-physiology of biochar treated plants growing under LED lighting systems.

Reaction of winter triticale breeding lines to *Fusarium* head blight and accumulation of *Fusarium* metabolites in grain in two environments

Wisniewska Halina*¹, Goral Tomasz², Ph.D., Ochodzki Piotr², Ph.D., Walentyn-Goral Dorota², M.Sc., Kwiatek Michal¹, Ph.D., Majka Maciej¹, M.Sc., Belter Jolanta¹, M.Sc.

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²Plant Breeding and Acclimatization Institute NRI, Poland

Fusarium head blight is a disease of cereals caused by fungi of the *Fusarium* genus. These fungi produce toxic metabolites - mycotoxins. Head infection by *Fusarium* leads to kernel infection and accumulation of mycotoxins in grain.

Resistance to *Fusarium* head blight of 106 Polish winter triticale lines and three cultivars (Trefl, Meloman, Fredro) was tested. The genotypes of triticale were analyzed in terms of the resistance types: resistance to infection (Type I), resistance to disease spread (Type II), kernel damage resistance (Type III) and resistance to accumulation of toxins in grain (Type V).

Triticale was sown in field experiments in two locations in Poland: Poznań–Cerekwica and Radzików. At flowering, triticale heads were inoculated by spraying with three *Fusarium culmorum* isolates. FHB index was scored and after the harvest percentage of *Fusarium* damaged kernels (%FDK) was assessed. Grain was analyzed for a content of trichothecenes B (deoxynivalenol and derivatives, nivalenol) and zearalenone using gas chromatography technique (trichothecenes) and AgraQuant® ZON test kit (zearalenone) and ergosterol (ERG) using HPLC technique.

Principle Component Analysis (PCA), revealed genotypes with combination of all types of FHB resistance : BOHD 1025-2, BOH 537-2, DS. 9, DANKO 14/15, MAH 33544-4, MAH 33881-1/3, DANKO 19/15 and BOH 534-4.

Audience Take Away:

- Nowadays modern cultivars of triticale were much more susceptible to *Fusarium* head blight than older ones
- Triticale genotypes were much more infected by *Fusarium* in recent years, on the similar level to wheat
- Concentration of trichothecenes in triticale grain was higher than in wheat grain comparing lines with similar resistance to head and kernel infection

Biography

1974 - Master of Sciences degree in the field of Botany, at the University of Adam Mickiewicz in Poznan.

1985 - Doctor of Philosophy degree in the field of Agricultural Sciences, at the Institute of Plant Genetics, Polish Academy of Sciences in Poznan

2007 - Doctor of Science degree in the field of Agronomy, at the University of Life Sciences in Poznan

2008-till now - The leader of Cereal Genomics Team at the Institute of Plant Genetics, Polish Academy of Sciences in Poznan

2014 - Professor degree in the field of Agricultural Sciences, at the Institute of Plant Genetics, Polish Academy of Sciences in Poznan

Taxonomy of plants in phylum using UV fingerprints and robust chemometrics

Maria Simion, PhD., Costel Sarbu*¹, PhD.

Babes-Bolyai University, Faculty of Chemistry and Chemical Engineering, Romania.

The increasing use of plant based treatments requires a fast, easy and cheap technique in order to verify the quality and authenticity of the products. In this study the UV-Vis spectrometry was applied on 42 commercially available hydro-alcoholic herbs extracts. The UV-range was utilized due to the lack of significant differences in Vis-range. The obtained data were digitized, normalized and then subjected to the Multivariate Data Analysis (MDA). The fuzzy methods compared with the classical ones produced better results. The Principal Component Analysis (PCA) and Cluster Analysis (CA) applied to original data and first derivative revealed a classification of the samples according to the therapeutic effects. A classification of the samples in phylum was obtained with PCA-LDA. The cluster analysis performed on the canonical scores indicates not only a grouping of the plants by phylum, but also by the next ranks: class and subclass, and in each subclass the plants have similar therapeutic uses. The UV-Vis spectrometry coupled with MDA proves to be a powerful method to classify the plants according to their phylum, class and therapeutic effects. The fuzzy methods compared with the classical ones produced better results. The batch of 42 samples is classified into three phyla according to "Flora medicinală a României". The spermatophyte phylum contains woody and herbaceous plants; they're origin being theoretically derived from the pteridophyte phylum. Depending on whether or not the seed is enclosed in fruit they are classified in gymnospermae and angiospermae. The pteridophyte phylum contains the first plants to which it can be distinguish true organ and tissues, they do not have flowers and the plant breeding is made by spores, they are used in therapy due to the presence of salicylic acid. The main plants that are present in this category are ferns. The magnoliophyte phylum contains the most evolved plants with the seed closed in fruits and a complex arrangement of petals. They are grouped in two categories: monocotyledons and dicotyledons.

Application of TaqMan probes to study the expression kinetics of celiac disease-related toxic epitopes and their presence in the gDNA of contrasted spelt accessions

Benjamin Dubois^{*1,2}, MSc., Pierre Bertin¹, PhD., Dominique Mingeot², PhD.

¹Université catholique de Louvain (UCL), Louvain-la-Neuve, Belgium

²Walloon Agricultural Research Center (CRA-W), Gembloux, Belgium

Gluten is the water insoluble protein fraction found in the flour of several cereals such as wheat and spelt. Its ingestion is responsible of celiac disease (CD) in genetically predisposed individuals (1-2% of the human population). Alpha-gliadins are a class of proteins of the gluten fraction encoded by a multigene family which play a key role in this pathogenesis with 4 main toxic epitopes recognized by the immune system. These epitopes display a full toxicity in their canonical form but amino acid substitutions or deletions naturally occur in some epitope sequences which lower or suppress their toxicity. On this basis, TaqMan probes targeting only the canonical form of each epitope have previously been developed and epitope expression data in contrasted spelt accessions have been collected. In this study, these TaqMan probes have been applied to the genomic DNA (gDNA) of the same spelt accessions. The results are globally correlated to epitope expression levels previously measured on cDNA samples with the same probes, despite the high proportion of pseudogenes displayed in α -gliadin sequences. Moreover, a kinetic study of the epitope expression was carried out to evaluate the best moment to apply these probes. The analysis was performed with a European and an Asian spelt accession, given that genetic differences between spelts from these two origins have previously been underlined by several authors. The results highlighted interesting differences, the expression peak being observed sooner in the European than in the Asian spelt. The results obtained with gDNA samples and from the kinetic analysis provide useful information with a view to studying the toxic content of spelt or bread wheat accessions and to tracking it in accessions involved in breeding programs aiming at developing safer varieties for CD patients.

Audience Take Away:

- Spelt and bread wheat are known to hold a high proportion of pseudogenes in the α -gliadin multigene family, which display the four major epitopes involved in CD. Consequently, the presence of these epitopes is generally studied in cDNA rather than gDNA samples to properly quantify the expressed toxic content by avoiding the pseudogene fraction. However, working with cDNA samples implies to wait for the grains to reach a precise development stage. The fact that the same trends have been pointed out when studying the epitope occurrence in gDNA and cDNA indicates that the designed probes might be used as a first approximation on genomic DNA from leaves, before the heading. This would represent an important time saving for instance in breeding programs aiming at developing safer varieties for CD patients.
- Furthermore, the results from the kinetic analysis provide new information to improve the accuracy of the experimental design by fine-tuning the sampling date.

Biography

Benjamin Dubois has completed bio-engineering studies at the age of 23 years in Gembloux Agro-Bio Tech (GxABT, Gembloux, Belgium). He is currently working on a research project at the Walloon Agricultural Research Center (CRA-W, Gembloux, Belgium) since October 2014. In parallel, he is carrying out a PhD thesis about this research project at the Université catholique de Louvain (UCL, Louvain-la-Neuve, Belgium).

Preliminary detection of pectins and arabinogalactan proteins during ovule embryogenesis in sugar beet (*Beta vulgaris* L.)

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¹Plant Breeding and Acclimatization Institute—NRI, Poland

The use of haploid and doubled-haploid plants facilitate fundamental genetic studies, breeding approaches, and molecular genetics research in most crops, including sugar beet (*Beta vulgaris* L. ssp. *vulgaris*). The main advantage of using in vitro cultures to achieve genetic homozygosity is the greatly time reduction. Unfortunately, sugar beet is recalcitrant in response to androgenic in vitro culture, so that gynogenesis proved to be the most successful method to produce haploids in this species. Even though great progress has been made in the use of unpollinated ovules embryogenesis, a certain number of constraints still hinder breeding programs. Among these limitations, a genotype dependency of embryogenic potential seems to be the most notable. In many cases it determines the rate of success in generating doubled haploid lines. In relation to morphogenetic potential, changes in plant cell wall composition have been previously described. Cell wall pectins and arabinogalactan proteins (AGPs) are involved in different biological processes such as cell expansion and differentiation or tissue development. Moreover, these molecules have also been proven to play an important role in differentiation of floral organs and sexual reproduction. Based on this, we compare the content of pectin and AGP epitopes in unfertilized ovules isolated from sugar beet genotypes of different embryogenic potential. Using the immuno-dot blot technique with two anti-pectin (JIM7 and LM5) and two anti-AGP (JIM13 and LM2) monoclonal antibodies the characterization of extracts was performed. The detection of carbohydrate antigens in the extracts revealed the presence of epitopes that typify both AGPs and pectins presence. The obtained results indicates the preliminary variation in above mentioned molecules composition depending on the ovary regeneration state.

Audience Take Away:

- The presentation will enable to summarize our current achievements in sugar beet embryogenesis of unfertilized ovules.
- It will enable the exchange of practical experiences connected with embryogenesis of unfertilized ovules.
- Presented results will be the starting point for further discussions about the role of pectins and arabinogalactan proteins (AGPs) in embryogenesis.

Biography

I studied biotechnology at UTP University of Science and Technology in Poland, where I graduated in 2009. From 2009 till now I have been working in Department of Genetics and Breeding of Root Crops at Plant Breeding and Acclimatization Institute-National Research Institute. Since 2014 I have been a PhD student at PBAAI-NRI. I have attendant 6 research programs concerning biological, cytological and molecular characterization of haploids and doubled haploids of sugar beet. Moreover, the second research direction is concentrated on genetic diversity among *Miscanthus* genus.

Abiotic stress tolerance in perennial grasses – recommended for the management of dry and degraded areas

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¹Forage Grasses and Legumes Dept., Plant Breeding and Acclimatization Institute-NRI, Poland

²Botanical Garden, Plant Breeding and Acclimatization Institute-NRI, Poland

Permanent grassland are a source of healthy forage for a large group of ruminant animals. They also serve to conserve biodiversity, reduce environmental pollution, including nitrogen oxide and sulfur in the air. They can contribute to the agro ecosystem sustainability by reducing soil erosion and conserving soil water. Ecotypes may provide genetic resources to improve resistance/tolerance for water stress limit or different soil type. Water conservation is the responsibility of every citizen, not just in areas with drought or low moisture conditions. Drought resistance is being increasingly labelled as being a ‘complex trait’. There are two different opinions regarding the impact of agricultural intensification on biodiversity. Some authors suggest that is that caused the extinction of many ecotypes and replacing them with new forms of crops. According to other authors the negative impact on the biodiversity is not observed, because the genetic resources in situ and ex situ form are included into the breeding programs and the wide variation within the newly created varieties could be maintained.

In the resent study as a plant material ecotypes and commercial hybrid which belong to 7 cool-season grass species were used: tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis* Huds.), red fescue (*Festuca rubra* L.), perennial ryegrass (*Lolium perenne* L.), Timothy-grass (*Phleum pratense*), Kentucky bluegrass (*Poa pratensis*) and *Deschampsia caespitosa*. Ecotypes were collected from semi-natural area representing different part of Poland. Next, based on the preliminary description, 15 – 17 genotypes which represent each species, were included into recent study. For the greenhouse test seedlings were taken from the experiment conducted under field conditions and after vegetative propagation they were planted into pots. Tolerance to different soil type: tree treatments – (1) soil with low phosphorus, magnesium n-organic, C-organic content, (2) soil with high clay content and low phosphorus and magnesium content, (3) control (mixture: 3 peat : 1 sand).). Plants were cut every 7 days at a height 7 cm (red fescue - 4 cm), and regrowth measured. Tolerance to water deficit test: plants grow for six weeks at an optimum moisture content of the soil (35 – 42%; soil type - mixture: 3 peat : 1 sand), cut every 7 days at a height 7 cm (red fescue - 4 cm), and regrowth measured. After this time resistance for water deficit and different type of soil was evaluated.

Different type of soil test was conducted in three treatments: control (mixture: 3 peat : 1 sand) and two types of soil taken from devastated area. Based on the results obtained in the water deficit test it was possible to conclude, that differences for red fescue, tall fescue and *Deschampsia caespitosa* regrowth under drought stress and under control conditions were not significant.

This work was supported by the project: Creation perennial grasses ecotypes collection and evaluation their suitability for the special purposes, 2014 – 2020. Programme: Basic Research for Biological Progress in Crop Production; Funded by the Ministry of Agriculture and Rural Development Proj. No. 4-7-00-3-01 (36)

Biography

Elzbieta Czembor is a plant pathologist with a MS degree in Plant Breeding Department, Agriculture University, SGGW-AR, Poland and Ph.D. degree in Plant Breeding and Acclimatization Institute (PBAI-NRI Radzikow), Poland. She participated in Postgraduate Study on Plant Pathology in Plant Pathology Department, Montana State University, Bozeman, USA. Her research is focused on: fungal diseases of maize and grasses, genetics and breeding, mechanisms of plant resistance, evaluation of genetic resources, food quality and safety, environmental protection, ecology and bioethics, IPM. She published more than 100 scientific papers. Member of Polish Plant Pathology and Polish Genetics Societies.

AtAIRP2, an arabidopsis RING E3 ubiquitin ligase, positively regulates ABA- and high salinity-mediated seed germination by stimulating ATP1/SDIRIP1 turn-over

Tae Rin Oh B.S., Jong Hum Kim B.S., Seok Keun Cho Ph.D., Moon Young Ryu Ph.D., Seong Wook Yang Ph.D., Woo Taek Kim*¹ Ph.D.
¹College of Life Science and Biotechnology, Yonsei University, Korea

A systemic network of proteolytic regulation via the ubiquitin-26S proteasome system plays significant roles in environmental adaptation and hormone signal transduction in plants. The abscisic acid (ABA) signaling is an essential pathway plants to survive against the abiotic stress, especially drought and osmotic stresses. AtAIRP2 is a cytosolic RING-type E3 ubiquitin (Ub) ligase that positively regulates an ABA response in Arabidopsis. Yeast two-hybrid screening using AtAIRP2 as bait identified ATP1 (AtAIRP2 Target Protein 1) as a substrate of AtAIRP2. ATP1, previously known as SDIRIP1 of which SDIR1 substrate protein, was identified as an interacting partner of AtAIRP2, a positive regulator of ABA-mediated drought response. ATP1 was accordingly renamed ATP1/SDIRIP1. A specific interaction between AtAIRP2 and ATP1/SDIRIP1 and ubiquitination of ATP1/SDIRIP1 by AtAIRP2 were demonstrated in vitro and in planta. The turn-over of ATP1/SDIRIP1 was regulated by AtAIRP2 in cell-free degradation and protoplast co-transfection assays. The ABA-mediated germination assay of 35S:ATP1/SDIRIP1-RNAi/atairp2 double-mutant progeny revealed that ATP1/SDIRIP1 acts downstream of AtAIRP2. AtAIRP2 and SDIR1 reciprocally complemented the ABA- and salt-insensitive germination phenotypes of *sdir1* and *atairp2* mutants, respectively, indicating their combinatory roles in seed germination. Subcellular localization and BiFC experiments in the presence of MG132, a 26S proteasome inhibitor, showed that AtAIRP2 and ATP1/SDIRIP1 were co-localized to the cytosolic spherical body, which lies in close proximity to the nucleus, in tobacco leaf cells. The 26S proteasome subunits RPN12a and RPT1 and molecular chaperones HSP70 and HSP104 were co-localized to these discrete punctae-like structures. These results raised the possibility that AtAIRP2 and ATP1/SDIRIP1 interact in the cytosolic spherical compartment. Collectively, our data suggest that down-regulation of ATP1/SDIRIP1 by the combinatory actions of AtAIRP2 and SDIR1 RING E3 ligases is critical for ABA and high salinity responses during germination in Arabidopsis.

Audience Take Away:

- Audience will learn about the most recent studies on ABA signaling pathway related to the ubiquitin-26S proteasome system.
- In addition, audience will be informed about molecular and cellular plant biology tools to study E3 ligase in plant.

Biography

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|----------------------------------|---|
| 1984 - 1988 | Ph.D. in Plant Physiology, Wash. State Univ., USA |
| 1988 - 1990 | Postdoc., Institute of Biological Chemistry, Wash. State Univ., USA |
| 1990 - 1994 | Postdoc., University of California, Davis, USA |
| 1995 - present 120-749, Korea | Professor of Department of Systems Biology, College of Life Science and Biotechnology, Yonsei University, Seoul |
| 2008 - 2017 | Chair, Graduate Program of Functional Genomics, Yonsei University |
| 2010 - 2012 | Review Board, National Research Foundation of Korea |
| 2010 - 2013 | Underwood Distinguished Professor, Yonsei University |
| 2012 - present | Member, The Korean Academy of Science and Technology |
| 2013 - 2014 | President, The Korean Society of Plant Biologists |

Functional characterization of ABC transporters in chloroplast

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Stress in plants is caused by sudden and restrictive changes in their environment, which disrupts the plant homeostasis and leads to worldwide yield losses. The deleterious effects of stress on plants physiology cause growth retardation, reduced metabolism and altered photosynthesis. Plant hormone auxin plays an important role in plant stress responses. Exogenous auxin treatments affect chloroplast structure, chlorophyll synthesis, nuclear and chloroplastic photosynthetic genes expression, and chloroplast protein levels. Auxin hypothetically has a protective function against photo-oxidative inhibition ¹. Approximately 30%–40% of the total free IAA pool is located in the chloroplast². Moreover, besides providing Tryptophan-derived precursors for Indole-acetic acid (IAA) biosynthesis, chloroplasts were shown to actively biosynthesize auxin ². Recently, it was shown that chloroplast redox state modulates auxin homeostasis ³. These data suggest a strong connection between chloroplast processes and auxin homeostasis. In *Arabidopsis*, five members of the ABCB subfamily of transporters have been reported to mediate cellular transport of auxin or auxin derivatives⁴. Based on AT_CHLORO database⁵ and sequences analysis⁶, we identified two chloroplast predicted ABCB transporters ABCB28 and ABCB29 in *Arabidopsis*

Our main goal is to uncover whether ABCB28 and ABCB29 participate in auxin transport across the chloroplast envelope and their roles in plant development and stress responses. In silico promoter gene analysis showed that motifs in the promoter of our target genes shared some similarities with the promoters of known auxin ABC transporters. Chloroplast subcellular localization was confirmed using 35S:ABCB28:GFP and 35S:ABCB29:CFP constructs and confocal microscopy. ABCB28 and ABCB29 overexpressors, *abcb29* knock out and *abcb28* knockdown mutants showed altered photosynthesis during early and late seedling development. ABCB28 and ABCB29 over expressing lines exhibited increased auxin induced lateral root development and reduced auxin induced root growth retardation compared to wild type plants. Interestingly, overexpressors showed increased number of siliques and seed production per plant. Moreover, in response to osmotic stress, lateral root development in these lines is stimulated. To find out the substrate specificity of our proteins, we are trying to implement different techniques by using isolated protoplast and chloroplast.

Audience Take Away:

- New techniques for chloroplast metabolites transport measurement.
- Detailed insight of ABCB transport machinery in *Arabidopsis* chloroplast.
- The understanding of how chloroplasts and auxin metabolism are interconnected will shed light on the mechanisms controlling plant growth and development as well as deepen our knowledge to improve the performance of crops under field conditions.

Biography

I am Prashanth Tamizhselvan hail from India. I did my bachelors in Biotechnology at SRM University, India and my Masters in Molecular genetics and physiology in Linkoping University, Sweden. I did my master thesis in KTH University, Stockholm titled "Comparison of Transcriptional circuits for wood formation in *Populus* and *Arabidopsis*". Now I am currently pursuing Ph.D. in Masaryk University CEITEC-MU under the supervision of Dr. Vanesa Tognetti Ph.D.

Transcriptome analysis of resistant and susceptible sweetpotato cultivars infected with root-knot nematode *Meloidogyne incognita*

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³Natural Product Research Center, Korea Research Institute of Bioscience and Biotechnology, Jeongeup, Republic of Korea

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Nematodes are one of the major limiting factors in sweetpotato production. Root-knot nematodes (RKN, *Meloidogyne* spp.) are widely distributed and economically important sedentary endoparasites of agricultural crops and they may inflict significant damage to field grown sweetpotato. As of today, no studies have been published on global gene expression profiling in sweetpotato infected with RKN or any other plant parasitic nematode. Therefore, in the present study, we performed root transcriptome analysis of resistant (cv. Juhwangmi) and susceptible (cv. Yulmi) sweetpotato cultivars infected with RKN *Meloidogyne incognita*, widespread root-knot nematode species and a major pest worldwide. A total of 407,106,902 pair-end reads were generated on an Illumina Hi-Seq 2000 platform and assembled into 148,666 transcripts from the fibrous roots of both cultivars. Bioinformatic analysis revealed a number of common and unique genes that were differentially expressed in susceptible and resistant lines as a result of nematode infection. Although the susceptible cultivar showed a more pronounced defense response to the infection, feeding sites were successfully established in its roots. Characteristically, basal gene expression levels under normal conditions differed between the two cultivars as well, which may confer advantage to one of the genotypes toward resistance to nematodes. Differentially expressed genes were subsequently assigned to known Gene Ontology categories to predict their functional roles and associated biological process. Candidate genes that contribute to protection against *M. incognita* in sweetpotato were proposed, and sweetpotato-nematode interactions with respect to pathogenesis-related 10 gene and trypsin inhibitor-mediated defense signaling are studied.

Audience Take Away:

- Transcriptome of sweetpotato fibrous roots during root-knot nematodes infection was de novo assembled and analyzed.
- A total of 1,750 differentially expressed genes (DEGs) were identified in sweetpotato fibrous roots during root-knot nematodes infection.
- Genes involved in transcription factors, pathogen defense, and insect resistance were generally up-regulated in resistant (cv. Juhwangmi) or susceptible (cv. Yulmi) sweetpotato cultivars during root-knot nematodes infection.

Biography

Ph.D. Yun-Hee Kim is an assistant professor at Gyeongsang National University where he is teaching on the plant physiology and microbiology. He's main research topic is omics based isolation of root-knot nematode resistance genes in sweetpotato and development of nematode-tolerant plants. His research areas of interests include stress physiology, transcriptome, and molecular marker analysis in useful crop plants.

Phytochemical composition of essential oil of Croatian endemic species *Centaurea tuberosa* Vis.

Valerija Dunkic, Mirko Ruscic, Nada Bezić*
University of Split, Croatia

The genus *Centaurea* L. is very important genera of Asteraceae family, with many local endemic species. According to Flora Croatica database (<http://hirc.botanic.hr/fcd>) described 88 *Centaurea* species, of which 30 is the endemic. The investigated *Centaurea tuberosa* L. (synonym: *Centaurea napulifera* subsp. *tuberosa* (Vis.) Dostál) is also Croatian endemic species and this species belongs to the vegetation community of East Adriatic submediterranean and epimediterranean lawns: *Chrysopogony-Koelerion splendensis*.

This is the first study on the chemical composition of *C. tuberosa* species. Plant material of investigated plants was collected from Tigarica (near Split) Croatia in the summer (July) 2015. Aerial parts of plants were performed in a shady place at room temperature for 10 days. Dried aerial parts of plant material (100 g) were subjected to hydrodistillation for 3 h in Clavenger type apparatus. This essential oil have been analysed by GC (Varian 3900) and GC/MS (Varian Saturn 2000 system) using VF-5ms capillary column. The individual peaks were identified by comparison of their retention indices of n-alkanes to those of authentic samples and literature, as well as by comparing their mass spectra with the Wiley 9.0 library (Wiley, New York) and NIST/02 mass spectral database. The percentage composition of the samples was computed from the GC peak areas using the normalization method.

Total yield of oil was 0.55%, based on dry weight of sample. Thirty-seven compounds representing 82.9% of the total oil. The essential oil of *C. tuberosa* was characterized by a high concentration of caryophyllene oxide (27.8%), followed by β -caryophyllene (7.1%), docosane (6.8%), spathulenol (5.4%). Also, compounds β -caryophyllene, spathulenol and caryophyllene oxide were the common for the *C. armena*, *C. appendicigera* and *C. helenioides*. According to literature data, the composition of essential oils of *Centaurea* species are frequently characterized by components with sesquiterpenes skeleton such as caryophyllene, eudesmol, germacrene and spathulenol, hydrocarbons and monoterpenes as pinene, terpinene, carvacrol.

The present study gives additional knowledge about phytochemical composition of the essential oil on the genus *Centaurea*.

Audience Take Away:

- The Asteraceae are arguably the largest family of flowering plants, which have a cosmopolitan distribution. The genus *Centaurea* L. is very important genera of this family, with many endemic species
- This is the first study on the essential oil composition of *Centaurea tuberosa* species, with biologically important components
- Wide range of biological activities displayed by the essential oils makes these compounds subject to different researches
- The essential oils are of great importance in several fields such as physiological function of growth, ecological function, development and resistance against diseases and insects

Biography

More than 45 papers published in international scientific journals in the field of virology, anatomy and physiology of xerophytes and also their implementation in phytoterapy. Plant species that are the subject of research are from Mediterranean part of Croatia. Laboratory researches, apart from exploring plant structures, are focused on the isolation of plant compounds and their chemical characterization, as well as the determination of their biological activity. In recent years we focusing on investigate is antiviral activity of essential oils. As a professor at the University of Split, I teach lectures and lead mentoring with students at the undergraduate, graduate and postgraduate level.

Evaluation of cultural and wild oat varieties for selected traits affecting the quality of human nutrition

Svetlana Slikova¹ PhD., Peter Hozlar¹ PhD., Edita Gregova¹ PhD., Michaela Havrlentova^{*1}, PhD.

¹NAFC – Research Institute of Plant Production, University of Ss. Cyril and Methodius, Slovakia

Present use of oats in making products for human nutrition mostly depends on nutritionally valuable compounds of oat grain. The aim of our research was to create a set of oat genotypes with a high variability of quality parameters and to characterize these genotypes for the presence of avenin blocks, ability to produce selected health beneficial substances (such as proteins, dietary fibre, beta-D-glucan, total lipids and others), resistance to infestation with toxicogenic fungi of *Fusarium* genus, as well as sensitivity to mycotoxins accumulation in the grain. A strong screening test was done to find such genotypes that could be perspective sources with a wide range of uses, e.g. (i) in development of new plant varieties with improved quality characteristics, (ii) as natural sources of beneficial substance(s) for the next use in food industry or (iii) to use the seed or extracted substance(s) in the pharmaceutical industry. In the work, cultural and wild forms of oat were evaluated for the traits that can improve the nutritional quality and contribute to the production of grain harmless to health. The set of genotypes was characterized by a high intra-species variability and enables to discover some new characters absent in cultural forms or characters that occur rarely. Among the aims of research, an output with a long-term character is to search and/or develop genetic markers for selected traits for Marker Assisted Selection as well as to create a new *Avena sativa* cultivar and its registration. In our experiment, oat genotypes were grown in two different locations, grain samples were analyzed for beta-D-glucan, dietary fiber, proteins and oil content and fatty acids composition. The identification and characterization of oat genotypes was made also using the electrophoresis of avenins. Artificial infection of plants by *Fusarium* spp. fungi, as producers of mycotoxins, revealed their sensitivity to infestation and mycotoxin production in grains. Results obtained in this three-year long experiment are discussed in the contribution. This work was supported by OP Research and Development: Development of new types of genetically modified plants with farm traits (ITMS 26220220189), by the European Regional Development Fund and by the Science and Research Support Agency (No. APVV-0398-12) of the Slovak Republic.

Audience Take Away:

- Large-scale characterization of oat (*Avena sativa* L.) genotypes potentially used for food industry and pharmacy
- Resistance / sensibility of oat genotypes to artificial infection by *Fusarium* spp. fungi and accumulation of mycotoxins
- Electrophoretic analysis of avenins as tool of oat originality characterization

Biography

Michaela Havrlentova was born in 1974. She lives with her family in Slovakia, in a small village. After graduating her study of biology at the Comenius University in Bratislava in 1997 she has been working at the Research Institute of Plant Production in Piešťany. Her activity is seeds quality (especially cereals and oilseeds) influenced by genotype and environment. Since 2012 she has been teaching at the Faculty of Natural Sciences of the University of Ss. Cyril and Methodius in Trnava. In her lectures she is oriented in general biology and plant biotechnology. She likes reading books, nature and discussing with people.

Global Conference on Plant Science and Molecular Biology

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Valencia, Spain

Identification and classification of U-box E3 ligases in barley and their responses to drought stress and fungal infection

Seok Keun Cho*¹, Ph.D., Moon Young Ryu, Ph.D., Yourae Hong, B.S., Hansol Bae, Ph.D., Jinho Kim, Ph.D., Jong Hum Kim, B.S., Eva Knoch, Ph.D., Birger Lindberg Moller, Ph.D., Woo Taek Kim, Ph.D., Michael Foged Lyngkjaer, Ph.D., Seong Wook Yang, Ph.D.

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An important way of plant defense against environmental and pathogen stresses is exploiting a controlled protein turnover pathway, the ubiquitin proteasome system (UPS). E3 ligases are key enzymes that play a central role in target determining by the UPS. Recently, it has been defined that U-box ligases, a specific class of E3 ligases, are largely implicated in the defence mechanisms against abiotic and biotic stresses in many plants. However, no studies on U-box E3 ligases have been performed in barley, one of the important staple crops in the world. In this study, we identified 68 putative U-box E3 ligases from the barley genome and corresponding expressed sequence tags (ESTs) data. Based on their domain compositions and arrangement, we classified barley U-box proteins into eight different classes. Similar to Arabidopsis and rice U-box E3 ligases, most of barley U-box E3 ligases have evolutionary well-conserved domain organizations. We identified a barley specific U-box gene with a GABA transporter 1 (GTA1) domain in addition to U-box domain, which is neither found in Arabidopsis nor in rice. Furthermore, we found that the expressions of some U-box genes were specifically up-and-down regulated by drought stress or by pathogen infection, implying the possible roles of barley U-box genes in stress responses. The identification and classification of barley U-box genes may provide a platform to functionally study the stress-related E3 ligases in barley.

Audience Take Away:

- Audience will learn about the classification of U-box E3 ligases in barley using bioinformatics tools. In addition, audience will also learn about the regulation of U-box genes in Barley against environmental stresses (abiotic and biotic stress)

Biography

2003 - 2009 Ph.D. in Plant systems biology, Yonsei University, South Korea
2009 - 2012 Postdoc., Institute of Life Science and Biotechnology, Yonsei University, South Korea
2012 - 2015 Postdoc., University of Copenhagen, Denmark
2015 - present Research Professor, Institute of Life Science and Biotechnology and BrainKorea21 Plus initiative for Biological function & Systems, Yonsei University, Korea

The role of antioxidant mechanisms in the tolerance of the Negev desert extremophyte, *Anastatica hierochuntica*, to abiotic stress

Prasanna Angel Deva^{*1}, Yana Kazachkova¹, Narendra Singh Yadav¹, Simon Barak¹

¹The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev

Investigation of stress-tolerant plants is crucial for understanding how plants can tolerate multiple abiotic stresses in the field. The extremophyte desert relative of *Arabidopsis thaliana*, *Anastatica hierochuntica*, is tolerant to several abiotic stresses. Because the secondary effect common to most abiotic stresses is massive production of damaging reactive oxygen species, (ROS), we investigated the response of the *Anastatica* ROS-scavenging machinery in comparison to *Arabidopsis* during methyl viologen (MV)-induced oxidative stress and heat stress. In vitro-grown *Anastatica* seedlings exhibited remarkable tolerance to increasing concentrations of MV, and to heat stress, compared to *Arabidopsis*. Notably, *Anastatica* was able to maintain total chlorophyll levels in response to high concentrations of MV and to heat stress whereas chlorophyll levels were considerably reduced in *Arabidopsis*. The severe stress symptoms observed in *Arabidopsis* were also reflected in the high accumulation of anthocyanins in response to MV and heat stress whereas only low levels of anthocyanins were observed in *Anastatica*. Nitroblue tetrazolium (NBT) staining of *Arabidopsis* seedlings indicated massive generation of superoxide radicals over time with increasing MV levels. No staining was apparent in control seedlings. However, *Anastatica* exhibited NBT staining in both control and MV-treated seedlings, which could reflect either a stress response caused by the experimental procedure that involved transfer of seedlings to treatment plates, or could be due to basal levels of ROS production. 3,3'-diaminobenzidine (DAB) staining of *Arabidopsis* seedlings for detection of H₂O₂, increased with elevated MV concentrations suggesting a rise in H₂O₂ production in response to oxidative stress. In contrast, *Anastatica* did not display any significant DAB staining in response to MV-induced oxidative stress, which could indicate a more highly active antioxidant system in *Anastatica* compared to *Arabidopsis*. ROS production in response to heat stress was different from the direct oxidative stress response. No DAB staining was observed in *Anastatica* at any time after onset of heat stress while in *Arabidopsis*, weak staining could only be detected after 3 and 4 h of heat stress. Surprisingly, *Anastatica* displayed stronger NBT staining that exhibited a clear dose response, compared to *Arabidopsis*. This result is unexpected and could indicate that *Anastatica* can tolerate high cellular superoxide levels or/and that high superoxide levels are necessary for heat stress signaling. To obtain further evidence for a more highly active antioxidant system in *Anastatica*, we have begun to examine expression of genes encoding various ROS-scavenging enzymes. Preliminary QPCR analysis of gene expression during heat stress showed that *Anastatica* exhibited a larger and more rapid induction of ASCORBATE PEROXIDASE 1 (APX1) expression than *Arabidopsis*. Overall, our data suggest that *Anastatica* is highly tolerant to direct oxidative stress and to heat stress. Work is in process to study the expression of a range of antioxidant genes, and antioxidant scavenging enzymes activities in response to oxidative stress and heat.

Audience Take Away:

- The study of naturally stress tolerant extremophytes is crucial in understanding how plants can tolerate multiple abiotic stresses in the field.
- This research provides knowledge concerning the antioxidant machinery in stress tolerant plants, which is a major mechanism allowing these species to cope with the harsh desert conditions.

Biography

I am Prasanna Angel Deva from India, and I obtained a B.Sc in Agriculture at Acharya N.G.Ranga Agricultural University, India, which included a Rural Agricultural Work Experience Programme (RAWEP) for 4 months in a rural village. This programme gave me an opportunity to interact with farmers and gain knowledge regarding agriculture challenges and their solutions. I also participated in a few national conferences on food security. I am currently pursuing M.Sc degree at The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Israel, studying abiotic stress tolerance in a desert extremophyte (*Anastatica hierochuntica*).

Transcriptome Profiling of Coffee (*C. arabica* L.) Seedlings Irrigated with Diluted Deep Sea Water

Mesfin Haile*, Cheol Soo Yoon, Won Hee Kang

Department of Horticulture, Kangwon University, Chuncheon 24341, Korea

Salinity is one of the important abiotic stress factors that limit plant growth and crop production. This research aimed to generate information about the gene expression of coffee seedlings under salt stress conditions and thereby to identify salt responsive genes. The treatments were normal irrigation water (0.2 dS/m) as a control treatment, and 5% diluted deep sea water (2.3 dS/m) as a salt treatment. The processed reads were mapped to the reference genes sequences (*C. canephora*) available on the coffee genome hub (<http://coffee-genome.org>) database and a total of 19,581 genes obtained. Gene ontology (GO) analysis was performed and among the 19581 genes; 7369 (37.64%) associated with the biological process, 5909 (30.18%) with cellular components, 5325 (27.19%) with molecular function and 978 (4.99%) genes categorized under no hit (unclassified) group. Differential gene expression analysis was performed with the DESeq2 package to identify differentially expressed genes based on the fold change and p-value. The result revealed that a total of 611 differentially expressed genes were identified (treatment/control). Among the differential expressed genes, 336 genes classified into up-regulated, and 275 genes were down-regulated. Among the total of 611 DEGs, 60 genes were significantly ($p < 0.05$) expressed and 44 genes classified into up-regulated and 16 genes were down-regulated. A total of four differentially expressed transcription factor genes identified, and two of them up-regulated, and the other two were down-regulated. The data generated in this study will help in understanding the response of coffee seedlings at the genomic level associated with abiotic stresses in general, salinity stress in particular. This study will also provide resources for functional genomic studies.

Keywords: Coffee, Coffee genome hub (CGH), Differential expressed gene (DEGs), Diluted deep sea water (DDSW), Gene Ontology (GO)

Biography

He studied and received a Bachelor of Science in the field of plant science at Aksum University, Ethiopia from 2008 - 2011. Then after, He joined the Ethiopian Institute of Agricultural Research (EIAR) as a researcher from 2012-2015 and he was doing researches on horticultural crops (garlic, shallot, onion, carrot and grapevine). Currently, he is a graduate (MSc) student and conducting experiments on coffee, pepper and tomato in the field of plant physiology and molecular biology at Kangwon National University, Korea.

Comparison of winter wheat and triticale genotypes for high callus induction and plant regeneration from mature embryo cultures.

Lidia Kowalska*¹ MSc, Edward Arseniuk¹

¹Plant Breeding and Acclimatization Institute, National Research Institute, Poland

Triticale and wheat belong to the three most important cereal crops of the world and is grown under a wide variety of climatic and agricultural conditions. These plants are the most common species of food and feed crops and it is a fundamental nutrient source of human calories worldwide. Over the last few decades, researches still strive to agronomic traits improvement and among those quality and disease resistance in to biotic and abiotic stresses. Increasingly, conventional methods are supported by the biotechnological tools, e.g. somatic embryogenesis. The ability of triticale and wheat callus induction and plant regeneration are influenced by culture medium, initial plant organ and genotype. Mature embryos were started to use as an alternative to immature embryos. During study was observed remarkable advantages: mature embryos are easy to handle, there is no time limitation and they are available in bulk quantities.

This study was undertaken to compare of winter wheat and triticale genotypes efficiency of somatic embryogenesis using mature embryos culture. To select genotypes with a high regeneration capability, we used 17 wheat genotypes (6 cultivars, 11 diallel crosses) and 26 winter triticale lines (5 cultivars, 21 diallel crosses). Callus induction was observed for all studied genotypes. The rate of embryogenic callus formation was generally better for cultivars and F1 hybrids of winter triticale. Explants that developed embryogenic calli ranged from 25.00% for SE62 to 83.33% for SE69, while for winter wheat genotypes the embryogenic callus rate was lower (ranged 7.32% for SE98 87.23% for SE104). Plants were regenerated for 17 triticale lines and only for 10 wheat genotypes. The genotypes with a relatively high regeneration capability were: SE85 for wheat (61 plants were obtained) and SE67 (92 plants were received). It is to conclude, that wheat lines used in this study showed lower ability to regenerate plants from mature embryos in vitro culture. In the future work an effort will be undertaken to improve the somatic embryogenesis efficiency for this species.

This work was financially supported by Ministry of Agriculture and Rural Development of Poland.

Audience Take Away:

- The comparison of wheat and triticale lines for high callus induction and plant regeneration is important because regeneration is genotype dependent, which is a factor inhibiting cell selection and genetic transformation. During future study we should improve the somatic embryogenesis efficiency for wheat winter genotypes.
- We have demonstrated significant effects of genotypes on embryogenic callus formation and plant regeneration from cultures initiated from mature embryos of wheat and triticale lines. We were selected few genotypes with a high regeneration capability. These plants can use for future practical application of mature embryo culture for breeding, transformation and other biotechnological objectives.

Biography

Lidia Kowalska received the MSc degree in Warsaw University of Technology and in Warsaw University of Life Science, Faculty of Horticulture, Biotechnology and Landscape Architecture. Her master thesis was concerned influence of medium on tissue culture response of rye recombinant inbred lines with high morphogenetic potential. In 2014, she joined the Department of Plant Pathology in Plant Breeding and Acclimatization Institute, National Research Institute. She started a project within the doctoral thesis. Her current research interests include anthers and embryos in vitro culture and resistance breeding of wheat and triticale winter cultivars.

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The use of modern physical and chemical methods for identifying adaptation genotypes *Prunus Cerasus L.*

Svetlana Motyleva*, Ivan Kulikov, Ludmila Marchenko, PhD, Sergei Medvedev

Federal State Scientific Institution "All-Russia Selection-Technological Institute of Horticulture and Nursery" (FSBSI ARHIBAN), The Federal Agency for Scientific Organizations (FASO Russia), Moscow, Russia.

Audience Take Away:

- A comprehensive approach to the study of the resistance mechanisms as part of plant physiology and biochemistry.
- Anatomical and morphological features of leaves as a factor of passive immunity.
- A statistical genetics approach in the study of the structure of variability of biochemical parameters as a binder component of immune system.
- Practical application: the rapid assessment of genetic resources by morphological and biochemical markers using of high technology equipment

Biography

Motyleva Svetlana Mikhailovna, associate professor, a leading research scientist, the head of the physiology and biochemistry laboratory of Federal State Scientific Institution "All-Russia Selection-Technological Institute of Horticulture and Nursery". Main activities and responsibility: studies the metabolome profile of different orchard plants using the energy dispersive spectrometry, the liquid chromatography and gas chromatography-mass spectrometry and the plant morphology using the scanning electron microscopy. Search for morphological and biochemical markers of resistance of fruit plants to biotic factors of the environment. The objects of research are traditional and rare fruit crops, cellular and biochemical structures of vegetative and generative plant parts.

Mineral composition and antioxidant activity of forest plants

Paulina Drozd^{*1}, MS, Krystyna Pyrzynska²

¹Forest Research Institute, Poland

²University of Warsaw, Poland

Heather (*Calluna vulgaris*) and wild berries (*Vaccinium myrtillus* L., *Vaccinium vitis-idaea* L.) are dominant species of forest shrubs growing in Poland. They are rich source of bioactive compounds such as flavonoids, phenolic acids, anthocyanins, stilbenes, tannins, sugars, essential oils, carotenoids, vitamins and minerals. Due to their beneficial properties they are commonly used as medicinal plants. Heather and wild berries samples were collected in three different locations in central Poland (the Mazovia plain).

The concentrations of 13 elements (Al, Ca, Cd, Cr, Cu, Fe, K, Mg, Mn, Na, Ni, Pb and Zn) were determined in several samples of these forest plants. The total metal contents after mineralization in acids and hot water extraction were analysed by inductively coupled plasma optical emission spectrometry. Ethyl acetate, water, ethanol and its mixture were used for the extraction of bioactive compounds from heather flowers and berries. The extracts from each plant were evaluated for the determination of some antioxidant capacity: total flavonoid content, reducing power by CUPRAC method, scavenging ability on DPPH radicals.

Forest berries and heather flowers are good sources of Ca, Na, Mg as well as Mn and Zn. Moreover, only low contents of toxic elements such as Pb and Cd were detected, ensuring the absence of risk for human health.

Antioxidant activity of prepared extracts strongly depends on the nature of extracting solvent due to the presence of different antioxidant compounds of varied chemical characteristics and polarities. Ethyl acetate and ethanol-water mixture were proved to be the best solvents. The observed differences in the antioxidant activities and metal composition of the extracts may correlate with the different ecological conditions in which they grow. One of the key factors is probably the composition of soil. The extracts of forest berries and heather contain plenty of compounds with high antioxidant properties.

Audience Take Away:

- The presented results could be used by other faculty researchers to expand their research with chemical analyses
- During presentation several practical information will be discussed: the influence of solvents used for the extraction, practical solution to a problems connected with the determination of antioxidant properties by different spectrophotometric methods
- The results may be helpful for better utilisation of forest plant extracts as potential pharmaceutical and nutraceutical ingredient

Biography

My name is Paulina Drózd. I am a young researcher and Ph.D. student at the Department of Chemistry at University of Warsaw. Since 2011 I have worked also in Laboratory of Natural Environment Chemistry in Forest Research Institute. I do research about the possibility of utilisation non-wood forest products (NWFPs) as a source of antioxidants in beneficial for health supplements. In my job I am also responsible for chemical analysis of forest plants: plant nutrition and soil analyses. I am co-author of few scientific articles concerning antioxidant activity of food samples and recently of forest plants. I have participated in some international scientific conferences presenting the results of my study.

Immunogenicity of GP4 and GP5 Recombinant proteins of Porcine Reproductive and Respiratory Syndrome Virus Expressed in Transgenic Plants

Chul Han An^{*1}, Yu Jeong Jeong, Sung-Chul Park Ph.D., Jae Cheol Jeong Ph.D., Cha Young Kim Ph.D.

Biological Resource Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Republic of Korea

¹Department of Bioscience and Biotechnology, Chungnam National University

Porcine reproductive and respiratory syndrome virus (PRRSV) is one of the most economically significant pathogens in the global swine industry due to reproductive disorders and growth retardation. Current vaccines against PRRSV rely on the use of an attenuated-live virus, but these are unreliable. Thus, effective vaccines against PRRSV should be developed. Plants are being considered as a promising alternative to conventional platforms for the large-scale production of recombinant proteins such as vaccine antigens. Here, our study aims at producing subunit vaccines for a set of structural proteins of PRRSV in plants. In an effort to develop plant-based subunit vaccines against PRRSV, codon-optimized and recombinant proteins (GP4, GP5) of PRRSV as antigens were expressed using plant-based subcellular targeting systems in transgenic Arabidopsis plants. Transgenic Arabidopsis plants with high-level expression of the GP4 and GP5 proteins in ER-targeting vector systems were confirmed by Western blot analysis. For animal immunogenicity study, four-week-old PRRSV-free pigs were administered three times using a finely ground leaf material of transgenic Arabidopsis plants. All pigs were aggressively challenged with PRRSV JA142 strain after a final administration and then immunogenicity of the GP4 and GP5 was assessed. As a result, the group of pigs fed transgenic plants expressing GP4 and GP5 antigens show that higher IFA titer and lower lung lesion scores than control in pig immune response test.

Audience Take Away:

- Approach for the development of plant vaccines using molecular agriculture
- Practical examples of the use of an organelle targeting vector for high expression of foreign proteins in plants
- How to develop a plant subunit vaccine for prevention of porcine reproductive and respiratory syndrome virus (PRRSV)
- Immunogenicity studies in pigs using various antigens of PRRSV

Biography

2013. 2. - present

(Ph.D. Candidate) Department of Bioscience and Biotechnology, Chungnam National University

2010. 3. - 2012.2.

(M.S.) Department of Forest Resources, Chungnam National University

2008. 11. - 2009.10.

Overseas internship at Forest Service

2004. 8. - 2006. 7.

Volunteers to prevent desertification in China

Response of kidney bean and pea plants to low temperature stress under polyamines treatment and its role to productivity

Ph.D. Jurga Jankauskiene^{1,2}, Ph.D. Sigita Jurkoniene¹, Ph.D. Virgilija Gaveliene¹, Ph.D. Rima Mockeviciute¹, Ph.D. Milda Jodinskiene¹, Ph.D. Dessislava Todorova³.

¹Nature Research Centre, Lithuania

²Lithuanian University of Educational Sciences, Lithuania

³Institute of Plant Physiology and Genetics, Bulgarian Academy of Sciences, Bulgaria

Temperatures below the optimal for plant growth and development influence a reduction in growth rate, stem elongation, leaf expansion and stomata movements, and cause changes in principal physiological and biochemical processes and thus reflect the plant growth and productivity (Browse and Xin, 2001). Plants subjected to unfavorable temperatures undergo an increased exposure to the reactive oxygen species (ROS), and the accumulation of free radicals provokes damages in membranes and build up of lipids peroxides. As polyamines possess free radical scavenging features and antioxidant activity, they stabilize negatively charged macromolecules and may confer plant tolerance to unfavorable temperatures. It could be proposed, that exogenous application of some polyamines should eliminate the harmful effects of temperature and influence garden pea (*Pea sativum* L.) and kidney bean (*Phaseolus vulgaris* L.) productivity. The goal of research was to improve garden pea and kidney bean temperature tolerance and productivity via different concentrations of polyamines applications to plants with different low temperature tolerance under controlled and natural growth conditions. We used polyamines – spermine, spermidine and putrescine at concentrations of 0.1 and 1.0 mM as plant physiological and biochemical processes modifiers. The hydrogen peroxide (H₂O₂) and malondialdehyde (MDA) were investigated as stress markers. Plant yield structural elements (silique number on plants, seed number per silique and 1000 seed weight) were assessed in the stage BBCH 89. Under controlled growth conditions MDA and H₂O₂ content in low temperature treated plants was increased. Application of polyamines caused a slight additional increase of MDA content, this effect in garden pea (more tolerant to low temperature) was more significant.

Under low temperature conditions H₂O₂ content in polyamines treated plants was higher. Among ROS species, H₂O₂ is an important signaling molecule which is produced by the chloroplast and involved in the response of the plant to different types of environmental stressors (Belkadhi et al., 2014; Jajic et al., 2015). Many researchers discuss about actual concentration of H₂O₂ in tissues – which one is optimal for plants to maintain homeostasis and which one is harmful (Belkadhi et al., 2014; Jajic et al., 2015). We supposed that higher content of H₂O₂ after polyamines applications in kidney bean played as signaling molecule to switch defense system in this plant.

Analysis of plant yield structural elements showed that polyamines noticeably enhanced the pea and kidney bean productivity elements.

Audience Take Away:

- The audience will hear some new data about polyamines as a tool for plant cold stress prevention and about plant productivity under polyamines applications.
- This knowledge will help them to expand their research or teaching. The data of this research provide a practical solution of cold stress problem.

Biography

My doctoral degree is in the Biomedical science area, research field of Biology. Thesis title is "Physiological-biochemical peculiarities of oilseed rape (*Brassica napus* L.) cold acclimation". I work in the Laboratory of Plant Physiology at Institute of Botany, Nature Research Centre as a researcher. Also, I am a lecturer in the Department of Biology at Lithuanian University of Educational Sciences. Main research interests: plant physiology, plant biochemistry. I am currently engaged in research of protein composition, phytohormones (IAA and ethylene) and plant growth regulators importance in plant resistance to adverse environmental factors. I am a member of Plant physiological society (Lithuania), Biochemical society (Lithuania) and the Botanical Society of Japan (Japan).

DAY 2

Keynote Forum

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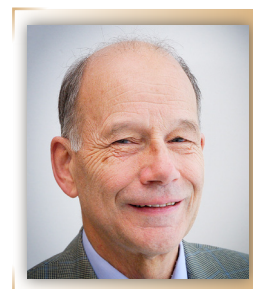
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Risk assessment of dietary exposure to deoxynivalenol in different age groups in Norway

Leif Sundheim*

Norwegian Institute of Bioeconomy Research, Ås, Norway



The Norwegian Scientific Committee for Food Safety has assessed the risk for adverse effects of deoxynivalenol (DON) in different human age groups. DON is the most prevalent mycotoxin in Norwegian cereals, and DON is present in virtually all samples of cereal grain and cereal flour, bran, oat flakes and other cereal based food products. In years with low and high mean concentration of DON in the flour the exposure to DON was calculated for different age groups, based on occurrence and consumption data. The estimated mean and high (95-percentile) exposure to DON, respectively, were in the range of, or exceeded the TDI by up to 2 times in 1-year-old infants and 2-year-old children. In years with high mean DON concentration the high (95-percentile) exposure exceeded the TDI up to 3.5 times for 1-, 2-, 4- and 9-year old children. Although the TDI is not a threshold for toxicity, the assessment concluded that exceeding the TDI in infants and children is of health concern. The estimated dietary intakes of DON in adolescence and adult populations are equal to or below the TDI and not of health concern. Acute exposure to DON is not of concern in any of the age groups.

Audience Take Away:

- Deoxynivalenol (DON) is the most common mycotoxin in cereals in Norway and can be detected in most flour samples and other cereal food commodities.
- The DON exposure in 1-4-year old children may exceed the tolerable daily intake and is of health concern.
- In adolescence and adult populations, DON is not of health concern.
- Acute exposure to DON is not of concern in any human age group.

Biography

PhD in Plant Pathology, University of Minnesota, St. Paul, Minnesota, USA. Senior lecturer and professor in Plant Pathology, Norwegian University of Life Sciences. Research Director, Norwegian Institute for Bioeconomy Research. Member of the Norwegian Scientific Committee for Food Safety since its establishment in 2004. Chairman of the Plant Health Panel and Member of the Scientific Steering Committee during seven years. Research on foliar plant diseases, soilborne plant disease, biological control of plant pathogens, mycotoxins.

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In vitro and molecular techniques combined with conventional methods for horticultural crop improvement

Samir C. Debnath*

St. John's Research and Development Centre, Agriculture and Agri-Food Canada, St. John's, Newfoundland and Labrador, Canada.



Plant tissue culture and molecular techniques are important biotechnological tools that can be used in combination with conventional methods for horticultural crop improvement. Micropropagation is now a multi-million dollar industry and is the most important biotechnological approach practiced all over the world. The technology is used commercially for mass propagation of selected cultivars and parental stocks in a hybrid development program, to maintain pathogen-free (indexed) germplasm and to produce plants all the year-round. DNA markers are used to identify variation of DNA sequences in horticultural plant species, to monitor trueness-to-type of micropropagated plants and to identify germplasm and assess genetic relatedness for practical breeding purposes through genotype selection and proprietary-rights protection. Small fruits and vegetables are health-promoting horticultural crops with anti-tumor, anti-ulcer, anti-oxidant and anti-inflammatory activities. The presentation focuses on: wild small fruit (*Vaccinium*, *Rubus* and *Fragaria* species) germplasm collection, characterization, maintenance and their utilization in hybrid development using *in vitro* and molecular techniques. Epigenetic studies in small fruit micropropagules and wild berry germplasm biodiversity using various molecular markers will contribute significantly in planning future breeding and production programs of horticultural crops. Emphasis is given with research conducted at St. John's Research and Development Centre, Agriculture and Agri-Food Canada in Newfoundland and Labrador, Canada.

Biography

Dr. Samir C. Debnath, P.Ag. is a Research Scientist at the St. John's Research and Development Centre of Agriculture and Agri-Food Canada (AAFC) in Newfoundland and Labrador and an Adjunct Professor of Biology at the Memorial University of Newfoundland. He has authored and co-authored more than 100 publications in peer-reviewed journals including review papers and book chapters. He has been a keynote speaker and an invited speaker at a number of international and national conferences and meetings, was the President of the Newfoundland and Labrador Institute of Agrologists (P.Ag.) and the Canadian Society for Horticultural Science, and the Editor-in-Chief of the journal: *Scientia Horticulturae*. He is the Country Representative for Canada and the Council Member of the International Society for Horticultural Science. His research concerns biotechnology along with conventional method-based value-added small fruit and medicinal plant production, propagation and genetic enhancement. Much of his current work focuses on wild germplasm, antioxidant activity, biodiversity and micropropagation for berry crop improvement using *in vitro* and molecular techniques combined with conventional methods.

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Understanding of plant innate immune response and engineering of novel innate immunity for pathogen clearance and disease protection

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Biosciences Division, Los Alamos National Laboratory, Los Alamos, NM, USA



A national consortium has been set up to study pathogenesis and develop diagnosis and therapy of citrus greening (aka Huanglongbing or HLB), the most devastating disease of citrus in the US and worldwide. HLB is caused by gram-negative *Liberibacter*, which is transmitted by insect vector, psyllid. There is no cure for HLB. Psyllid control and tree removal are the only disease management options. Psyllid control, which does not eliminate the causative *Liberibacter*, is only partially successful. The problem is further exacerbated by the fact that the disease symptoms appear 2-5 years after the initial *Liberibacter* exposure. By then disease is often too widespread to be effective by the current disease management protocols. Therefore, robust strategies for pre-symptomatic diagnosis and therapy are urgently needed for effective HLB management.

It is our hypothesis that quantitative knowledge of citrus innate immune response induced early upon *Liberibacter* exposure would guide the development of both pre-symptomatic diagnosis and therapy. In support of our hypothesis, we have carried out genome-wide transcriptomic analysis in the greenhouse to identify citrus mRNA and microRNAs that are induced early (within 4-24 weeks of *Liberibacter* exposure) and belong to the five coupled gene networks: PTI (PAMP-triggered immunity), ETI (Effector-triggered immunity), and Salicylic Acid (SA)/ Jasmonic Acid (JA)/ Ethylene (ET) signaling.

The final output of the coupled networks is the production of citrus defense proteins that can clear or block infection. We identified key genes that are induced in these networks and determine the disease outcome, i.e., *Liberibacter* modifies the expression pattern of these genes, which, in turn, abrogates the citrus innate immune defense allowing *Liberibacter* to escape killing, cause infection, and develop HLB. We identified informative microRNAs that also determine the disease outcome by regulating post-transcriptionally specific genes belonging to the five coupled PTI/ETI/SA/JA/ET networks. We believe that a combination of citrus mRNA and microRNA, induced early during infection, will serve as the biomarkers for pre-symptomatic diagnosis of HLB.

From our transcriptome analysis, we identified citrus thionin, an antimicrobial or lytic peptide and an end-product of the PTI/ETI/SA/JA/ET networks, to be severely down-regulated. We argued that thionin expression can be rescued by removing the control of the PTI/ETI/SA/JA/ET networks and putting it under the control of a constitutive promoter. In addition, we made targeted modifications in the endogenous thionin amino acid sequence to improve activity and reduce toxicity. Transgenic citrus expressing the modified thionin showed *Liberibacter* clearance and protection against HLB. We are in the process of designing a chimera, in which we have added a recognition domain to the modified thionin (a lysis domain). Transgenic citrus expressing the chimera of recognition and lysis domains is expected to be more effective in *Liberibacter* clearance and disease protection. Introduction of a modified thionin or a chimera introduces a novel innate immune defense in citrus.

In summary, we propose a platform technology that combines transcriptome analysis and protein engineering (i) to identify informative plant mRNA and microRNA for pre-symptomatic disease diagnosis and (ii) to engineer novel innate immunity for pathogen clearance and disease protection.

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Audience Take Away:

- The audience will learn to use genome biology to decipher how a pathogen subverts plant innate immune response and how this knowledge can be utilized to develop novel diagnosis and therapy
- The research and industry participants will learn the utility of pre-symptomatic diagnosis and engineered immunity to protect against pathogen-induced diseases and to develop a robust strategy for food security
- Researchers will learn (i) about transcriptome analysis tools for understanding disease pathogenesis during the early stages of infection and (ii) protein design tools for engineering novel plant innate immunity to facilitate pathogen clearance and disease protection
- The participants will learn the progress made for the therapy of Pierce's Disease in grape and HLB in citrus

Biography

The author obtained his PH. D. in the area of structural biology of DNA. Interestingly, he discovered the role of DNA repeats in human diseases based upon their ability to adopt unusual structures. He then turned his attention to the immunological aspects of various infectious diseases: for example, how HIV surface antigen varies its sequence and structure to escape host immune pressure. Currently, he has been working on various pathogen-induced plant and human diseases to understand innate immune response and to develop diagnosis and therapy. He has over 100 papers in peer-reviewed journals.

DAY 2
Speakers

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Sessions on: Plant Pathology: Mechanisms Of Disease | Applications In Plant Sciences And Plant Research | Plant Diseases

Session Chairs

Leif Sundheim

Norwegian Institute of Bioeconomy Research
Norway

Antonio Domenech-Carbo

University of Valencia
Spain

Session Introduction

Title: Treating plants with plastic: Macromolecular therapies to combat infections in plants

Victoria A Piunova, IBM Almaden Research Center, United States

Title: Metabolomics analysis of the effect of changed CO2 concentration on the wheat's response to Fusarium Head Blight

Miroslava Cuperlovic-Culf, National Research Council Canada, Canada

Title: Defense mechanisms in multi-actor relationships: Pathogenesis related gene response in agricultural important crops

Paola Leonetti, IPSP-CNR, Italy

Title: A barley powdery mildew candidate effector regulates host immune responses through destabilizing HvCAT1

Qian-Hua Shen, Institute of Genetics & Developmental Biology, China

Title: Analysis of metabolites modulated by Plasmopara viticola infection in Bianca grapevine leaves

Giulia Chitarrini, Fondazione Edmund Mach, Italy

Title: Electrochemolomic methodology for plant taxonomy

Antonio Domenech-Carbo, University of Valencia, Spain

Title: Characterization of transcription factors involved in early defense response during interaction of oil palm (Elaeis guineensis) with Ganoderma boninense

Nurshafika Mohd Sakeh, Universiti Putra Malaysia, Malaysia

Title: Performance of Grafted Galia and Ananas Melon Types under Different Salinity Concentrations

Adel Saleh Hussein Al-Abed, National Center for Agricultural Research and Extension, Jordan

Title: TaqMan PCR assay for detection and quantification of Stagonosporopsis tanacetii in pyrethrum seed and seedlings

Md Abdullahil Baki Bhuiyan, The University of Melbourne, Australia

Title: GFP tagging of Ralstonia solanacearum facilitate its easy tracking in tomato cultivars without affecting virulence

Manju Sharma, Amity Institute of Biotechnology, India

Title: Activation of Innate Plant Immunity as a Sustainable Strategy for Pest Management

Sergio Molinari, IPSP-CNR, Italy

Title: Development and application of DNA and metabolic markers for characterisation and selection of garlic cultivars

Jaroslava Ovesna, Crop Research institute, czech Rpublic

Title: Bursting to life as a Biotech Entrepreneur, Why accelerators matter

John B. Carrigan, RebelBio SOSV, Ireland

Title: Characterization of Kumquat (Fortunella margarita) peel essential oil and hydrosol fraction and their potential as antimicrobial, antioxidant, anti-inflammatory and anti-carcinogenic agents

Bardouki Haido, VIORYL S.A., Greece

Title: Perspectives on the use of reflectance spectra in the visible/near infrared region to detect the Citrus tristeza virus

Natalia Tomas Marques, Universidade do Algarve, Portugal

Title: Response of Stevia rebaudiana bertonii to foliar application with yeast or seaweed extracts on growth, anatomical and chemical structure

Azza M. Salama, Cairo University, Egypt

Title: Transcriptome profiling during low temperature storage of sweetpotato tuberous roots to elucidate the mechanism of chilling injury

Chang-Yoon Ji, University of Science & Technology, Korea

Title: Managing root-knot nematodes in potatoes using cucurbitacin-containing phytonematicides: A success story in South Africa

Kgabo Martha Pofu, Agricultural Research Council, South Africa

Treating Plants with Plastic: Macromolecular Therapies to Combat Infections in Plants

Victoria A. Piunova^{1*}, Ph.D., Noah F. Fine-Nathel¹, Ph.D., James L. Hedrick¹, Ph.D., Michael Knoblauch², Ph.D.

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Continuous population growth places a great demand on the sustainable farming practices and effective crop disease management. Breeding of varieties with higher crop yield is usually accompanied with higher susceptibility to pathogens and production in monocultures promotes pathogen spread. Here we demonstrate an application of polymer-based therapy for mitigation of infectious diseases in plants. The design, synthesis and evaluation of antimicrobial activity in plant tissue is discussed. Effects of macromolecular therapy on soil microbiome are evaluated.

Audience Take Away:

- Application of macromolecular therapeutics in agriculture.
- Mechanism of action and efficacy of macromolecular therapeutics in plants.
- Effect of macromolecular therapeutics on plant microbiome.

Biography

Dr. Victoria Piunova is a research staff member at IBM Almaden Research Center. She earned her Ph.D. in chemistry from the University of Southern California conducted post-doctoral studies at the California Institute of Technology. Dr. Piunova's current research interests are focused on the development of materials for biological and biomedical applications.

Metabolomics analysis of the effect of changed CO₂ concentration on the wheat's response to Fusarium Head Blight

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Diseases of agricultural crops caused by fungi have devastating economic and health effects. Fusarium head blight (FHB) is one of the most damaging diseases of wheat and other small grain cereals. FHB contamination of wheat has been steadily increasing over the last decade leading to an increase in the associated risk of mycotoxin contamination in food and feed. Climate change and associated rise in CO₂ levels are hypothetical causes of this rise but their effects on Fusarium graminearum and the spread of FHB are still unknown. In this study the defense response of wheat plants grown at ambient (400 ppm) and elevated (800 ppm) CO₂ was evaluated and compared. Plant and fungal metabolites play a major role in defense and virulence with significant differences in metabolic response in resistant and susceptible plants. 1D and 2D 1H NMR spectroscopy performed in this work have provided detailed metabolite information leading to possible metabolic markers discriminating metabolic changes in wheat subtypes with different resistance and at changing CO₂ levels. Methodology previously established in our group for metabolite quantification from NMR data that automatically aligns spectra of standards and samples prior to quantification utilizing multivariate linear regression optimization of spectra of assigned metabolites to samples' 1D spectra is described and used. Fusarium infection-induced metabolic changes in different conditions will be discussed in the context of metabolic network and resistance.

Audience Take Away:

- Methods for metabolomics analysis will be presented and audience will learn how to use them in plant sciences
- Major metabolic differences between wheat resistant and susceptible to FHB will be shown with indication of type of resistance in different conditions. Audience will be able to use these markers of resistance to explore different wheat varieties and understand resistance to pathogens
- Effect of CO₂ level change on resistance to FHB will be discussed providing knowledge about the effect of climate change on fungal pathogens in agricultural crops
- Methods for analysis of metabolomics data will be introduced allowing audience to enhance their data analysis capabilities
- Database of resistance related metabolites and their relationship to climate change will be introducing audience to publically available resource

Biography

Miroslava Cuperlovic-Culf is a Senior Research Officer and leader of Scientific Data Mining team at National Research Council of Canada. She has a Ph.D. in BioPhysical Chemistry from University of California, USA and Postdoctoral training in Biophysics from University of British Columbia, Canada. Miroslava has worked for a number of years in the application of metabolomics and transcriptomics in life sciences. She has authored a book in the application of NMR Metabolomics as well as many articles and book chapters. With several collaborators in Canada and USA she is working on the application of metabolomics and metabolism modeling for the development of improved wheat varieties. She lives and works in Ottawa, Canada.

Defense mechanisms in multi-actor relationships: Pathogenesis related gene response in agricultural important crops

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Which are the main objectives of the study of the interactions between plants and pathogenic organisms? It's possible to outline at least three: first of all, detailed analysis of plant-microbe interactions should provide sustainable solutions for the control of plant pests worldwide. Second, such study should help to identify the signaling mechanisms by which plant cells respond to biotic stresses. Last but not least, researchers, through the study of plant-pathogen interaction, may find out how organisms from different kingdoms communicate. Keys of this signaling pathways and communications are genes and proteins. Plant gene expression, in fact, can be modified by various types of pathogens and parasites, including bacteria, fungi, viruses and nematodes; in literature, pathogenesis related (PR) genes are well known as inducible genes at the onset of biotic challenges and their role is to encode proteins which participate in the complex mechanisms of defense. New PR genes were identified and sequenced in Apulian accessions of leguminous plants. Moreover, an analysis of PR-gene expression patterns by qRT-PCR and the determination of nematode infection levels were carried out after that tomato (*Solanum lycopersicon* L) plants, phytoparasitic nematodes (*Meloidogyne* spp.) and symbiont fungi (*Trichoderma* spp.) were allowed to interact. Such a study has contributed to understand the role of Systemic Acquired Resistance (SAR) and Induced Systemic Resistance (ISR) in this multi-actor relationship.

In the presentation, three different interactions will be analyzed: plant-nematode, plant-fungi and plant-nematode-fungi to better understand the relationships between these common soil organisms. Successful pathogen infection occurs only if environmental conditions are favorable, if the preformed plant defenses are inadequate, and if either the plants fails to detect the pathogen or the activated defense responses are ineffective.

The major plant defense pathways adopted by tomato plants would be described along with the signal molecules and the genes induced by SAR or ISR. New pathogenesis related genes encoding for PR proteins in Apulian accessions of leguminous plants were identified, cloned and sequenced; the sequences are being deposited in NCBI gene bank and should be useful to extend the investigations from horticultural to those leguminous species that are becoming more and more important as source of proteins in humans and animals diets.

Audience Take Away:

- The audience should be able to better understand defense mechanisms in plant-organism interactions
- The presentation's topic is very important for anyone researching, teaching, working in plant pathology; the signal molecules, the adopted strategies, the technique presented should suggest ideas for pests biocontrol, useful for safety of human and environment.

Biography

Dr Leonetti obtained in 2000 the Specialization Degree in Biochemistry and Clinical Chemistry, University of Bari, and became researcher in 2001 at the National Council of Research, Institute for Sustainable Plant Protection, in Bari (Italy). Recent Scientific Activities regard host organism-environment interactions: biology and functional genomics; in particular, pathogen-host interactions with an emphasis on molecular biology, biochemistry and epigenetic aspects. In nematode sustainable control strategy, the work mainly concerns the investigation on plant-derived biocidal compounds and chemical control: evaluation of potential of newly formulated nematicides and suitable strategies of application. Referee of research projects for the Italian Ministry of Education. Teacher activities in Master and referee for International Journals.

A barley powdery mildew candidate effector regulates host immune responses through destabilizing HvCAT1

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Biotrophic fungal pathogens secrete effector proteins to regulate host immunity and to establish successful colonization. Barley powdery mildew, *Blumeriagraminisf.sp.hordei* (Bgh), is an obligate biotrophic fungus that is predicted to have more than 500 candidate secreted effector proteins (CSEPs). However, only a small number of these CSEPs have been characterized and their biochemical functions are poorly understood. Here, we describe the characterization and functions of a candidate Bgh effector. Bgh CSEP27 was identified to trigger cell-death and enhance H₂O₂ accumulation using *Agrobacteria*-mediated transient expression in *N. benthamiana*. A barley catalase, HvCAT1, was further identified to interact with CSEP27 in yeast, *in vitro* and *in planta*. HvCAT1 was recruited and accumulated into plant nucleus in the presence of CSEP27. Transient expression of HvCAT1 suppressed CSEP27-induced cell-death and H₂O₂ accumulation in *N. benthamiana*. Interestingly, CSEP27 could promote proteasomal degradation of HvCAT1. Silencing of HvCAT1 in barley enhances the susceptibility to Bgh, while overexpression of CSEP27 in barley increased Bgh haustorium formation in epidermal cells, indicating that HvCAT1 is essential for barley disease resistance and CSEP27 is likely a virulent factor from Bgh. Taken together, our data suggest that Bgh candidate effector CSEP27 regulates host immune responses by destabilizing a host factor, HvCAT1.

Key Words: Fungal Pathogen, Effector, Virulence, Plant Disease Resistance

Biography

Dr. Shen is Principal Investigator of the Plant-Microbe Interaction Group at the Institute of Genetics & Developmental Biology, Chinese Academy of Sciences (Beijing). He earned a PhD in Genetics at the Max Planck Institute for Plant Breeding Research (Cologne, Germany), and an MSc in Plant Breeding and Biotechnology at the John Innes Center (Norwich, England), and Huazhong Agricultural University (Wuhan, China).

Analysis of metabolites modulated by *Plasmopara viticola* infection in Bianca grapevine leaves

Giulia Chitarrini^{*1}, Evelyn Soini¹, Domenico Masuero¹, Marco Stefanini¹, Luca Zulini¹, Antonella Vecchione¹, Samantha Riccadonna¹, Gabriele Di Gaspero¹, Urska Vrhovsek¹

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Downy mildew is one of the most destructive disease of grapevine caused by the biotrophic oomycete *Plasmopara viticola* in particular for the cultivated species *Vitis vinifera*. Due to their levels of resistance, grape from North America have been crossed with *Vitis vinifera* to introgress resistance. The use of grapevine varieties showing durable resistance to downy mildew is a promising strategy to control the disease. Grapevine-*Plasmopara viticola* interaction is still poorly understood from metabolic point of view therefore applying metabolomic approach can extended the up to date knowledge how the plant system is perturbed after stress and let us known which are the metabolites more affected after perturbation probably involved in resistance mechanisms. In this work we evaluated metabolic perturbation in the hybrid grape leaf discs after artificial infection with a suspension of *Plasmopara viticola*. In particular we investigated primary and secondary metabolism at 12, 24, 48 and 96 hours post infection (hpi) using methods of identification and quantification for lipid (LC-MS/MS), phenols (LC-MS/MS), primary compounds from acids, aminoacids, amines/others, sugars (GC-MS), semiquantification for volatiles compounds (GC-MS). This work offers some important information in the study of grapevine *Plasmopara viticola* interaction. A general principal component analysis shows a high variance on the first dimension explaining a separation according to the sampling time. Focusing on each class of compounds we found changes during the first 24-48 hpi regarding the primary metabolism in response to the pathogen infection with a modulation of some metabolites belonging from lipids, aminoacids, acids and sugars. Afterwards the secondary metabolism was affect more strongly by the pathogen with a changes of volatile compounds at 48-96 hpi. The classes of compounds more affected after the infection turns out to be phenylpropanoids, flavonols, stilbenes and stilbenoids at 96 hpi. Our results gave a picture of plant metabolome perturbation and it is up to our knowledge the first time that an extensive metabolites study using a hybrid grape variety has been done to better understand the metabolomics perturbation after *Plasmopara viticola* infection.

Audience Take Away:

- Our results are interesting for the understanding of plant-pathogen interaction and in future grapevine breeding programs.
- It is strongly necessary the knowledge of hybrid metabolism and perturbation to understand resistance mechanisms. It is interesting to discover how the metabolism can be perturbed after pathogens infection and which are the metabolites strongly involved in this interaction.
- Our results represents a start point to understand resistance using metabolomics approach. This work can be done using different grapevine species and to study other plant-pathogen interactions.
- Resistance and knowledge of resistance mechanism are a start point to the fight against pathogen without the massive use of chemical compounds.
- To assist a design problems we performed a randomization of our samples using leaf discs that make possible a homogenous samples among biological replicates.

Biography

Giulia Chitarrini worked on her PhD project in Metabolomic Unit at Fondazione Edmund Mach (Italy) on the project aimed at deciphering the mechanisms responsible for resistance against *Plasmopara viticola* in vine plants applying metabolomics and transcriptomics approaches and will focus on identification of respective early bio-markers. Giulia Chitarrini studied Health and Nutrition biology at the University of L'Aquila. She worked on a thesis project "Relationship between *Aspergillus flavus* and antioxidant profile of *Fagopyrum* spp., potential ingredient for functional foods production" in collaboration with ENEA Casaccia laboratories. Her research activities were focused on the correlation between buckwheat antioxidant profile and AB1-producer *Aspergillus* growth on achenes.

Electrochemolomic methodology for plant taxonomy

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¹University of Valencia, Spain

A methodology for characterizing vegetal taxonomic groups, based on microextraction-assisted voltammetry of immobilized particles applied to microsamples of vegetal matter is described. It is based on recording the voltammetric response of microparticulate films deposited from ethanol, acetone, etc. extracts of different parts of plants put in contact with aqueous electrolytes. The obtained voltammetric profiles, associated to electroactive metabolites in vegetal matter, define an electrochemolomic response which can be applied for discriminating different taxonomic groups using bivariant and multivariate chemometric techniques. Application of the reported methodology for a set of species of different orders suggests the possibility of correlating electrochemical data with phylogenetic trees (see Domenech-Carbo et al. *Electrochemistry-based chemotaxonomy in plants using the voltammetry of microparticles methodology*. *New Journal of Chemistry*, 2015, 39, 7421-7428; Domenech-Carbo et al. *Access to phylogeny from voltammetric fingerprints of seeds: the Asparagus case*. *Electroanalysis*, 2017, 29, 643-650).

Audience Take Away:

- The proposed electrochemical methodology can be used for complementing genetic, molecular and morphological/functional classifications.
- Due to its simplicity and versatility, is of potential interest in screening varieties, discriminating taxonomic groups at different levels.
- Application for real-time monitoring of growth, environmental aggression, etc. in plants is available.

Biography

Prof. Antonio Domenech-Carbo, PhD in Chemistry (Univ. Valencia, 1988), is currently Professor at the Department of Analytical Chemistry of the University of Valencia (Spain). He has published more than 215 articles in indexed journals (two for IUPAC's *Pure Appl. Chem.*) and several books (among them, *Electrochemical Methods in Archeometry, Conservation and Restoration* (2009, Springer), *Electrochemistry of Porous Materials* (2010, Taylor & Francis) and *Electrochemistry of Immobilized Particles and Droplets*, 2nd edit. (2014, Springer). He is topical editor of *Journal of Solid State Electrochemistry* (Springer) and reviewer of ten National Research Agencies and 95 indexed journals. His research is focused on solid state electroanalytical techniques.

Characterization of transcription factors involved in early defense response during interaction of oil palm (*Elaeis guineensis*) with *Ganoderma boninense*.

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Oil palm production generates large export earnings to many countries especially in Southeast Asian region. Manifestation of the disease caused by necrotrophic fungi, *Ganoderma boninense* on oil palm results in basal stem rot which compromises oil palm production leading to significant economic loss. Effective detection and disease control techniques are lacking while oil palm varieties that are resistant to the disease are not available to overcome the problem. Thus, understanding molecular defense mechanisms underlying early interactions of oil palm with *G. boninense* may be vital to promote preventive or control measure of the disease. In the present study, four months old of oil palm seedlings were infected via artificial inoculation using rubber wood blocks fully colonised with *G. boninense*. Roots of six biological replicates of treated and untreated oil palm seedlings were harvested at 0, 3, 7 and 11 days post inoculation (d.p.i). Next-generation sequencing (NGS) was performed to generate high-throughput RNA-seq data and identify differentially expressed genes (DEGs) during early oil palm-*G. boninense* interaction. Based on de novo transcriptome assembly, a total of 427,122,605 paired-end clean reads were assembled into 30,654 unigenes. Sixty-one transcription factors were categorized as DEGs according to stringent cut off-values of genes with log2 ratio [Number of treated oil palm seedlings/ Number of untreated oil palm seedlings] \geq |2.0| (corresponding to 2-fold or more upregulation) with p-value \leq 0.01. Transcription factors that respond specifically to *G. boninense* interaction were selected and separated from those that were also responsive to abiotic stress (empty rubber wood block control) by preliminary screening using reverse transcriptase polymerase chain reaction (RT-PCR). Transcription factors unique to early *G. boninense* interaction were further verified using quantitative real-time polymerase chain reaction (qRT-PCR). The promoter sequences of these genes were identified from the oil palm genome sequence and cloned into β -glucuronidase (GUS) reporter vector and used for functional characterisation using transient expression assay in *G. boninense* infected oil palm roots. This presentation will further elaborate on the promoter activity of the *G. boninense* induced oil palm genes and the different promoter motifs that may be involved in early defense response of oil palm against this devastating pathogenic fungi.

Audience Take Away:

- The findings suggest transcription factor as biomarker involved in early plant defense response.
- The findings will facilitate researchers to pinpoint defense response mechanism specific against necrotrophic fungal attack on oil palm.
- Promoter analysis in this project will exercise novel method of protoplast-Agrobacterium mediated transformation on root tissues of oil palm's explant.

Biography

Nurshafika Mohd Sakeh was born on December 24th, 1989 in Kuala Lumpur, Malaysia. She received her early education at Sekolah Kebangsaan Dato' Demang Hussin and attended Sekolah Menengah Sains Muar for her secondary education. She completed her matriculation level at Kolej Matrikulasi Perak (KMPK) before graduating her tertiary level with Bachelor of Science in Biochemistry (Hons.) at Universiti Putra Malaysia (UPM). During her degree study, she was nationally awarded with Best Thesis and Best Final Year Project in Biochemistry for her final year project entitled the "Development of An Inhibitive Enzyme Assay For Heavy Metals Using Plant Protease" by both Faculty of Biotechnology and Biomolecular Sciences (FBSB), UPM and Malaysian Society for Biochemistry and Molecular Biology (MSBMB). In 2011, she was awarded with two scholarships, Graduate Research Fellowship (GRF) by UPM as well as MyBrain15 by Ministry of Education to pursue her Master's degree in Animal Cell Biotechnology at FBSB, UPM. She is currently enrolling her Ph.D programme in Plant Pathology under MyPhD scholarship by Ministry of Education, Malaysia.

Performance of grafted galia and ananas melon types under different salinity concentrations

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Salinity is a major factor in reduced crop productivity in many arid and semiarid regions. An environmentally friendly approach to avoid or reduce salinity impairment in crop production is grafting of salt-sensitive plants onto salt-tolerant rootstocks. To evaluate the response of grafted Galia and Ananas type melons to salinity, two greenhouse experiments were conducted in NCARE Jordan. Two melon cultivars; Raymond (Ananas type) and Ra'anah (Galia type) were grafted onto two Cucurbita rootstocks; '53009' and '53004'. The grafted melons were grown in ten liter pots filled with perlite. The plants were irrigated with different saline water of 1.5, 3, 6 and 9 dS m⁻¹ concentrations. In general, increasing salinity decreased plant growth parameters. Fresh shoot weight and leaf area were the most sensitive parameters that were affected by increasing salinity stress. Non-grafted "Ananas" melon was more salt tolerant compared to "Galia" type, however, this salt tolerance had no significant effect on improving salt tolerance of the rootstocks. Rootstock '53009' appeared more salt tolerant compared to '53004'. Reduction of dry shoot weight and leaf area under salinity stress may be alleviated by grafting.

Growing grafted melons is a relative new agro-technology used to overcome damages caused by soil borne diseases and also for cultivation of this crop using waste and saline water. Thus dealing with limited sources of fresh water. The overall purposes of this study is to gather information on the performance of grafted melons in order to establish growing protocols optimizing this new agro-technology for the benefit of melon growers on Jordan, Israel and Egypt.

The results of this study were from a regional project between Jordan, Israel and Egypt. Solving problems associated with soil borne pathogens and limited sources of fresh water will not be limited to the life time of the project, as the basis for screening for resistance will be integral for future development of this crop. In addition, local decisions will have a major impact at the regional level mainly due to similar climatic and biological conditions in common to Jordan, Israel and Egypt. Therefore, mutual future decision making based on the results of this research project, at the agricultural level in the field will be immediately implemented by both countries.

Biography

I am Adel Saleh Al-Abed. Ph.D 51 years old .working at the National Center for Agricultural Research and Extension(Jordan). My Ph.D degree in Plant Nematology

"Epidemiological Studies on the Cereal Cyst Nematode *Heterodera latipons* on barley"

Faculty of Graduate Studies, University of Jordan, Amman 2001. And MSc. Degree in plant disease "Antifungal Effects of Some Common Wild Plant against Certain Soil Borne Plant Pathogenic Fungi"

University of Jordan, Faculty of Graduate Studies, Amman 1992 .

I am working as a researcher and plant disease unit manager. Preparing, designing, conducting, and analyzing experiments and reports related to program activities (integrated pest management) on protected and open field cultivation.

Working Projects:

- Development of a novel glucosinolate-containing desert plant (*Ochradenus baccatus*) for control of soil borne diseases in the Middle East. (USAID)
- Grafting Melon as a novel technology for improving yields and reducing chemicals in infested soils (USAID)
- Use of fungal endophytes to increase cucurbit plant performance by conferring abiotic and biotic stress tolerance (USAID)
- Study the environment-friendly control methods of soil borne diseases (*Fusarium* and Nematode) of cucumber and tomato by using cruciferous plant.(SRF)

TaqMan PCR assay for detection and quantification of *Stagonosporopsis tanacetii* in pyrethrum seed and seedlings

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Pyrethrum seed has an important role in the transmission of *Stagonosporopsis tanacetii*, the cause of ray blight disease of pyrethrum. A TaqMan probe based polymerase chain reaction (PCR) assay was developed to quantify the level of *S. tanacetii* inocula in pyrethrum seed and seedlings. Primer pair (St_qF3, St_qR2) was designed based on the intergenic spacer (IGS) region of *S. tanacetii*, which produced a 125 bp amplicon specific to *S. tanacetii*. TaqMan PCR assay using St_qF3, St_qR2 and a probe was highly specific against the genomic DNA of *S. tanacetii*, but did not amplify DNA of 14 related.

Stagonosporopsis species or other foliar pathogens of pyrethrum. The sensitivity limit of this assay was measured using the cycle threshold (Ct) value which ranged from 17.59 for 10 nanograms (ng) to 36.34 for 100 femtograms (fg) genomic DNA of *S. tanacetii*. There

was a significant negative correlation ($r = -0.999$, $P \leq 0$) between the Ct value and the percent of *S. tanacetii* infected seed. In addition, this TaqMan PCR assay detected latent infection within seedlings. This assay could be applied to test commercial seed and seedlings before deciding on the appropriate management practices.

Audience Take Away:

- This research would be utilized by the seed company to detect a specific pathogen in the seed.
- The audience could also learn the specificity and sensitivity of the TaqMan PCR over the traditional culture assay and conventional PCR for detection and quantification of infection within the seed.

Biography

The presenter has submitted PhD thesis at The University of Melbourne which is now under examination. He has published 3 research articles from his PhD research in different Plant Pathology Journals. Before joining as a PhD student, he was working as an Assistant Professor, Plant Pathology at the Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh. He has completed his Master of Science (MS) in Plant Pathology from the Bangladesh Agricultural University, Mymensingh.

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GFP tagging of *Ralstonia solanacearum* facilitate its easy tracking in tomato cultivars without affecting virulence

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Green fluorescent protein (GFP) labelling of phytopathogenic bacteria *Ralstoniasolanacearum* strain UTT-25 (Race 1, bv 3) has been used to study their infection, localization activity, movement at cellular level and monitoring bacterial disease development at whole-plant level in tomato resistant (Hawaii-7996) and susceptible (Pusa Ruby) cv. at different time intervals. This is a new method of isolation for direct-transformation of bacterial cells and easily introduced by electroporation, which was stably maintained with selective pressure (Kanamycin) in *R. solanacearum* (UTT-25) by using the binary vector pCambia1302 carrying *gfp* sequence as a reporter. After direct-transformation the cells were screened by selectable marker and further confirmed with PCR, fluorescence microscopy and Confocal Laser Scanning microscopy (CLSM). Important parameters which are critical for the quality of transformed cells of *R. solanacearum* and efficiency was standardized using green fluorescence protein assay, due to which we recorded the strong green fluorescence emitted from pCambia1302+UTT-25 cells. The infection in tomato plant tissues (leaf, stem and root) was done by using infiltration method. Accordingly, after 24hrs of infection it can be easily monitored using CLSM at wavelength (480-540nm), which targets live bacteria showing abundant green-fluorescing particles along the host cell periphery in CLSM, apparently in between the plasma membrane and the cell wall. These results suggested, pCambia1302 can serve as a direct easy-to-use GFP-tagging tool for any given strain of *R. solanacearum* in cytological as well as field studies. The use of GFP-labelled bacteria has a wide range of applications in host-bacterial interaction studies and bacterial ecology-related research.

Keywords: *Ralstoniasolanacearum*, Tomato, pCambia1302, Fluorescence Microscopy, Confocal Laser Scanning microscopy (CLSM)

Biography

Manju Sharma is professionally active since 1999 presently, working as Assistant Professor at Amity Institute of Biotechnology, Amity University Haryana, Gurgram, Delhi NCR, India since May, 2013. Before, joining Amity, she served her two teaching contracts as Assistant Prof. with Jimma University, Department of Horticulture and Plant Sciences, College of Agriculture and Veterinary Medicine, Jimma, Ethiopia, from 2009-2012 under UNDP programme. She earned her doctorate degree in Feb. 1999 In vitro improvement studies in *Brassica juncea* L. and *Sesamum indicum* L." at Department of Botany, University of Rajasthan, Jaipur, as UGC project-JRF. She obtained her M.Sc. degree in Botany from the same department in 1989. She joined Department of Botany, Delhi University as UGC Project fellow from 1990-92. She has actively participated & presented papers in many national & International conferences. She has published 17 research papers in international journals of repute, 5 books chapters and also wrote Book of poetry *Wojo rah gayeeankahee* released in 5th Delhi Literature Festival, New Delhi. Presently, she is guiding 5 Ph.D scholars. She also supervised exchange programme Ph. D work of RTF-DCS fellow on wheat resistance to *Septoria* from Addis Ababa University, Ethiopia from 29th Nov. 2015- 23rd May, 2016 funded by NAM-ST center, New Delhi. She has basic research background in plant tissue culture and gene transfer in important oil yielding crops. Presently, she is working on Expression of defense-related genes and signaling pathways in tomato, genetic relatedness and biochemical role of XopR-T3SS effector protein in *Xanthomonas oryzae* pv. *Oryzae*, molecular analysis of Phosphine resistance in Lesser grain borer *Phytoperthadominica* infesting Wheat.

Activation of innate plant immunity as a sustainable strategy for pest management

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Plants adopt sophisticated molecular mechanisms to activate immune response against pathogen and parasite attacks. Immune response in plants is regulated by several low molecular weight molecules known as phytohormones, i.e. salicylic acid (SA), jasmonic acid (JA) and ethylene (ET) which also regulate many aspects of plant growth, photosynthesis, flowering, reproduction, seed production and response to environmental abiotic challenges. Defense following pest attacks and also colonization from beneficial microorganisms by plants goes through a relatively unspecific response, a basal defense (PTI, PAMPs Triggered Immunity), in which some molecular patterns (PAMPs, Pathogen Associated Molecular Patterns), such as chitin from fungi, peptidoglycans/flagellin from bacteria, and lipochitooligosaccharides from symbionts are recognized in the apoplastic spaces by cell-surface receptors known as NLR proteins (nucleotide binding domain (NDB), leucine-rich repeats (LRR)). However, adapted pathogens can circumvent PTI by delivering effector molecules directly into the cells. Specific effectors can be recognized by resistant plants carrying intracellular NLRs known encoded by resistance genes (R-genes) in the so-called Effector-Triggered Immunity (ETI). ETI is characterized by a Hypersensitive Reaction (HR) in which production of Reactive Oxygen Species (ROS), SA, and antimicrobial enzymes occur leading to tissue necrosis which stops the spread of the infection. Primary infections of necrotrophs in the green parts of the plant produce diffusible immune signals moving upwards to uninfected leaves, which prime plants against subsequent infections by a wide array of biotrophic pathogen/parasites; this defense mechanism has long since been recognized as Systemic Acquired Resistance (SAR). The executors of SAR are the so-called Pathogenesis Related Proteins (PR-proteins). Over-expression of PR-genes is strictly associated with SAR induction in leaves. Our study has proved that SAR can be induced also in roots against soil-borne parasites such as the biotrophic root-knot nematodes (RKNs). SAR can be induced by minimal amounts of exogenously-added SA and natural functional analogs like methyl-SA, or synthetically produced analogs such as benzothiadiazole (BTH) and 2,6-dichloroisonicotinic acid (INA). Research is on-going to monitor some other classes of chemicals, such as strobilurins, used as fungicides at present, as potential inducers of resistance against nematodes and insects. Furthermore, enrichment of soil of potted tomato and egg plants by Arbuscular Mycorrhizal Fungi (AMF) or antagonistic symbiotic fungi such as some strains of *Trichoderma* spp., commercially available in mixtures, has been proved to induce resistance (MIR, Micorrhiza Induced Resistance; TIR, *Trichoderma* Induced Resistance) to RKNs; propagules of *Glomus* spp. (MIR) mixed with soil induced resistance against the miner insect *Tuta absoluta* in tomato. MIR has been recognized by over-expression of PR-1 either in roots or in leaves.

Application of this strategy in PMI programs will foster the development of all omics techniques, such as metabolomics for immune signal identification, epigenomics for assay of DNA methylation and acetylation in chromatin rearrangements following priming, genomics and proteomics for assays of PR-gene expression, PR-protein enzyme activities, protein identification by specific antibodies, etc. Activation of plant immunity will make plants more responsive to environmental challenges and open the way to a more sustainable pest control as indicated by scientific European communities.

Audience Take Away:

- This presentation is addressed to lab people and farming stakeholders who wants to study pest control in plants by the standpoint of sustainability of the strategies and want to recognize that plants have an immune system which operate in every plant cells and is not functional in specialized tissues and organs as in animals and humans. Like in humans, this system can be fostered and activated firstly by recovering life in farming lands by favoring growth and spread of beneficial microorganisms. Non-toxic chemicals can be associated in strengthening plant immunity which must not kill pests which induce chemical resistance in pest communities.

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- What people can take away from our presentation is a different way to think of plants as organisms completely responsive to environmental changes with a highly specialized immune system, although, in their case, strictly associated with growth; therefore, trade off of fitness with defense may be a problem that should carefully evaluated in different farming systems. The harsh impoverishment and pollution of farming lands by pesticides which kill soil life, lately, is one of the main reason of the severe epidemics outbreaks which are causing big economical problems to our farmers. What people can take away from our presentation is that plant interaction with (a)biotic stresses must be studied in association with plant interactions with environment, otherwise such a study will be of no practical interest

Biography

Senior scientist at CNR and responsible of the Biochemistry Lab. of IPSP located in Bari. Main research topic : study of plant immune system mechanisms; in particular, genetic resistance and induced resistance (SAR, ISR, MIR, TIR) by treatments of plants with hormones, or with symbiont mycorrhizal or antagonist fungi such as *Glomus* and *Trichoderma* spp. Models are Solanaceae plants infected by soil-borne nematodes and mining insects. 67 papers published on International Journals (about 900 citations, H-index 13). Reviewer of projects in industrial research, experimental development, and technology transfer within regional and national applications issued by UE, Italian Ministry (Mise, Miur), Apulia Region.

Development and application of DNA and metabolic markers for characterisation and selection of garlic cultivars

Ovesna Jaroslava*, PhD., Mitrova Katarina¹ MSc., Hrbek Vojtech² PhD, Kucera Ladislav¹ Ing.PhD, Hajslova Jana², PhD.

¹Crop Research Institute, Czech Republic

²University of Chemical Technology, Czech Republic

Vegetables constitute a substantial part of human diet. Consumers require high quality, fresh products, full of health promoting compounds. Among various vegetable species garlic (*Allium sativum* L.) is considered not only culinary, but also medical species rich in secondary metabolites. Both flavour and biological activity are determined mainly by organo-sulfur compounds, S-alk(en)yl-L-cysteine sulfoxides (ACSO). A wide range of factors may have an impact on content of these compounds in the garlic tissue, such as the genetic background of the respective cultivars, growing and storage conditions.

Garlic is a vegetatively propagated diploid species with extremely large genome that lost the ability to flower. Only recently a very few genotypes have been found to be able to produce true seed to some extent. That is why selection of clones from available genetic resources and off types from currently registered cultivars is used.

Careful characterization of available genetic resources and cultivars using molecular and metabolic markers is essential for selection of desirable genotypes and protect the breeders right. DNA fingerprints of almost 150 cultivars and genetic resources identified them and divided them in principle according their origin. We shown that garlics that associated according to their genetic background as identified by DNA fingerprinting grouped similarly according the production of health promoting compounds. Molecular markers associated with ASCO content were identified and transcription of genes associated with ASCO biosynthesis was investigated, characterized along with their transcription activities in different developmental phases.

Bolting cultivars are desirable in the Czech Republic by local consumers while in Spain or France non bolting cultivars are produced which usually are more stable during postharvest period. Non target metabolomic profiling (DART-Orbitrap analysis) and target analysis (LC-MS/MS) revealed the differences among marketed products of different origin.

Production of health promoting compounds was shown to depend upon the environment, including temperature, precipitation and sulphur content in soil. Especially ASCO content was negatively affected by low sulphur supply. The ratio of health promoting substances in different cultivars tends to be constant across environments.

We identified local genotypes that have been used for development of new cultivars that fulfil requirement of farmers and consumers. We uncovered also clonal micro-variability within cultivars and these off-types are used for further breeding.

We suggest that careful characterization of available genetic resources, breeding lines and cultivars along with markers assisted selection may help to select the best garlic genotypes suited for farmers and consumers requirements.

Acknowledgement: The work was supported by the project of the Ministry of Agriculture of the Czech Republic NAZV-QJ1210158 and RO0414.

Audience Take Away:

- Although vegetatively propagated, garlic maintain enough variability for breeding of new cultivars with required properties
- DNA markers are highly suitable for authentication of garlic cultivars, prevent adulteration and facilitate protection of breeders right

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- DNA sequencing and ddPCR revealed multigenic nature of alliinase gene family in garlic
- Tools were developed for transcriptomic profiling of genes involved in ASCO biosynthesis and applied for gene transcription investigation in various environments
- Content of desired compounds depend upon environment as revealed by metabolomic approaches
- All the tools may be applied for garlic improvement
-

Biography

Crop Research Institute in Prague since 1984. Experiences in plant tissue cultures, plant transformation, marker development and assisted selection, DNA fingerprinting, gene expression studies. Current position: Head of the division of Plant Genetics and Breeding. Project leader, supervisor of bachelor's, master's and doctoral theses, lecturer of professional seminars (GMOs, plant breeding). Research Director of national and international scientific projects. Author of more than 120 scientific publications author of applied results. National representative in various management bodies and working groups of DG JRC EC. Award of the Czech Minister of Agriculture (2012), Award of CRI Director (2014, 2016).

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Bursting to life as a Biotech Entrepreneur, why accelerators matter

John B. Carrigan*

RebelBio SOSV, Penrose Wharf, Alfred Street, Cork, Ireland

RebelBio is SOSV's Cork-based global bioaccelerator initiative, which is dedicated to funding and building startups for the purpose of aiding humanity. Having founded the world's first life sciences accelerator in Cork in 2014, SOSV now operates two accelerator programs, IndieBio based in San Francisco and RebelBio again based in Cork. These accelerators are responsible for establishing many biotech startups around the world including Perfect Day Foods, Memphis Meats, Microsynbiotix and the German based Saphium Biotech. We provide the mechanism by which young scientists, entrepreneurs and tinkerers can shape their own destiny and make something that matters. RebelBio provides seed funding and mentorship to drive the transition of science to a business in only four months, before launching its graduate companies into the world of biotechnology to make their fortune, buffered by the company's many alumni, partners and partner investors. This year's cohort contains Plantedit, a plant gene editing company founded in Italy and Swalife, who, with our help are commercialising the production of plants' natural compounds for the treatment of skin cancers. Both of these companies are developing their products and business in our labs at University College Cork in 2017.

Audience Take Away:

- The audience will have learned that there is a direct and easy way to obtain investment and begin the commercialisation of their research
- The audience will also learn how an accelerator program has driven the formation of companies such as Plantedit and Swalife, both formed by postdocs from plant sciences
- The audience will learn how by becoming involved with Venture capital they can allow their institutions to be at the centre of a innovation hubs.

Biography

John Carrigan has completed his PhD in 2005 from University College Dublin and carried out postdoctoral both in Dublin and in Copenhagen. He has been involved with several startups, most recently biobased advanced materials company, Cellulac Ltd. He is the CSO in SOSV responsible for scientific due diligence, recruitment, product development analysis in addition to other work. He has published several papers in the area of protein engineering, enzymology, metabolomics and cellulosic biofuels.

Characterization of Kumquat (*Fortunella margarita*) peel essential oil and hydrosol fraction and their potential as antimicrobial, antioxidant, anti-inflammatory and anti-carcinogenic agents.

H. Bardouki^{*1}, M. Vamvakias¹, E. Papavassilopoulou¹, D. Georganakis¹, E. Fitsiou², G. Mitropoulou², K. Spyridopoulou², A. Tiptiri-Kourpeti², M. I. Panayiotidis³, A. Galanis², Y. Kourkoutas², K. Chlichlia², A. Pappa², E. Tzima⁴, I. Serifi⁴ and T. Papamarcaki⁴

¹VIORYL S.A., Chemical & Agricultural Industry, Research S.A., Greece

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³School of Life Sciences, Heriot-Watt University, Scotland

⁴Laboratory of Biological Chemistry, Medical School, University of Ioannina, Ioannina, Greece

Nowadays, there is an increasing concern in plant extracts as potential antimicrobial, antioxidant, anti-inflammatory and anti-carcinogenic agents. In the research project (BIOFOOD) supported by the GRST, biologically active extracts derived by indigenous Greek edible and medicinal plants were characterized and used for the production of novel functional foods. Kumquat (*Fortunella margarita*) was one of the studied species that is actually cultivated in Greece (Corfu Island), with high economic significance. Peel essential oil and hydrosol fraction were characterized with GC/MS and LC/MS. Essential oil consists of a variety of components with the most prominent being limonene, myrcene and δ germacrene. No phenolic acids were detected in the hydrosol fraction. Antimicrobial activity and anti-cancer potential was further studied for both fractions. Essential oil in vivo effect in embryonic development in zebrafish was also determined. The main research objective was the development of novel functional foods incorporating Kumquat fractions and the validation of their health promoting effects.

Research project co-financed by the European Union (European Regional Development Fund–ERDF) and Greek national funds through the Operational Program “National Action “COOPERATION 2011 – Partnerships of Production and Research Institutions in Focused Research and Technology Sectors” (Project Nr. 11SYN_2_566).

Audience Take Away:

- In this study we focus on the results received for Kumquat but the whole project in general opens new horizons in the research by taking a rather innovative multidisciplinary approach. The main objective covers the determination of biological activities for fractions (mainly essential oils) isolated from Greek endemic species. Meanwhile, their efficient utilization for novel functional foods production aims at health improvement.
- The future innovation would be the development of an industrially applicable technology, with end products having enhanced microbial safety and potential antioxidant, anti-inflammatory and anti-cancer properties.

Biography

Haido Bardouki received her PHD (2003) from the Department of Chemistry, University of Crete (Greece) where she had earlier received her Chemistry Degree (1997) and a Master of Science (2000). Thesis and master subjects focused on analytical and environmental chemistry that gave her the opportunity to participate in research projects taking place in Kuujjuarapik, (2001, Hudson Bay, Canada) and Kerguelen Islands complex, (2002, Indian Ocean). Since 2003 she works in VIORYL S.A. (Greece), a chemical company focusing on Fragrances, Flavors, Plant Protection and Biological Insect Control, in the Mass Spectrometry Laboratory, R&D Department. She is responsible for the implementation of various GRST supported research programs. She is specialized in the analysis of fine chemicals, essential oils, flavors and high added value compounds using GC-MS and LC-MS.

Perspectives on the use of reflectance spectra in the visible/near infrared region to detect the Citrus tristeza virus

Andreia M. Afonso¹, MsS., Rui Guerra¹, PhD., Ana M. Cavaco¹, PhD., Patrícia Pinto¹ PhD., Amílcar Duarte¹, PhD., Deborah M. Power¹, PhD., Natália T. Marques^{*1}, PhD.

¹Universidade do Algarve, Portugal.

Citrus plants are affected by Citrus tristeza virus (CTV), the most economically important viral disease. In this study we address the problem of identifying asymptomatic infected plants by multivariate analysis of reflectance and transmittance spectra of the leaves in the visible/near infrared region. Twenty young healthy and CTV infected Citrus macrophylla plants were assayed. Reflectance and transmittance spectra of selected leaves were acquired through a portable spectrometer, with measurements performed monthly over 10 months. The spectra study was complemented with biochemical analyzes and photosynthesis rate evaluation to estimate the condition of plants. In this communication we present the results conveyed by multivariate analysis of the spectra. Standard unsupervised classification methods such as Principal Component Analysis or clustering show promising results by yielding a correct separation of classes (infected vs. non-infected) for some of the months but not for others. We discuss optimization of the measurements directed at obtaining reliable results under field conditions.

Audience Take Away:

- Spectroscopic techniques may be employed in a easy and non-invasive way to help diagnose plant diseases
- This research may be reproduced with other plants and pathologies
- The analysis presented is an example that may be adapted to each case
- Spectroscopic techniques allow to gather more information
- The use of reflectance and transmittance spectra in detection of citrus tristeza virus in the field: applications and limitations.

Biography

Natalia Tomas Marques has a PhD in Biological Sciences from the Classical University of Lisbon, Portugal. From 2004 until now is Assistant Professor at Faculty of Sciences of Universidade do Algarve. She is specialized in plant cell & molecular biology and in vitro culture. Her current research projects include Citrus tristeza virus (CTV)-citrus interaction, interaction of proteins encoded by Citrus tristeza virus to look for protein synergistic effects, studies on application of reflectance spectra in the visible/near infrared region to detect the CTV, performed in cooperation with Dr. Rui Guerra from Department of Physics of Universidade do Algarve.

Response of *stevia rebaudiana* Bertoni to foliar application with yeast or seaweed extracts on growth, anatomical and chemical structure

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¹Cairo University, Egypt.

²Sugar Crops Research Institute, Agricultural Research Center, Egypt.

³Food Technology Research Institute, Agricultural Research Center, Egypt.

The current study was carried out during the two successive seasons of 2013-2014 and 2014-2015 at Giza Agricultural Research Station, Agricultural Research Center, Giza, Egypt, to investigate the effect of foliar spray with yeast or seaweed extracts and their interaction on some morphological, anatomical as well as chemical characters of stevia (cv. China-1).

Audience Take Away:

- This investigation is an attempt to bring to light more information about the effect of foliar spray with yeast or seaweed extracts and their interaction on some morphological, anatomical and chemical characters of stevia.
- The maximum significant increase was recorded when plant sprayed with a mixture of 2 g yeast extract/L and 1.0 ml seaweed extract/L.
- spray with mixture of 2g yeast extract/L + 1.0 ml seaweed extract/L recorded the highest percentage of rebaudioside-A (7.0%), also the highest stevioside percentage (3.94%).

Transcriptome profiling during low temperature storage of sweetpotato tuberous roots to elucidate the mechanism of chilling injury.

Chang Yoon Ji^{1,2*}, Won-Hyong Chung³, Ho Soo Kim¹, Won Yong Jung¹, Sang-Soo Kwak^{1,2}

¹Plant Systems Engineering Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Republic of Korea

²Department of Environmental Biotechnology, Korea University of Science Technology (UST), Republic of Korea

³Division of Nutrition and Metabolism Research, Korea Food Research Institute (KFRI), Republic of Korea

Sweetpotato [*Ipomoea batatas* (L.) Lam.] is a globally important root crop with a high industrial value. The optimal storage temperature for sweetpotato is 13-16°C. However, because sweetpotato tuberous roots undergo chilling injuries that negatively affect their quality at temperatures below 10°C, postharvest damage during the winter season is a major constraint for industrialization at the northern hemisphere. So far, the molecular mechanism of postharvest storage at low temperature has not been elucidated in sweetpotato. To elucidate the mechanism of injury during postharvest low-temperature storage, we used next-generation sequencing technology to comprehensively analyze the transcriptome of tuberous roots stored at optimal (13°C) or low temperature (4°C) for 6 weeks. From nine cDNA libraries, we produced 298,765,564 clean reads, which were de novo assembled into 58,392 unigenes with an average length of 1,100 bp. A total of 3,216 differentially expressed genes (DEGs) were detected and categorized into six clusters, of which clusters 2, 4, and 5 (1,464 DEGs) were up-regulated under low temperature. The genes in these three clusters are involved in biosynthesis of unsaturated fatty acids, pathogen defense, and phenylalanine metabolism. By contrast, genes in clusters 1, 3, and 6 (1,752 DEGs), which were generally down-regulated at low temperature, encode antioxidant enzymes or are involved in glycerophospholipid, carbohydrate, or energy metabolism. We confirmed the results of the transcriptome analysis by quantitative RT-PCR. We are currently focused on RNA-Seq based comparative transcriptomics analyses for both cold-sensitive and -tolerant sweetpotato tuberous roots during low temperature. Our transcriptome analysis will advance our understanding of the comprehensive mechanisms of chilling injury during low temperature storage and facilitate improvements in postharvest storage of sweetpotato tuberous roots.

Audience Take Away:

- Transcriptome of sweetpotato tuberous roots during low temperature storage was de novo assembled and analyzed.
- A total of 3,216 differentially expressed genes (DEGs) were identified in sweetpotato tuberous roots stored at 13 °C and 4 °C.
- Genes involved in lipid metabolism were differentially expressed under low temperature.
- Genes involved in pathogen defense, and phenylalanine metabolism were generally up-regulated at low temperature.
- Genes involved in antioxidant enzyme, carbohydrate, or energy metabolism were generally down-regulated at low temperature.

Biography

Mr. Chang Yoon Ji is a graduate student at Korea University of Science and Technology where he is studying environmental biotechnology. He received his BS (2011) from Kyungpook National University, Republic of Korea. His research areas of interests include sweetpotato biotechnology, abiotic stress, and transcriptome analysis.

Managing root-knot nematodes in potatoes using cucurbitacin-containing phytonematicides: A success story in South Africa

Pofu, K.M.*¹, PhD., Mashela, P.W.², PhD., Venter, S.L.¹, PhD, Du Plooy, C.P.¹, PhD., Oloefse, D.¹, PhD.

¹Agricultural Research Council, South Africa

²University of Limpopo, South Africa

All commercially available potato cultivars in South Africa do not have resistance to all root-knot (*Meloidogyne* species) nematodes in the country. In the past, the potato industry relied heavily on the use of fumigant nematicides for successful production of economic potato crop. However, with the withdrawal of fumigant synthetic nematicides from the agrochemical markets and the high residues of systemic nematicides in tubers, alternative management strategies were researched and developed. The objective of this study was to compare the efficacy of cucurbitacin-containing phytonematicides and existing non-fumigant nematicides on nematode suppression and growth of potato plants. Field studies were initiated to assess the efficacy of Nemarioc-AL phytonematicide, Nemafric-BL phytonematicide, Aldicarb and Velum on suppression of *Meloidogyne* species on potato cv. 'Mondial G3'. At harvest, in some cases the phytonematicides had outdone the synthetic nematicides, whereas in other cases the efficacies on nematode suppression were comparable. Generally, when the phytonematicides were used in granular formulation during planting in a separate trial, the products were not phytotoxic, but they successfully suppressed nematodes and improved tuber yield. In conclusion, cucurbitacin-containing phytonematicides are highly effective in managing population densities of the South African *Meloidogyne* species.

Audience Take Away:

- Efficacies of cucurbitacin-containing phytonematicides were comparable to those of synthetic nematicides in management of *Meloidogyne* species.
- Cucurbitacin-containing phytonematicides stimulate tuber yield in potato production – when used according to empirically-determined concentrations.

Biography

Dr K. M. Pofu is a researcher at the Agricultural Research Council in South Africa and she specialises in nematode-plant interactions with specific to using nematode resistance as alternatives to synthetic nematicides. Dr Pofu focuses on assessing the efficacy of active ingredients on nematode management from ethnomedicinal plants in vivo.

Sessions on: Plant Biology | Plant Biosystems | Plant Nutrition And Soil Sciences

Session Chairs

Monica Ruffini Castiglione
University of Pisa
Italy

Piergiorgio Stevanato
University of Padova
Italy

Session Introduction

Title: Facilitation of adventitious root formation by nitrogen remobilization on reversible dark-induced carbohydrate depletion and potential application in horticulture

Siegfried Zerche, Leibniz-Institute of Vegetable- & Ornamental Crops, Germany

Title: Omics responses of sugar beet to changes in sulfate availability

Piergiorgio Stevanato, University of Padova, Italy

Title: The switch from skotomorphogenesis to photomorphogenesis triggers the regulatory transition of miRNA biogenesis in *Arabidopsis thaliana*

Seong Wook Yang, Yonsei University, Republic of Korea

Title: Cryo-EM Structure of the chloroplast ATP synthase from Spinach

Alexander Hahn, Max Planck Institute for Biophysic, Germany

Title: Hormone-modulated response modules in the plasma membrane initiating early events in plant cell elongation

Klaus Harter, University of Tuebingen, Center for Plant Molecular Biology, Germany

Title: Dissection of the remorin gene function in rice

Laigeng Li, Institute of Plant Physiology and Ecology, China

Title: Herbicide Resistant *Amaranthus palmeri* poses major evolutionary and ecological challenges to broad acre farming operations in the United States

Thomas C Mueller, University of Tennessee, United States

Title: Model of Entrepreneurship Capacity Building of Seaweed Farmers in Takalar District, South Sulawesi, Indonesia

Djusdil Akrim, Bosowa Polytechnic, Indonesia

Title: Eco-physiology of abiotic stress tolerance in selected bryophytes

Ingeborg Lang, University of Vienna, Austria

Title: Ferns and Lycopytes in Balinsasayao, Philippines: Participatory Inventory, Assessment and Conservation Initiatives

Victor B. Amoroso, Central Mindanao University, Philippines

Title: The Mexican *Salvia blepharophylla* and *Salvia greggii* in an ecological context: Scents, biotic relationships and exudates

Gelsomina Fico, University of Milan, Italy

Title: Microalgae: An excellent tool to study the effects of sulphur nutrition starvation on plants in general

Carfagna Simona, Naples, University "Federico II", Italy

Title: Effect of tris(3-hydroxy-4-pyridinonate) iron(III) complexes in iron deficiency chlorosis

Maria Conceicao Rangel, University of Porto, Portugal

Title: Hydric stress and silicon in the activity of antioxidant enzymes in cv Micro-Tom tomato

Janaina Oliveira Cruz, UNESP - Univ. Estadual Paulista, Brazil

Title: Induction of barley silicon transporters HvLsi1 and HvLsi2 is responsible for silicon accumulation in shoot under concomitant drought and K deficiency

Seyed Abdollah Hosseini, Agro Innovation International - Roullier group, France

Title: Hormonal dynamics during salt stress response of salt-sensitive *Arabidopsis thaliana* and salt-tolerant *Thellungiella salsuginea*

Prerostova Sylva, Institute of Experimental Botany AS CR, Czech Republic

Title: Synergism of the false root-knot nematode *Nacobbus aberrans* and *Phytophthora capsici* manifested by alteration of phenylpropanoid metabolism in *Capsicum annuum*

Noe Lopez-Martinez, Universidad Autonoma Chapingo, Mexico

Title: Axenically culturing the bryophytes: Problems, achievements and prospective of in vitro cultures

Marko Sabovljevic, University of Belgrade, Serbia

Facilitation of adventitious root formation by nitrogen remobilization on reversible dark-induced carbohydrate depletion and potential application in horticulture

Siegfried Zerche^{*1}, Klaus-Thomas Haensch¹, Mohammad-Reza Hajirezaei¹, Dieter Lohr², Elke Meinken², Uwe Druege¹

¹Leibniz-Institute of Vegetable- & Ornamental Crops, Germany

²University of Applied Sciences, Institut fuer Gartenbau

Adventitious root (AR) formation in axillary shoot tip cuttings is utilized in global production chains of vegetative-propagated ornamentals. Therein, the nitrogen and carbohydrate metabolisms in cuttings are affected by their total nitrogen content (Nt), temporary dark exposure and irradiance levels at the different production sites and phases with a specific plasticity to readjust metabolite pools to complex environments. We investigated in *Petunia hybrida* cuttings how elevated Nt contents with a combined dark exposure of cuttings change their different internal N-pools including free amino acids. In addition, early anatomic events of AR formation and further root development were studied.

Enhanced Nt contents and dark exposure of unrooted cuttings resulted in elevated levels of total free amino acids. With rising Nt contents, in particular glutamate and glutamine accumulated in leaf and basal stem. N-allocation to mobile N-pools increased whereas the allocation to insoluble protein-N declined. A dark exposure of cuttings conserved initial Nt and nitrate-N, while it reduced insoluble protein-N and increased soluble protein. Predominantly, free amino acids and soluble amino-N and amide-N pools increased under darkness. This mainly applied to asparagine, aspartate and arginine in leaves and resulted in tissue specific responses in stem and leaf at a rise in N-supply.

In the early stages of AR formation, meristematic cells developed until 72 h post excision with a negligible difference for two (eg, high vs low) Nt contents. After 168 h, AR formation was accelerated at a high Nt and gave rise to first obvious fully developed roots while only meristems were formed with a low Nt. After 384 h, a strong positive effect of a high Nt level in cuttings on their AR formation (root number and total length) was observed. However, a dark exposure for 168 h promoted AR formation particularly in cuttings with a low Nt close to compensation with that at high Nt level. The results indicate that both increased Nt contents and a temporary dark exposure of cuttings induce N signals and remobilize N resources in basal stem that are facilitated by senescence-related proteolysis in leaves. Based on our results, a metabolic model of N remobilization by temporary and reversible carbohydrate depletion and its significance for AR formation is presented. To illustrate application, we show the achievement potential of near infrared reflectance spectroscopy as noninvasive measurement for nitrogen and carbohydrate pools in ornamental plant species with economic value in horticulture.

We conclude that conventional strategies might consider nitrogen fertilization of donor plants and subsequent dark storage for enhanced survival and rooting capacity and thus highest propagation rates.

Audience Take Away:

- Explain how the audience will be able to use what they learn? How will this help the audience in their job?
- The take home message of this presentation is that enhanced nitrogen contents in petunia shoot tip cuttings do not influence the establishment of new root meristematic cells in the early stages but it stimulates root development with strong rise in the number of emerged ARs at final stage of root development. Further, a temporary and reversible dark-induced carbohydrate depletion which triggers proteolysis and nitrogen remobilization is favorable for facilitation of AR formation and thus for a rapid and increased propagation rate. In addition, it needs to be ensured, that the carbohydrate depletion during darkness is not too strong and thus irreversible for the survival of cuttings, and that a non-limiting photosynthesis rapidly can replenish carbohydrates during subsequent cultivation under light.
- Is this research that other faculty could use to expand their research or teaching?
- This research will help other faculty to expand their research or teaching with regard to plant nutrition of stock plants and rooting response to metabolic changes.

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- Does this provide a practical solution to a problem that could simplify or make a designer's job more efficient?
- This research presents potential application in horticulture that faces questions regarding the quality assurance in the global value-added chain of vegetative-propagated ornamentals.

Biography

Dr. Siegfried Zerche did his PhD in Agricultural Sciences at the Academy of Agricultural Sciences, Berlin in the Institute of Fertilization Research, Leipzig, Germany.

Before that he graduated in Agronomy from the Russian State Agricultural University, formerly Moscow Timiryazev Agricultural Academy after five-years of studies as a German student abroad. He is member of the International Society for Horticultural Science, the German Society of Plant Nutrition and the German Society for Horticultural Science.

He has research experience in plant physiology and molecular functions of plant nutrients, plant nutrition, nitrogen and carbohydrate metabolism, generative and vegetative reproduction, floriculture industry, horticulture, fertilization systems in agricultural and horticultural crop cultivation.

Omics responses of sugar beet to changes in sulfate availability

Piergiorgio Stevanato^{*1}, Chiara Broccanello, Massimo Cagnin, Andrea Baglieri, Luigi Lucini, Serenella Nardi, Giuseppe Concheri
¹University of Padova, Italy

In this study, a system based on omics profiling were set-up for sugar beet (*Beta vulgaris* L. subsp. *vulgaris*) evaluation after changes in sulfate availability. Root morphology, plant ionome and metabolome together with gene expression profiling were evaluated in leaves and roots of sulfate deprived and supplied plants. Particularly, we evaluated the capability of “omics” techniques to depict pictures about complex plant-sulfate interactions.

Audience Take Away:

- Learn about how “omics” techniques can be used in research and diagnostics to evaluate plant response to nutrients.
- Learn about the impact of novel instrumentations and reagent selection on plant biology.
- Discover how to use digital PCR in plant biology, including how to use it for validation in genetic expression experiments.

Biography

Graduated in Agricultural Sciences in 1999 at the University of Padova (Italy), he obtained in 2008 the Ph.D. degree in Plant Ecophysiology. Visiting researcher at the Michigan State University (USA) in 2003 and 2005-2006. His current position is researcher at the DAFNAE Dept. of University of Padova. Main current activity is aimed to improve the tolerance to biotic and abiotic stresses in sugar beet. Dr. Stevanato is a member of the International Institute for Beet Research (IIRB) and of the Executive Committee of the International Association of Professionals in Sugar and Integrated Technologies (IAPSIT). He has presented research papers at national and international conferences. He has co-authored over 100 publications including peer review journal papers, book chapters and international conference proceedings. He is managing editor of Sugar Tech for the sugar beet section and member of the editorial board of International Sugar Journal and Iore Journal of Genetics.

The switch from skotomorphogenesis to photomorphogenesis triggers the regulatory transition of miRNA biogenesis in *Arabidopsis thaliana*

Seok Keun Cho, Moon Young Ryu, Sukwon Choi, Andras Viczian, Attila Molna, Ferenc Nagy, Seong Wook Yang*
Yonsei University, Republic of Korea

Light signaling pathways are central to the development and growth of plants. The pathways render plants to perceive the discrete wavelength, intensity, and duration of light, by which information of light can be transmitted and coordinated, resulting in intricate physiological and developmental responses. Extensive studies on the light-triggered switch from skotomorphogenesis to photomorphogenesis have elucidated many important biochemical entities in light signaling pathways. However, the studies have mostly focused on photoreceptors, signaling intermediates and their proteolytic repression by negative regulators. Recently, we found that the core components of miRNA processing - Dicer-like 1 (DCL1), SERRATE (SE) and HYPONASTIC LEAVES 1 (HYL1) - are differentially expressed by the light-induced developmental transition. The core processing proteins are constitutively degraded by unknown proteolytic pathways in etiolated seedlings but dramatically stabilized in de-etiolated seedlings. In contrast to the up-regulated microprocessor components, the levels of miRNAs are notably diminished by light. Based on detailed molecular and biochemical analyses, we here suggest that a new interaction between light signaling and miRNA biogenesis.

Audience Take Away:

- Audience can take a concept of the crosstalk between light signaling and miRNA biogenesis.
- Novel mechanism of miRNA biogenesis in response to different lights, red, far-red and blue

Biography

PhD. Yonsei University

Post Doctoral Associate, Plant Molecular Biology,

Rockefeller University, New York, NY, USA

Research Fellow, Group of Host pathogen interaction, Temasek Life science Lab, National University of Singapore, Singapore

Associate Professor (tenured position; VT-10), Section of Plant Biochemistry, Center for UNIK synthetic biology, Department of Plant and Environmental Sciences, Faculty of Science, University of Copenhagen, Denmark

Associate Professor, Department of Systems Biology, College of life science and Biotechnology, Yonsei University

Cryo-EM Structure of the chloroplast ATP synthase from Spinach

Alexander Hahn^{1*}, Thomas Bauseweis¹, Deryck Mills¹, Werner Kühlbrandt¹, Thomas Meier^{1,2}

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²Imperial College London, United Kingdom

The F-type ATP synthase (F₁F_o) in the thylakoid membranes is responsible for the bulk ATP production of plants, cyanobacteria and green algae. It utilizes the proton-motive force across the thylakoid membrane to generate ATP from ADP and inorganic phosphate by rotary catalysis. The basic architecture can be subdivided in three functional elements: The F_o-rotor complex, the catalytic F₁ complex and the peripheral stalk. While all major functional aspects of rotary ATP synthases are preserved throughout all kingdoms of life, the chloroplast ATP synthase (CF₁F_o) has a unique dithiol redox switch, formed by the insertion of a short amino acid loop in the central rotor subunit gamma. This redox switch is thought to keep CF₁F_o in an inactive state during phases of light deprivation. We determined the structure of the chloroplast ATP synthase isolated from Spinach by single particle cryo-EM at 4.2 Å. We identified three distinct conformations which represent the three catalytic positions within the binding change mechanism. We were able to build a complete CF₁F_o model that includes amino acid side chain information about the unique dithiol redox switch of the gamma subunit. The complete structure allows a comprehensive description of this bacterial-type ATP synthase with respect to the underlying rotary mechanism and its redox regulation in plant chloroplasts.

Biography

2001 - 2007: Study of Biology at the Goethe University, Frankfurt, Germany

2007 - 2008: Diploma Thesis in the group of Prof. Lutz Nover. Title: "The heat stress response in Plants"

2008 - 2013: PhD Thesis in the Group of Prof. Enrico Schleiff. Title: "The Multidrug Efflux, Secondary Metabolite and Protein Secretion Network of Cyanobacteria."

2013 - Now: PostDoc in the Group of Werner Kühlbrandt at the Max-Planck-Institute of Biophysics, Frankfurt, Germany.

Current occupation: Structural investigation of ATP synthesis from yeast and plant by single particle cryo-EM.

Hormone-modulated response modules in the plasma membrane initiating early events in plant cell elongation

Nina Glockner¹, Friederike Wanke¹, Ruth Grosseholz², Sven zur Oven-Krockhaus¹, Sebastian Wolf², Ursula Kummer², Margret Sauter³, Klaus Harter^{1*}

¹Center for Plant Molecular Biology (ZMBP), University of Tuebingen, Germany

²Center for Organismal Studies (COS), University of Heidelberg

³Plant Developmental Biology and Plant Physiology, University of Kiel, Germany

Plant cell elongation growth is regulated by many factors including phytohormones. The onset of cell elongation is regulated by brassinosteroids and phytosulfokines via specific receptor complexes (BRI1 or PSKR1 complex). These receptor complexes initiate responses such as H⁺ extrusion and wall acidification, plasma membrane (PM) hyperpolarization and wall expansion within few minutes after hormone application. These perception/response modules appear to have a common basic composition, which – in addition to the specific receptors – comprises co-receptors, proton pumps and ion channels. For the BRI1 response module we depicted the molecular and functional properties by using state-of-the-art spectro-microscopical tools with quantitative readout such as high resolution CLSM, FLIM and FRET. The data were used for the establishment of a quantitative computational model predicting missing components, regulatory determinants and parameters.

We also observed that the information about cell wall integrity, that rapidly modulate cell elongation as well, appear to be processed by a BRI1-dependent response module as well.

In future we would like address problems such as, how are these response modules distributed in the PM spatially, what are their dynamics and what are the functional consequences, when complex formation and dynamics are disturbed? The data will be used for the refinement of our multi-dimensional computational model deepening our understanding of the response modules' action in vivo.

Audience Take Away:

- New knowledge and concepts about regulation of plant cell elongation growth and subcellular physiology, application of high-resolution spectromicroscopy in plant cell biology, theoretical and computational plant cell science

Biography

Name: Harter, Klaus, Prof. Dr.

Current position and status: Full professor, University training and degrees

1984-1989 Study of biology (plant physiology, biochemistry, geobotany, physical chemistry), University of Freiburg

Advanced academic qualifications

1993 Dr. rer. nat. in biology, University of Freiburg

2001 Habilitation and Venia Legendi in plant physiology, Faculty of Biology, University of Freiburg

Postgraduate professional career

since 2004 Full professor for Plant Physiology, Center for Plant Molecular Biology (ZMBP), Department for Plant Physiology, University of Tübingen, Germany

2002-2004 Full professor for Botany, Institute of Botany, University of Cologne, Germany

1997-2002 Scientific Assistant, Institute for Biology II / Botany, University of Freiburg, Germany

1996-1997 Postdoc, Department for Plant Biology, UC Berkeley, USA

1994-1996 Postdoc, Plant Gene Expression Center, Albany, USA

1993-1994 Postdoc, Institute for Biology II / Botany, University of Freiburg, Germany

Dissection of the remorin gene function in rice

JinshanGui, ZhuaiZheng, Chang Liu, JunhuiShen, Laigeng Li*¹

¹Institute of Plant Physiology and Ecology, China

Remorins are plant-specific proteins that display a variety of function in plant development and defense. The presentation will discuss the remorin gene function in rice. That includes 1) we identified a rice T-DNA insertion mutant (grain setting defect 1-Dominant, *gsd1-D*), with a grain setting deficient phenotype caused by over-expression of *GSD1*, a remorin gene with unknown function. *GSD1* is expressed specifically in phloem companion cells and is localized in the PD and plasma membrane. The study demonstrates that *GSD1* plays a role in regulating photoassimilate translocation through the symplastic pathway to impact grain setting in rice; 2) we found that another remorin *OsREM4.1* is transcriptionally regulated by ABA and functions as an *OsBRI1* substrate and *OsSERK1*-interacting protein to regulate the formation and subsequent activation of the *OsBRI1*-*OsSERK1* receptor in coordinating the ABA and BR signaling in rice. The results reveals that *REM4.1* functions as coordinator for balancing plant growth and its adjustment to stress environments in rice. These finding illustrates new mechanisms in understanding of the remorin functions as well as provides innovative strategies to improve crops.

Audience Take Away:

- Understanding of the plant-specific Remorin protein function
- How can the remorin genes be applied to improve rice production

Biography

Professor & Associate Director

2007-present, Institute of Plant Physiology and Ecology, Chinese Academy of Sciences

2003-2007, NC State University, Associate Professor,

1999-2002, Michigan Technological University, Research Assistant Professor

1997, Michigan Technological University, Ph.D.

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Herbicide Resistant *Amaranthus palmeri* poses major evolutionary and ecological challenges to broad acre farming operations in the United States.

Thomas C. Mueller*, PhD.
University of Tennessee, USA

A major purpose of plant biology is the interaction of plants that produce food for humans (crops) and those that compete and challenge those crops (weeds). The evolutionary struggle between crops and weeds is as old as agriculture itself. In recent decades, new technologies have simplified weed control and broad acre production agriculture, with herbicides commonly used to reduce weed competition with crops. However, the intense selection pressure placed upon vast areas of farmland has resulted in weeds developing immunity, or resistance, to these same herbicides. This report details the weedy plant *Amaranthus palmeri*, a plant that is infamous in the United States for rapid growth (up to 8 cm per day), large seed production potential (> 100,000 seeds per female plant), and wide genetic variability that has allowed it to develop resistance to multiple herbicide modes of action (MOA).

A common response of many farmers in highly developed countries to herbicide resistance is to simply change to a different MOA. One reason why glyphosate resistant crops were so widely and rapidly accepted by producers in the Americas was that glyphosate applied to foliar plants controlled many weedy species, including *A. palmeri*, that have developed resistance to other MOA. However, once glyphosate resistance was apparent farmers change to use other MOAs, including PPOs. This report details PPO-resistant *A. palmeri* in the United States.

Three putative PPO-resistant populations were collected from the Mississippi River Valley from the states of Tennessee and Arkansas, United States. These populations or biotypes were compared to a population that was known to be susceptible to the PPO herbicide fomesafen. *A. palmeri* response on a 0 to 100 scale (no effect to complete death) 14 days after treatment was 98% for the susceptible population and less than 25% for all three of the resistant populations. A separate study showed that the weed size at the time of planting affected control with less control of plants that were 12 cm compared to 4 cm in height. Studies examining alternate modes of action showed that the PPO-Resistant were also insensitive to glyphosate and ALS inhibiting herbicides. Additional studies growing the *A. Palmeri* plants in the absence of herbicide applications showed no phenotypic differences between Resistant and Susceptible biotypes, indicating no apparent fitness penalty for the observed herbicide resistance. Plants with herbicide resistance to multiple modes of action is a very real challenge to producers and all available choices should be considered to maintain viable production systems that are effective, economical and environmentally sustainable.

Biography

Dr. Mueller grew up on a small grain farm in rural Illinois, where his family farm produced corn, soybeans, and wheat. Through several experiences in the private sector, he came to understand the pragmatic aspects of agronomic production systems. He joined the University of Tennessee in April, 1991 as an assistant professor, was promoted to associate professor in 1996 and to professor in 2003. The primary goal of Dr. Mueller's research is to develop and validate weed control systems that are effective, economical, and environmentally sustainable. Specific research areas include weed control in soybeans and corn, especially under no-tillage production systems, the environmental fate of herbicides, and a focused research effort examining glyphosate-resistant weeds.

Model of entrepreneurship capacity building of seaweed farmers in Takalar District, South Sulawesi, Indonesia

Djurdil Akrim^{*1}, Abdul Mun'im², Nurlita Pertwi³, Andi Rumpang Yusuf⁴

¹Universitas Negeri Makassar. Deputy of Bosowa Agro Group and Executive Director of Polytechnic Bosowa, Makassar, Indonesia

²Universitas Negeri Makassar. Senior Lecturer of Science Faculty, Science Education Program, Universitas Negeri Makassar, Indonesia

³Doctor of Environmental Management and Head Department of Environmental Education Studies, Post Graduate Programme Universitas Negeri Makassar, Indonesia

⁴PhD Student Department of Environmental Education Studies, Universitas Negeri Makassar. Senior Lecturer of Faculty of Engineering, Civil Engineering Program, Bosowa University, Makassar, Indonesia

The seaweed cultivation development in Indonesia is growing rapidly, but not yet supported by the entrepreneurial ability of farmers in its management. This study aims to describe the socio-economic objective conditions of seaweed farmers and analyze the strategy of developing the entrepreneurship capacity of seaweed farmers. Description of competence of farmer's entrepreneur used quantitative descriptive method while farmer entrepreneurship capacity building strategy used Analytical Hierarchy Process. The results showed that the entrepreneurial competence of farmers is very low which is indicated by three indicators which are knowledge about post harvest, product quality and processing technology, and also market access. The strategy of developing the entrepreneurial capacity of farmers shows that private sector holds a dominant role compared to the peasants and local government institutions. The dominant development program affecting the entrepreneurial capacity of farmers is the improvement of farmers' knowledge about market access and product quality.

Keyword: Entrepreneurship, Farmers, Seaweed and Capacity Building

Biography

Djurdil Akrim, male, seaweed commerce specialist, graduated from Chemistry Department, IKIP Ujung Pandang, in 1990. He worked for PT. Bantimurung Indah which is a part of seaweed industry in Makassar, South Sulawesi, Indonesia since 1990. During 2006-2014, he became the Director of PT. Bantimurung Indah (Bosowa Group). From January 2015, he is appointed as Deputy Bosowa Agro Group and Executive Director in Polytechnic Bosowa. Now he is a PhD student, Department of Environmental Education Studies, Universitas Negeri Makassar, Indonesia. He has published papers and books on seaweed development, environment learning and entrepreneurship. He was also a member of Indonesian Seaweed Association (ARLI).

Eco-physiology of abiotic stress tolerance in selected bryophytes

Marko Sabovljevic¹, Marieluise Weidinger¹, Anjeta Sabovljevic¹, Margret Eckhart¹, Wolfram Adlassnig¹, Stefan Sassmann¹, Ingeborg Lang^{1*}
¹Cell Imaging & Ultrastructure Research, Faculty of Life Sciences, University of Vienna, Austria

We are living in a rapidly changing world. The increase of harsh environments like the barren, metal spiked substrate of former mining sites exposed to high irradiation and drought are good examples. However, some organisms like bryophytes are pioneers to settle even in such inhospitable habitats. The reasons for this astonishing tolerance are remain largely unknown.

Here, we focus on four different bryophyte species (*Physcomitrella patens*, *Pohlia drummondii*, *Mielichhoferia elongata*, *Atrichum undulatum*), some occurring on metal spoil heaps, some are from uncontaminated sites. In laboratory experiments, the specimen were introduced to controlled amounts of copper or zinc (provided as -Cl₂, -SO₄, or -acetate) by addition to the substrate or application as simulated rain containing toxic metals. The bryophyte samples were analysed for growth parameters, primary and secondary metabolites, stress physiology markers and cellular localisation of metal deposition. Thereby, we can determine physiological traits that allow certain species to settle on barren substrate. The inclusion of model species like *Physcomitrella patens* allows for complementary analyses of abiotic stress tolerance at the proteomics level.

In general, it can be assumed that bryophytes contain evolutionary conserved resistance to some extent of zinc and copper contamination, and that the tolerance to zinc is higher compared to copper. The accumulation of copper can be documented better than zinc within moss tissues, which could be the reason for the higher toxicity of copper and higher tolerance to zinc. The mechanisms of resistance and tolerance, however, remain unclear and need to be further examined.

Audience Take Away:

- Insights to the fascinating habitat of metal spoil heaps
- Which abiotic stress factors are most relevant for the settlement of plants
- Species dependent differences in metal tolerance and how we analyse them

Biography

In biological systems, structure and function are intrinsically tied to each other. Both areas have been fascinating to me as a plant scientist since the beginning of my studies. My scientific work is focussed on two major topics: (1) ecological aspects, like tolerance of plants towards heavy metals and their potential, intracellular uptake and (2) physiological aspects of salt- and UV-stress as well as water balance of cells and tissues. I am passionate about teaching and I am regularly giving lectures and lab courses in cell biology, plant physiology and anatomy, light microscopy and scientific documentation. For a couple of years now, I am leading a small group consisting of PhD, master and bachelor students at the Core Facility Cell Imaging & Ultrastructure Research, at the University of Vienna, Austria.

Ferns and Lycophytes in Balinsasayao, Philippines: Participatory Inventory, Assessment and Conservation Initiatives

Victor B. Amoroso^{*1}, Fulgent P. Coritico¹, M.S.
¹Central Mindanao University, Philippines

The Philippines has a total of 14 Long-Term Ecological Research (LTER) sites. One of the potential LTER sites is Balinsasayao Twin Lakes Natural Park (BTLNP) in Negros Island, Philippines. Declared as protected area in November 21, 2000, it is home to endangered and endemic species of flora and fauna. However, ferns and lycophytes have not been studied thoroughly. This research was conducted to determine the species richness, assess the conservation and ecological status of the species and conduct conservation strategies to enhance awareness and protect the endangered, endemic, rare and economic species of ferns and lycophytes through the participation of the members of the non-government organization (NGO). Transect walk and establishment of a 2-hectare permanent plot and delineated into fifty 20 x 20 m subplots were done to determine the species richness and diversity. The conservation status of species was assessed using IUCN and National List Red List while the ecological status assessment was based on field observation, key informant interview and secondary data. Repeated transect walk and complete inventory in 2-hectare permanent plot with selected members of the non-government organization revealed a total of 232 species. Of these, 219 species ferns (86 genera, 31 families) and 13 species (3 genera, 2 families) are lycophytes. This species richness is about 21% of the species found in the Philippines. The diversity value of H' 1.40 was obtained with *Asplenium tenerum*, *Nephrolepis hirsutula*, *Alsophila negrosiana*, *N. cordifolia* and *Angiopteris leytensis* garnering the highest Species Importance Value. Of the 232 species of ferns and lycophytes, 14 species are threatened and 4 are endemic. Among the threatened species, 5 of which are endangered, 5 vulnerable and the 4 species are in the other threatened species category. The 2-hectare permanent plot served as an in situ conservation strategy for long term monitoring and protection. Likewise, the members of Balinsasayao Twin Lakes Farmers Association Incorporated (BTLFAI) were trained to establish their Community Economic Fern Garden (CEFG) as part of the ex situ conservation initiative to avoid overharvesting from the wild. Moreover, this CEFG supply fern materials to their restaurant for salad and vegetable as additional NGO income. All these activities including the Information, Education, Communication (IEC) materials have enhanced awareness about ferns and lycophytes in the community.

Audience Take Away:

- Through my presentation, the audience will take away the following:
- Enhanced awareness on the species richness and diversity of ferns and lycophytes in lowland tropical forest.
- Strategy that research should be participatory by involving the local people.
- Knowledge that the species of ferns and lycophytes have economic uses but are now endangered.
- Information that permanent plot is important for long term biodiversity study, monitoring and in situ conservation and that the economic garden is an ex situ conservation strategy to augment community income.
- Community capability building is necessary to make sustainable research and extension activities.

Biography

Victor B. Amoroso is a Career Scientist III and University Professor and presently the Director of the Center for Biodiversity Research and Extension in Mindanao in Central Mindanao University, Philippines. For a decade, he has worked on the morphology and taxonomy of ferns and lycophytes, gymnosperms and some flowering plants. With his research collaborators, he has named new species and a new records of ferns and flowering plants in the Philippines. Currently, he is the research program leader on Saving Biodiversity of Terrestrial Ecosystem in Selected Mindanao Long-Term Ecological Research Sites, Screening Indigenous Plants as Biopesticides for Vegetables and Sugarcane and a study leader on Exploring Potentials of Philippine Ferns and Lycophytes as Therapeutics for Chronic Inflammation and Cancer.

The Mexican *Salvia blepharophylla* and *Salvia greggii* in an ecological context: Scents, biotic relationships and exudates

Claudia Giuliani¹PhD., Manuela Giovanetti²PhD., Roberta Ascrizzi³, Daniela Lupi¹, Roberta Pastorelli⁴, Marco Palamara Mesiano¹, Fabrizio Gelmini¹, Laura Santagostini¹, Giangiacomo Beretta¹, Guido Flamini³, Gelsomina Fico^{*1}

¹University of Milan, Italy

²University of Lisbon, Portugal

³University of Pisa, Italy

⁴CREA-ABP, Florence

Strategies adopted by plants to interact with other organisms are very sophisticated and the studies of these relationships are full of charm for researchers and extremely important to understand evolutionary perspectives. Our work arises in this framework. We focused our attention on two Mexican *Salvia* species (Lamiaceae) preserved at the Ghirardi Botanic Garden of the University of Milan: *Salvia blepharophylla* Brandege ex Epling and *Salvia greggii* A. Gray. Both species show nice red flowers, of the kind usually pollinated by hummingbirds.

We explored the phytochemical characterization related to the productivity in volatile organic compounds (VOCs) from both flowers and leaves, and the epicuticular depositions, in concert with the biotic interactions established by the target species. We evaluated the biodiversity of insect pollinators visiting the flowers and of the microorganisms inhabiting the phyllosphere. Moreover, we performed a micro-morphological investigation on the glandular trichomes. Our aim is giving a first attempt to sketch a link of the plant productivity in secondary metabolites to observed biotic relationships concurrently occurring at the botanic garden.

Phytochemical survey revealed that sesquiterpene hydrocarbons were the most abundant chemical class of volatiles in the leaf of both species (42.34% in *S. greggii* and 54.97% in *S. blepharophylla*), while monoterpenes dominated the flower emission profiles. As a whole, different emission profiles characterized the two species thanks to exclusive compounds: the floral bouquets are dominated by limonene and β -pinene in *S. greggii*, and by 1,8-cineole in *S. blepharophylla*. On the other hand, common principal compounds occurring in high relative percentages in flowers are β -caryophyllene and germacrene D, both also detected in the leaf emission profile. Slight differences were found for the composition of the secondary metabolites present in the leaf exudates, with isopimaric acid and a compound structurally related to the cloredane diterpenes blepharolide A and B prevailing in *S. greggii* and *S. blepharophylla*, respectively.

Biological surveys were equally interesting. Although the relatively high biodiversity of pollinators recorded at the botanic garden, the target species attracted only two functional pollinator groups: small (*Lasioglossum* morphotypes) and large bees (*Xylocopa violacea* L.). These insects applied different but interesting handling strategies to reach flower resources: the described strategies are significant from an evolutionary point of view, considering the probable link of the Mexican *Salvia* with bird pollinators. The microbiological analysis revealed that *S. greggii* harbours a more abundant and diverse phyllospheric bacterial community than *S. blepharophylla* did, although a considerable variability between the replicates was observed within each species.

Our data can be linked to existent literature concerning chemical compounds and biotic responses. With regards to VOCs, an attractive role towards bees is documented only for limonene, β -pinene and 1,8-cineole. Conversely, β -caryophyllene and germacrene D are common deterrents. Our data, as existent literature sustain the hypothesis that local bees do adapt to novel food sources. The chemical compounds we found may moreover allow to infer that bees are able to recognise the chemical signals emitted by the target-species and possibly use them to locate the plants. In this view, also chemicals produced by leaves may be used by bees: more data are needed to investigate this potential role of leaf chemistry. Compounds in leaves are so far known to exert defensive functions. Finally, our is the first report on the microflora inhabiting the phyllosphere of the two *Salvia* species and represents an initial step towards the understanding of the adaptive mechanisms between microorganisms and leaf exudates.

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Audience Take Away:

- The multidisciplinary of this work, combining phytochemical data with ecological information is important to understand the interactions that the target species established with the biotic environmental components
- This allow us to infer hypotheses on the relationships between the VOC emission profile and the pollinators, and between the composition of the leaf exudates and the microflora inhabiting the phyllosphere
- We believe that this research approach may stimulate other researchers to investigate the close connection between the productivity in secondary metabolites and the biotic mutualistic interactions
- These issues are full of charm also in the teaching approach, since investigating the novel relationships that exotic species establish with local pollinators or microorganisms is a core-topic in an evolutionary perspective.

Biography

Gelsomina Fico is Associate Professor in the subject of Pharmaceutical Biology (Italian code: area BIO/15), at the Department of Pharmaceutical Sciences (DISFARM) of the University of Milan. Her research activity includes studies on the morphology and chemistry of secondary metabolites from medicinal plant species. These studies are often in relation to ecological/physiological aspects, also including analyses on the biological activity of secondary metabolite. She also works on chemotaxonomic and ethnobotanical topics. Since 2003 she has been scientific coordinator of the Botanic Garden Ghirardi (Toscolano Maderno, Brescia), which belongs to DISFARM and is focused on medicinal plants. Since 2008 to 2011 she was Vice-President, and further from 2012 to 2015 President, of the Network of Botanical Gardens of Lombardy. From 2009 to 2015 she was member of the Council of the Italian Society of Phytochemistry.

Microalgae: An excellent tool to study the effects of sulphur nutrition starvation on plants in general

Carfagna Simona^{*1}, Ph.D., Giovanna Salbitani¹, Ph.D., Vincenza Vona¹

¹University "Federico II" of Naples, Italy

Sulfur (S) deficiency is a recent but serious problem in some European countries, attributed to the decline in industrial emissions and to less intensive application of mineral fertilizers. In all plants, S is assimilated into numerous essential compounds such as the amino acids cysteine and methionine, glutathione, hormones, vitamins, cofactors, and numerous secondary products. In addition, some S-containing compounds are involved in stress responses; for example, glutathione is an important antioxidant that prevents ROS (Reactive Oxygen Species) from damaging cellular components and it is a substrate for phytochelatin synthesis. Consequently, insufficient S nutrition reduces plant growth and resistance to abiotic and biotic stresses. Vascular plants have evolved organ-specific modes of nutrition: a photosynthetic shoot closely interacts with a heterotrophic root using xylem and phloem as communication highways. The complex communication between autotrophic and heterotrophic metabolism could be studied in unicellular organisms and the results could be transferred to the multiorgan system of higher plants. The utilization of unicellular algae as model system to study enzymes involved in plant metabolism is advantageous because their metabolism depends only on the nutrients that each cell takes up from the medium and not from a metabolite exchange between cells. Microalgae reproduce fast, which provides an opportunity to introduce a wide range of nutritional changes in culture and to study their effects in a short span of time. Then, the unicellular algae represent a suitable experimental system to study phenomena that occur in plant cells as a consequence of sulphur shortage or S supply. A tight regulatory cross-talk between glutathione and ascorbic acid metabolism and the activation of ROS-scavenging enzymes, in the green alga *C. sorokiniana* subjected to S deficiency, was demonstrated. In plants and algae, sulfate assimilation and cysteine synthesis are regulated by S availability from the environment. In addition, we present the first report detailing the effects of S starvation under both autotrophic and heterotrophic culture conditions in the microalga *Galdieria phlegrea* inhabiting hot springs with high S and sulphate levels. Our results show that in *G. phlegrea* both in autotrophic cells but especially in cells cultured in heterotrophy, the glutathione content is much higher than that found in *C. sorokiniana*. The results presented are discussed in the context of physiological changes that occur in an S deficient plant cell and aim to provide new insights on metabolism regulation under S limited conditions.

Biography

Simona Carfagna is a Permanent Researcher in the Biology Department of the University "Federico II" of Naples. Since completing her PhD and postdoctoral fellowships, she has focused her research on various aspects of plant mineral nutrition. In particular, she studies the effects of different nutrient availability on the metabolism of sulfur and nitrogen and related control mechanisms in photosynthetic organisms that live in very different environments.

Effect of tris(3-hydroxy-4-pyridinonate) iron(III) complexes in iron deficiency chlorosis

M. Rangel*¹, Ph.D., C. S. Santos², M. Sc., Andreia Leite¹, Ph.D., Tania Moniz¹, Ph.D., M. W. Vasconcelos², Ph.D.

¹REQUIMTE, Instituto de Ciencias Biomedicas de Abel Salazar, Universidade do Porto, Portugal

²CQBF, Escola Superior de Biotecnologia, Universidade Catolica Portuguesa, Porto, Portugal

Successful cultivation of crops with the best nutritional properties is an issue of paramount importance in the Agricultural and Health fields. Iron (Fe) is an essential mineral nutrient and legumes are one of the major sources of Fe. However the absorption of Fe by the roots of plants is compromised when grown in alkaline soil. As a consequence, plants may suffer from Fe deficiency chlorosis (IDC), characterized by chlorosis, yield losses, and lower concentrations of Fe in edible plant parts. Soil application of synthetic Fe(III) chelates (e.g. Fe-EDTA or FeEDDHA) remains one of the most common measures to correct IDC.

Here, we tested the capacity of two tris(3-hydroxy-4-pyridinonate) Fe(III) complexes, [Fe(dmpp)₃ and Fe(mpp)₃], to amend IDC in hydroponically grown soybean (*Glycine max*) plants, and we compared them to FeEDDHA. Plants treated with 20 μM of [Fe(dmpp)₃ and Fe(mpp)₃] were significantly greener (Fig. 1), bigger and had 47% and 55% higher total Fe content (respectively) than those treated with the same amount of FeEDDHA. Plants supplied with [Fe(mpp)₃] were able to translocate 64% more Fe to the shoots than Fe(dmpp)₃-supplied plants, which tended to accumulate Fe in the roots. Given the positive results obtained with 20 μM Fe(mpp)₃, we hypothesized that even lower concentrations, such as 5 and 10 μM, could also be effective in preventing IDC, and a second trial was performed. Plants supplied with 20 μM and 10 μM [Fe(mpp)₃] presented two expanded trifoliolate leaves whereas plants grown with 5 μM had only one expanded trifoliolate leaf. Total fresh weight (TFW) was not significantly different between 10 and 20 μM supplied plants, but was different to 5 μM grown plants, which had about 30% lower TFW. Chlorosis development was assessed using SPAD measurements and total chlorophyll quantification. SPAD values were 10% higher in 20 μM-supplied plants when compared to the other two concentrations ($p < 0.05$), although no significant differences were found in total chlorophyll leaf accumulation. Also, the accumulation of antioxidant defense related pigments - carotenoids and anthocyanins- was not significantly different between treatments. The amount of Fe was quantified in roots and leaves, using atomic absorption spectroscopy, and in both tissues no differences were detected. This work indicates that [Fe(mpp)₃] has potential as an Fe fertilizer that, even at low doses, is able to avoid IDC symptoms development, and that could be economically and environmentally favorable in agricultural contexts.

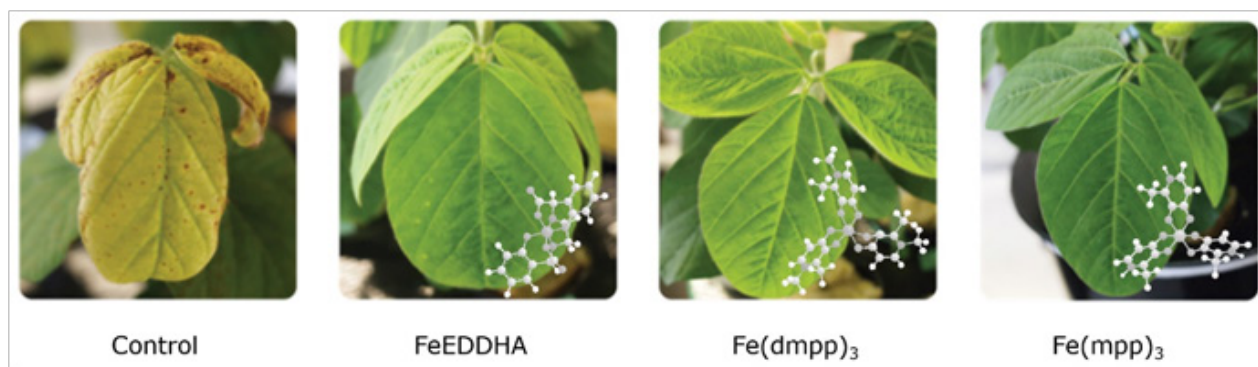


Figure 1

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Audience Take Away:

- The presentation is focused on the development of a new Fe fertilizer. We will explain the concept.
- The new compound is part of a set of compounds that are made in our laboratory and we have the possibility to tailor-made the compounds to adjust their properties and improve efficacy.
- The new compound improves Fe content both in roots and in leaves.
- Application of the new fertilizer can be made either in soil or sprayed on leaves.

Biography

Maria Rangel is an Associate Professor at University of Porto. She is a Bioinorganic Chemist whose research interests are focused in the role of metal ions in living organisms. In recent years she has worked on the design of Iron chelators for: (a) novel strategies to fight Infection through Fe deprivation; (b) treatment of Fe Overload and (c) Fe Sensing. Her interest in Iron Biology has been extended to Plant Nutrition and she is currently developing projects that aim the understanding of mineral nutrition processes and the design of Fe-chelates to address agricultural problems related with Fe deficiency.

Hydric stress and silicon in the activity of antioxidant enzymes in cv Micro-Tom tomato

Janaina Oliveira Cruz^{*1}, Ph.D., Carla Veronica Correa¹, Ph.D., Nathalia de Souza Parreiras¹, Ph.D., Carmen Silvia Fernandes Boaro¹, Joao Domingos Rodrigues¹

¹Sao Paulo State University, Brazil

Water usage has become controversial because it is an increasingly scarce resource. Furthermore, summer periods may drastically affect agricultural non-irrigated cultures productivity. Hydric stress can lead to decreased productivity due to physiological, metabolic and morphological changes. Silicon is considered a beneficial element, and its supplementation has been efficiently adopted for greater resistance to biotic and abiotic stresses. Under stress conditions, there is increased production of reactive oxygen species (ROS) which cause a cascade of oxidative reactions that may interfere with metabolism. However, complex protection systems are formed to compete with oxidative stress, consisting of several antioxidant enzymes such as superoxide dismutase, peroxidase and catalase. The beneficial effect of silicon has been associated with increased antioxidant defense capacity in water deficiency. Therefore, this study aimed to evaluate the effect of silicon and hydric stress on the activity of antioxidant enzymes in cv Micro Tom tomato. Four weekly applications of silicon were carried out at the following concentrations: 0; 0.5; 1; 1.5; 2; 2.5 g L⁻¹ via leaf. After these applications, water stress was established, with total water withdrawal and rehydration. Sampling for analysis were performed before, during and after hydric stress. Superoxide dismutase, catalase and peroxidase were evaluated enzymes; leaf lipid peroxidation was also evaluated. It was observed that without water stress the plants with the highest concentration of silicon (2.5 g L⁻¹) had high lipid peroxidation, which also caused higher activity of antioxidant enzymes. During stress and rehydration, it was also observed that the higher concentration of silicon provided a reduction in enzymatic activity and lipid peroxidation. Thus, it can be stated that, under the conditions evaluated, silicon had a beneficial effect during hydric stress and rehydration, promoting greater membrane stability.

Audience Take Away:

- Silicon; oxidative estress; enzymes; rehydration.
- This research suggests a new role for silicon during water stress by increasing the available information and allowing a new approach to reduce the oxidative effects that water stress can cause on vegetables.

Biography

Bachelor in Biological Sciences with experience in Botany, with emphasis on Plant Physiology and Ecophysiology. Master's degree in Agronomy - Horticulture by the Faculty of Agronomic Sciences of Botucatu, belonging to the State University Paulista Julio Mesquita Filho - UNESP, and is currently a doctoral candidate for the Graduate Program in Biological Sciences – Botany, by the Institute of Biosciences of Botucatu, belonging to the same institution, and currently works with mineral nutrition.

Induction of barley silicon transporters HvLsi1 and HvLsi2 is responsible for silicon accumulation in shoot under concomitant drought and K deficiency

Seyed Abdollah Hosseini*¹, Anne Maillard, Jean Claude Yvin¹
¹Centre Mondial de l'Innovation Roullier Saint Malo, France

The important role of potassium (K) in the mitigation of different stress such as drought, heat or frost has been well documented. Recently, researchers have been more focused on silicon (Si) topic and wide-ranging benefits of Si for stressed plants are exploited for agricultural gain. Si has been widely reported to alleviate drought responses and plant nutrient deficiency. Also, few studies have been also shown that Si ameliorated the K-deficient response. Although there is evidence that both K and Si can improve drought tolerance on their own, their combinatorial effect on drought stress tolerance has so far not yet been reported. In order to investigate the role of Si nutrition under concomitant drought and K deficiency, a barley line was submitted to polyethylene glycol (PEG)-induced osmotic stress under low or high K supply and two Si regimes to investigate the related mechanisms contributing to better drought tolerance. The results showed that the regulation of barley silicon transporters HvLsi1, HvLsi2 and HvLsi6 controlled accumulation of Si in the shoot only when plants suffered of K deficiency. Furthermore, our results indicated that higher Si accumulated in shoot of barley plants contributed to better drought tolerance by maintaining the photosynthetic machinery active and increasing the chlorophyll level.

Audience Take Away:

- The new mechanisms by which Si mitigates K deficiency in particular when additional abiotic stress like drought interfere
- The importance of applying Si for reaching to sustainable agriculture.
- Scientists will be encouraged to work more on Si topic as an important nutritional alleviating stress responses.

Biography

Seyed Abdollah Hosseini has 10 years of research experience in plant physiology and biotechnology. His scientific career has been started in Agriculture Biotechnology Research Institute of Iran (ABRII) as research assistant and lab manager. He then moved to Germany for his PhD at Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), addressing the role of the potassium nutritional status on drought stress-induced leaf senescence in barley. Since 2017, he is employed as Project manager at Agro Innovation International of Roullier Group. He is currently focused on potassium and silicon nutrition in plants in particular under drought condition. All his scientific works and research studies in different topics in the past were published in 6 papers in outstanding international journals.

Hormonal dynamics during salt stress response of salt-sensitive *Arabidopsis thaliana* and salt-tolerant *Thellungiella salsuginea*

Mgr. Sylva Prerostova^{*1,2}, Ing. Petre I. Dobrev¹, CSc., RNDr. Alena Gaudinova¹, Ing. Petr Hosek¹, Ph.D., RNDr. Petr Soudek¹, Ph.D., Bc. Vojtech Knirsch¹, RNDr. Radomira Vankova¹, CSc.

¹Institute of Experimental Botany AS CR, Czech Republic

²Faculty of Science, Charles University, Czech Republic

Salinization represents a serious problem of modern agriculture. Elucidation of the tolerance mechanisms is highly desirable. Phytohormones play an important role in stress responses as well as in regulation of plant growth and development. In our study, we focused on the impact of salinity on hormonal dynamics. Salt stress responses of salt-sensitive *Arabidopsis thaliana* and its close relative, salt-tolerant *Thellungiella salsuginea* (*Eutrema halophila*) exposed one week to the concentration range 2 – 150 mM and 150 – 350 mM NaCl, respectively, were followed in hydroponics. Time course of the early response (15 min to 24 h) to severe salt stress was also studied. Responses were characterised by phytohormone contents, selected gene transcription, membrane stability, and Na⁺ and K⁺ levels.

Thellungiella exhibited higher basal levels of abscisic acid (ABA) and jasmonic acid (JA) in shoot apices in comparison with *Arabidopsis*. However, the levels of active cytokinins (CKs) were lower (except of cis-zeatin). The halophyte reacted faster and stronger to salt stress (increase of ABA level, and RD26 and COR47 transcription). According to salt stress intensity, four groups may be distinguished on the basis of hormonal and transcriptome changes. Very mild stress (2 – 25 mM NaCl in *Arabidopsis*) slightly changed transcription of genes involved in CK metabolism. Mild stress in *Arabidopsis* (50 mM NaCl) induced stress reaction only in apices, while in *Thellungiella* (150 mM) the hormonal response was detected in whole plant. Severe stress was defined above 75 mM NaCl in the case of *Arabidopsis*, and above 225 mM in the case of *Thellungiella*. Lethal stress caused death of *Arabidopsis* plants (150 mM NaCl).

Generally, JA levels were transiently elevated during the early response. By contrast, salicylic acid content stayed unchanged. Auxin (indole-3-acetic acid) and CKs (primarily trans-zeatin) decreased in roots of both genotypes. The low active CK, cis-zeatin, seems to play an important role during salt stress responses. The results demonstrated that in severe stress the halophyte preferentially protected apices, which died first in *Arabidopsis*.

This work was supported by MEYS CR, project no. LD 15093.

Audience Take Away:

- Plants protect shoot apical meristem (apex) under salt stress.
- Wide phytohormone range was followed during salt stress response for the first time.
- Hormonome and transcriptome reflect the salt stress strength.

Biography

Mgr. Sylva Prerostova is a PhD student at Charles University. Since 2011, she has worked in the Institute of Experimental Botany of Academy of Science, Czech Republic. She has focused on salinity stress in plants. She uses molecular biology methods for understanding of plant phytohormone signalling and interactions during salinity stress.

Synergism of the false root-knot nematode *Nacobbus aberrans* and *Phytophthora capsici* manifested by alteration of phenylpropanoid metabolism in *Capsicum annuum*

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²Departamento de Ingeniería de Alimentos y Equipamiento Agrícola. Universidad Politécnica de Cartagena (UPCT), Cartagena (Murcia).

³Department of Chemistry, University of Warsaw, Poland.

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The significant role of plant parasitic nematodes in the development of diseases caused by soilborne pathogens has been demonstrated in many cultivated crops throughout the world. In most cases, such interactions involve root-knot nematodes like *Meloidogyne* spp. and the false root-knot nematode *Nacobbus aberrans*. Our research group has been using with the interactions among *Nacobbus aberrans* and pepper (*Capsicum annuum* L) CM334 resistant to *Phytophthora capsici* Leoninan, to determine what biochemical and molecular changes are induced by the nematode, which in turn could affecting the host resistance. Resistance in the genotype of chilli pepper CM334 against the three major species of root-knot nematodes and the oomycete *Phytophthora capsici* has been associated with the phenylpropanoid pathway of secondary metabolism. Therefore, L-phenylalanine ammonia-lyase (PAL) activity and the content of total soluble phenols (TSP) were determined in CM334 plants inoculated with *N. aberrans*, *P. capsici* or both pathogens. Besides, the phenylpropanoid profile was analyzed by HPLC-ESI/MS and the in vitro effect of phenylpropanoid compounds on second-stage juveniles (J2s) of *N. aberrans* and *Meloidogyne incognita* was also tested. The highest values of PAL activity and content of TSP were registered in plants inoculated only with *P. capsici*, while those plants inoculated with *N. aberrans* alone or in combination with *P. capsici* showed the lowest level ($P < 0.05$). Phenolic acids (p-HBA, gallic, caffeic, syringic, sinapic, ferulic, vanillic, p-coumaric and chlorogenic) and flavonoids (rutin, apigenin and luteolin) were found CM334 plants. Chlorogenic acid and luteolin were the phenylpropanoid compounds in highest quantity in CM334. Concentration of p-hidroxy benzoic and chlorogenic acids and flavonoids was lower in plants inoculated with *N. aberrans* than in the control ($P < 0.05$) at any sampling date. On the other hand, the flavonoid rutin has a differential particular toxic effect in each of nematodes used in this work. This flavonoid had a nematocidal effect as shown in the experiment carried out on with J2s of *N. aberrans*, whereas it only had a nemastatic effect on J2s of *M. incognita*. These results indicate that *N. aberrans* alters the phenylpropanoid metabolism during the infection of chilli pepper, possibly to create a favorable environment that allowed it to complete their life cycle.

Audience Take Away:

- Try to understand some biochemical changes induced by the root the false root-knot nematode *Nacobbus aberrans* in *Capsicum annuum*, possibly to create a favorable environment that allowed it to complete their life cycle.
- Root infection by the root the false root-knot nematode *Nacobbus aberrans* modify the host response to subsequent infections, in this case infection by the oomycete *Phytophthora capsici*. Explain how the audience will be able to use what they learn?
- This paper reports new findings concerning the interactions among two different pathogens of *C. annuum* and their synergism in affecting host resistance

Biography

Noe Lopez-Martinez was born at 1981 in Veracruz state, Mexico. He is Engineer in Crop Production and accepted Post Graduate studies in Plant Physiology. He is Professor in the Crop Production Department at Universidad Autónoma Chapingo, México. He teaches courses of plant physiology and plant biochemistry. His recent area of interest concerns the study of interactions between plant parasitic nematodes and soilborne pathogens. He has serve as chair of the host-nematode interaction sessions in international meetings.

Axenically culturing the bryophytes: Problems, achievements and prospective of in vitro cultures

Marko S. Sabovljevic*¹, Aneta D. Sabovljevic¹, Milorad Vujcic¹

¹University of Belgrade, Serbia

Although the second biggest group of terrestrial plants, bryophytes remained under-studied as well as neglected in biotechnology. They comprise very heterogeneous morphology, anatomy, physiology, ecology, chemical constituents, environmental stress reaction types, biochemical pathways and mechanisms and a lot can be learnt from them. Here, we present the insights into many of these features of case studies bryophytes as well as potentials of these plants in future biotechnological applications like remedies, medicines, ecosystem engineering, crop improvement or even food. The main problem in dealing with bryophytes is achievement of clean material in a significant amount. Although they are present almost in all Earth ecosystems (except seas), they are small in biomass and often intermingled with other organisms. This problem can be overcome by in vitro culturing, but it is not easy to establish and maintain the axenic culture of bryophytes having in mind their one cell layer thallus and that they represent the whole habitat for many small groups of organisms. Once, these problems overcome, the optimization of growth factors and enough biomass achievement present the challenge. The production of targeted natural compound can be managed by growth condition or by genetic tools, but the establishment of monoculture in open wide is not a way due to small competitive capacity of bryophytes and its rapid interaction with other organisms. Besides, biotechnological processes applied on bryophytes can also lead to good and valid ex situ conservation of these tiny and nice organisms. The Belgrade Biology Research group has an immense collection of 260 bryophytes species (including hornworts, leafy and thallose liverworts, acrocarpous and pleurocarpous mosses and peat mosses) from all over the World. It is the world biggest live collection of bryophytes, many of which are used in various biological and biotechnological research and many examples from the own and new research will be presented.

Audience Take Away:

- Since, there are very few research groups dealing in applied bryophyte biology world-wide, the audience will have the opportunity to hear many novelties and also to learn about our achievements and problem solutions. The audience can get new ideas in their work, either research or industry, and new cooperation(s) or product(s) can be developed.

Biography

Marko S. Sabovljevic (1974), is a biologist dealing with Bryophyte Biology and leading a group of researchers in University of Belgrade (Serbia). He received his PhD at the University of Bonn (Germany), and has over 350 references including peer-reviewed papers (184), conference communications (151), university text books (5), and book chapters (11). He is Associate Professor at Faculty of Biology, University of Belgrade, Serbia. The main focus of his research includes bryophytes and various aspects of their fundamental and applied features.

Poster Presentations

Global Conference on
**Plant Science and
Molecular Biology**

September 11 - 13, 2017 | Valencia, Spain

GPMB 2017

Enhanced Production of Stilbene Compounds in Plant and Cell Culture Systems

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¹Biological Resource Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Republic of Korea

Anthocyanins and stilbenes share common phenylpropanoid precursor pathways. We previously reported that overexpression of sweetpotato R2R3-type MYB gene IbMYB1a (MYB-OX) induced anthocyanin pigmentation in transgenic Arabidopsis and tobacco plants. Here, we also generated transgenic plants overexpressing a stilbene synthase gene RpSTS to obtain a high-level production of stilbene compounds in transgenic plants. However, low levels of resveratrol compounds were produced in transgenic tobacco plants (STS-OX) plants. Therefore, to improve the production of stilbene compounds in plants, we cross-pollinated flowers of STS-OX or ROST-OX and MYB-OX transgenic lines (SM and RSM). HPLC and LC-MS analyses exhibited the increased production of stilbene compounds such as piceid, piceid methyl ether, resveratrol methyl ether O-hexoside, and 5-methyl resveratrol-3,4'-O- β -D-diglucoopyranoside in SM and RSM lines. Thus, we suggest that coexpression of RpSTS and IbMYB1a via cross-pollination can induce the enhanced production of resveratrol compounds in plants by increasing metabolic flux into stilbenoid biosynthesis. In addition, as an alternative approach, we employed the cell culture system of grape (*Vitis vinifera*) for production of resveratrol derivatives. Here, we established the elicitation and secretion conditions for high-level production of resveratrol and its oligomers such as viniferin, a resveratrol dehydromer in grape cell cultures. In particular, we developed the conditional production of resveratrol and viniferin in the culture media using different solubilizers. In this presentation, our current studies will be addressed.

Audience Take Away:

- Strategies for enhanced production of anthocyanin and stilbene compounds in plant system
- Enhancement of metabolic flux into stilbenoid biosynthesis by co-expression of RpSTS and IbMYB1a via cross-pollination
- Establishment of elicitation and secretion conditions for high-level production of resveratrol and viniferin in grape cell cultures
- Conditional production of resveratrol and viniferin in the culture media using different solubilizers

Biography

| | |
|-------------|---|
| 2016 – 2017 | Director, Biological Resource Center (KCTC), KRIBB |
| 2007 – 2016 | Senior Researcher/Principal Researcher, KRIBB |
| 2002 – 2006 | Post-Doctoral Fellow, The Pennsylvania State University (PSU) |
| 2000 – 2002 | Post-Doctoral Fellow, University of Missouri-Columbia |
| 1998 – 2000 | Ph.D., Gyeongsang National University |
| 1991 – 1993 | M.S., Gyeongsang National University |
| 1987 – 1991 | B.S., Gyeongsang National University |

Expression of Heavy Metal ATPase HMA1 and HMA2 in Brassica juncea and Brassica nigra grown at Different Levels of Cu and Cd.

Nuriye Merakli*, MerveNurSahan and Abdul Razaque Memon

Brassica species are well known as metal accumulators and some of them are being used for phytoremediation in contaminated soils. Approximately 25% of the documented metal hyper accumulating species have been found in Brassicaceae family. In this report we have evaluated the accumulation capacity of two well known Brassica sps (B. juncea and B. nigra) grown at different levels of Cu and Cd. Heavy metal transporting proteins have an important role in maintenance of metal homeostasis in plants and are involved in a number of different processes including metal uptake, delivery of metals to cellular compartments and metal detoxification. P1B-ATPases are one of the largest and diverse protein families in membrane proteins responsible for transporting metals from roots to shoots. We have done the phylogenetic analysis of these proteins by using the sequence data of these genes from B. juncea. Homology analysis of these genes were performed by using different data banks. Additionally we have analyzed the gene expression pattern of metal ATPases (HMA1 and HMA2) in plant leaves and roots grown at different levels of Cu and Cd by using R-T PCR. Our data showed that HMA1 and HMA2 play an important role in metal accumulation and detoxification in B. juncea leaves. Over all our aim in this project is to find out the Cu and Cd induced gene regulation in accumulator plant B. nigra and tolerant plant B. juncea.

Audience Take Away:

- The metal accumulation of Cu and Cd in two species from the genus Brassica was examined to determine if these plants showed sufficient tolerance and metal accumulation to be used to phytoremediate a site contaminated with these two heavy metals

Biography

Nuriye Merakli. She is a master student in the Department of Molecular Biology and Genetics at Usak University. She graduated from Usak University in June 2016 with a bachelor's degree 3,23/4. She has also awarded with a certificate of honor from University.

Inferring movement of potato psyllids among host plants using NextRAD sequencing

Zhen Fu^{1*}, Brendan Epstein², Joanna L. Kelley², Qi Zheng³, Alan O. Bergland^{4,5}, Carmen I. Castillo Carrillo^{1,6}, Andrew S. Jensen⁷, Jennifer Dahan⁸, Alexander V. Karasev⁸, William E. Snyder¹

¹ Department of Entomology, Washington State University, USA

² School of Biological Sciences, Washington State University, USA

³ Department of Bioinformatics and Biostatistics, University of Louisville, USA

⁴ Department of Biology, Stanford University, USA

⁵ Department of Biology, University of Virginia, USA

⁶ Department of Plant Protection, Santa Catalina Experimental Station, National Institute of Agricultural Research, INIAP, Ecuador

⁷ Northwest Potato Research Consortium, USA

⁸ Department of Plant, Soil and Entomological Sciences, Moscow, USA

Herbivores often move among spatially interspersed host plants, tracking high-quality resources through space and time. This dispersal is of particular interest for vectors of plant pathogens. Existing molecular tools to track such movement have yielded important insights, but often provide insufficient genetic resolution to infer spread at finer spatiotemporal scales. Here, we explore the use of Nextera-tagmented reductively-amplified DNA (NextRAD) sequencing to infer movement of a highly-mobile winged insect, the potato psyllid (*Bactericera cockerelli*), among host plants. The psyllid vectors the pathogen that causes zebra chip disease in potato (*Solanum tuberosum*), but understanding and managing the spread of this pathogen is limited by uncertainty about the insect's host plant(s) outside of the growing season. We identified 1,978 polymorphic loci among psyllids separated spatiotemporally on potato or in patches of bittersweet nightshade (*S. dulcumara*), a weedy plant proposed to be the source of potato-colonizing psyllids. A subset of the psyllids on potato exhibited genetic similarity to insects on nightshade, consistent with regular movement between these two host plants. However, a second subset of potato-collected psyllids was genetically distinct from those collected on bittersweet nightshade; this suggests that a currently unrecognized source, i.e., other nightshade patches or a third host-plant species, could be contributing to psyllid populations in potato. Oftentimes, dispersal of vectors of pathogens must be tracked at a fine scale in order to understand, predict, and manage disease spread. We demonstrate that emerging sequencing technologies that detect genome-wide SNPs of a vector can be used to infer such localized movement.

Audience Take Away:

- Next generation sequencing approach was used in this case to explain the movement of very small insects, what could be very difficult to be explained in other way.
- This research opens the opportunity to explore the origin and migration of other guilds moving from sites.
- This molecular tool shows versatile applicability in research.

Biography

Ph.D. and M.Sc. in Entomology (WSU, USA and WUR, Netherlands, respectively). I had internships and work and laboratory practices in Japan, Spain and New Zealand. My research runs about developing integrated pest management of agricultural pests, including vector-pathogen relationships and biological control. I'm focused on molecular characterization and identification of pathogens and insect vectors of emerging plant diseases. I develop research projects to help low-income farmers and to improve agriculture in the Ecuadorian Highlands. I have been working in the National Institute of Agricultural Research of Ecuador for two decades.

The lack of AtEgy1 protease leads to quantitative changes of photosystem II apoproteins in *Arabidopsis thaliana*.

Małgorzata Adamiec, Jędrzej Dobrogojski, Maria Ciesielska, Lucyna Misztal, Robert Lucinski*¹

¹Adam Mickiewicz University Poznan, Faculty of Biology, Institute of Experimental Biology, Department of Plant Physiology, Poland

AtEgy1 chloroplast protease is the first intramembrane protease identified in plants, that belongs to the site-2-proteases (S2P), which are a relatively recently discovered class of proteases capable of catalyzing the proteolysis process within the biological membranes. AtEgy1 protease is a 59-kDa protein with 8 transmembrane domains. In the primary structure of this protein the motifs, characteristic for S2P proteases, responsible for the zinc ion binding e.g. HExxH and NxxPxxxxDG are present. Previous studies have shown that *A. thaliana* mutants lacking AtEgy1 protein exhibit marked changes in the number and ultrastructure of chloroplasts. Egy1 mutants are characterized by a poorly developed system of thylakoid membranes, lack of granum and markedly reduced plastoglobules size. Moreover, egy1 mutants showed the reduced chlorophyll level, resulting in the yellow color of the leaves. The lack of AtEgy1 protease can also cause disorders in the normal development of amyloplasts, which are important for the perception of gravitational stimulus. As a result, egy1 mutants exhibit the disorders of gravitropism. The aim of this work was to analyze the quantitative changes in the proteins that build the core of photosystem II (PsbA, PsbC and PsbD) and the proteins that build up its major energy antennas (Lhcb1-6). It has been shown that the lack of AtEgy1 protease leads to significant changes in the levels of almost all tested proteins. The apparent decrease in the amount of Lhcb1-6, PsbC and PsbD had also impact on the parameters describing the quantitative effectiveness of PSII functioning. This work was supported by the Polish National Science Center based on decision number DEC-2014/15/B/NZ3/00412.

Audience Take Away:

- Potential role of chloroplast intramembrane protease AtEgy1
- Changes in the number of photosystem II proteins in *A. thaliana* mutants lacking AtEgy1 protease
- Changes in the parameters describing the functioning of the photosystem II as a result of the lack of AtEgy1 protease.

Biography

1999 – M.Sc. in Biotechnology, Faculty of Biology, Adam Mickiewicz University.

2003 – Ph.D. in biological sciences with specialization in biology, plant physiology, Faculty of Biology, Adam Mickiewicz University.

Professor assistant in The Department of Plant Physiology, Faculty of Biology, Adam Mickiewicz University.

Dead pericarps function as storage for active hydrolases and germination inhibitory substances

Godwin James*, Buzi Raviv, Gila Granot, Gideon Grafi

French Associates Institute of Agriculture and Biotechnology of Drylands, The Institutes for Desert Research, Ben-Gurion University of the Negev, Israel.

Fruits can be divided into two classes; dry fruits and fleshy fruits. Dry fruits, in which the coat (pericarp) undergoes death and hardening at maturity categorized as either dehiscent, whereby the dry fruit is opened at maturity to allow seed dispersal or indehiscent, whereby the dry fruit does not open at maturity and act as a dispersal unit. The pericarp enclosing the seed is believed to provide a major physical shield against harmful environmental conditions as well as assisting in seed dispersal. A recent study in our lab demonstrated that the maternally-derived dead organs enclosing the embryo (seed coat) in Brassicaceae and Fabaceae species as well as hardened floral bracts of wheat dispersal units (e.g., glumes) store and release upon hydration hydrolytic enzymes and other growth regulatory substances that might assist seed germination and seedling establishment. We wanted to address if similar function is carried out by dead pericarps. We focused on *Sinapis alba* (white mustard) because the fruit is composed of dehiscent and indehiscent parts, and investigated the potential of the dead pericarps to store active proteins and nutrients and their potential to support or inhibit seed germination.

Preliminary proteome analysis revealed that *S. alba* pericarps released upon hydration multiple proteins including stress related proteins, hydrolases and extracellular proteins. In gel nuclease assays of proteins released from *S. alba* dehiscent and indehiscent pericarps showed the both pericarps possess active nucleases. This appears to be a general phenomenon in plants in as much as the dead pericarps of other plant species including *Arabidopsis thaliana*, *Coriandrum sativum* L. (Apiaceae), *Spartium junceum* L. (Fabaceae) and *Trigonella arabica* Delile (Fabaceae) store and release upon hydration active nucleases. Elemental analysis revealed the abundant accumulation of major and minor nutrients in the *S. alba* pericarp and surprisingly there is more accumulation of nutrients in indehiscent pericarp compared dehiscent pericarp. Preliminary germination experiments showed that substances released from the pericarps inhibited seed germination of *S. alba*. Thus, our results explored previously unknown features of the pericarp serving as a reservoir of substances that might play an important role in seed germination and seedling establishment.

Audience Take Away:

- I am studying a unique, previously unexplored field in plant sciences - the role of dead organs enclosing embryos (seed coats, pericarps, glumes etc.) in long term preservation of active proteins and nutrients and their role in seed persistence and germination.
- This study would interest the audience in the conference and help me gain ideas for future research directions

Biography

My name is Godwin James. I am currently an M.Sc student in Desert studies specializing in Agriculture and Biotechnology for sustainable dryland development at Ben Gurion University of the Negev, Israel. I am working on white mustard (*Sinapis alba*) fruits, to understand the potential of dead pericarp enclosing the seeds to store active proteins and nutrients upon hydration and their potential to support or inhibit seed germination. I gained professional bachelor's degree in Biotechnology in 2015 from Tamil Nadu Agricultural University, India. I was offered a prestigious summer research fellowship by Indian Academy of Sciences in 2014 to carry out an internship project for two months.

Genome-wide characterization and analysis of MADS-box transcription factor gene family related to flower induction in Pineapple (*Ananascomosus*)

Hu Fuchu*, Chen zhe, NianYuwei, Zhang Zhili

Institute of Tropical Fruit Trees, Hainan Academy of Agricultural Science/Key laboratory of tropical fruit tree biology of Hainan Province/Haikou Investigation Station of Tropical Fruit Trees, Ministry of Agriculture, China

MADS-box transcription factors are vital regulators participating in plant growth and development, but a little information is available regarding the MADS-box gene family in Pineapple (*Ananascomosus*), a very important tropical fruit in the world. Herein, 40 MADS-box genes were identified in Pineapple, and could be divided into two types, in which 26 AcMADSs were grouped in type II (MIKC), while 14 in type I. Transcriptome analysis of pineapple buds revealed that many MADS-box genes were activated by ethephon after 1 d treatment. Some candidate AcMADSs participating in flowering were identified for further functional characterization in pineapple, and all data provide new insight into AcMADS-mediated flowering related to ethylene in Pineapple.

Key words: Pineapple, MADS-box, Genome-wide, Phylogenetic analysis, AcMADS-mediated flowering

Tempe lake management strategies as the clean water source society in wajo district, south sulawesi, indonesia

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³PhD Student Department of Environmental Education Studies, Universitas Negeri Makassar. Deputy of Bosowa Agro Group and Executive Director of Polytechnic Bosowa, Makassar, Indonesia

⁴PhD Student Department of Environmental Education Studies, Universitas Negeri Makassar. Senior Lecturer of Science Faculty, Science Education Program, Universitas Negeri, Makassar, Indonesia

Lake Tempe as one of the water resources in Indonesia has permanent puddle problems in settlement area. This problem limits public access to clean water sources. This study reviews the society's limited access of clean water around Lake Tempe and the management strategy of Lake Tempe as a source of clean water for the society. The research method is descriptive quantitative with survey approach. Descriptive statistical methods describe the condition of the society water access and the method of Analytical Hierarchy Process. The results showed that society water access was very low in accordance with the three indicators, namely the quality of water sources, the location of the source of clean water and the sustainability of the clean water availability. The analysis result of tempe lake management strategy as a source of clean water showed that government plays an important role compared with private institutions and society institutions. The main strategy in clean water management is the provision of communal water treatment supported by participation of the society.

Keyword: Clean Water, Society and Lake

Biography

Nurlita Pertiwi, Female, Doctor of Environmental Management, graduated from Department of Environmental and Natural Resources Management, Institute Pertanian Bogor, in 2011. Recently, she is Head Department of Environmental Education Studies, Post Graduate Programme Universitas Negeri Makassar. Since 1998 Lecturer of Faculty of Engineering, Department of Civil Engineering Universitas Negeri Makassar. She has published some international journals about environment issues and also published books with subject Sustainable Development in Indonesia. She has participated in several international seminars. In addition, she has involved as co chair of annual meeting of 2nd International Conference on Education, Science and Technology (ICEST) in Makassar, Indonesia.

New locus of barley resistance gene to powdery mildew

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Blumeria graminis f. sp. hordei is one of the most economically important pathogen of barley. This windborne fungus causes powdery mildew foliar disease and yield losses due to this pathogen may reach up to 20-30%. In addition to yield losses it is observed lowering of grain quality, particularly disadvantageous for malting barley. Resistance for powdery mildew is the aim of numerous breeding programmes. Searching for new resistance genes can be based on barley landraces.

Barley landrace Bgh255-3-3 resistant to broad spectrum powdery mildew isolates was investigated. Analyses of mapping population with microsatellite markers lead to define new resistance locus on 2H barley chromosome. Genetic association map of 2H chromosome with resistance gene origin from Bgh255-3-3 was obtained.

Broadening available barley gene pool has practical application. Introducing and pyramiding new resistance genes to new cultivars reduce impact of disease on yield.

This work was supported by programme: “Creation of scientific basis for biological improvement and plant genetic resources protection as source of innovation and support of sustainable agriculture and national food security” funded by Ministry of Agriculture and Rural Development (Poland). Project No. 3-2-00-0-02 (WP 2.2): “Broadening of barley gene pool.”

Biography

Jerzy Henryk Czembor has completed his PhD in 1995, Montana State University, Bozeman, USA; 2012 – professor of agriculture. 2008-2016 Head of Laboratory of Applied Genetics, 2011 – 2016 Head of Department of Plant Breeding and Genetics; 2016 - Head of National Centre of Plant Genetic Resource (Polish GeneBank). Coordinator and partner in several national and international projects. Member of several domestic and international scientific associations. Author of more than 200 scientific papers and communications. Interested in: agricultural sciences, plant pathology, plant genetic resources management, biodiversity, molecular biology, marker-assisted selection (MAS), cereals, plant genetics, plant breeding, integrated pest management (IPM).

Effect of silicate-coated rice seed on bakanae disease (*Gibberella fujikuroi*) reduction in the rice cultivation

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Crop seeds are often coated with either chemicals or fertilizers to reduce the production cost. So far, to protect bird damage in direct wet seeding rice paddies, seedlot was coated either with Iron or Ocher mud soil. Our R&D team investigated the effect of silicate-coated rice seeds (SCS) on the reduction of bakanae epidemics and the rice growth performance in direct wet seeded paddy field and also in raising seedlings boxes for mechanical transplanting as well. We developed SCS to protect and to apply the silicate fertilizer as follows. Naturally infested rice seedlots not previously subjected to any fungicidal treatment were dressed with a mixture of 25% silicic acid at pH-11 and 300-mesh zeolite powder at a ratio of 50 g dry seed : 9 mL silicic acid : 25 g zeolite powder. In direct wet seeding blocks, uniform scattering of rice seeds on the soil surface with better seedling establishment were observed in SCS plots. As of heading stage, the infection rate was the highest by 9.9% in the non-SCS control. While in SCS plots, the infection rate was limited to below 0.01%. The viability of the bakanae fungal conidia in the SCS and non-SCS seedlots previously inoculated with panicles of infected plants from experimental field plots was assessed in the incubator. In the non-SCS control, pinkish colonies were observed to recover on the panicle grain of infected plants where mycelium, macro- and micro-conidia were developed actively in interior of infected grain. While in the SCS plots there was no sign of pathogen survival in vivo. In seedling boxes, seedlings emerged 2-3 days earlier for the SCS than they did for the non-SCS control and damping-off and bakanae disease incidence were remarkably reduced. Specifically, bakanae disease incidence in the SCS was limited to only 7.8% for 80 days after sowing, as compared to 91.6% of the non-SCS control. For the 45-days-old SCS nursery seedlings, the fresh weight was increased by 11% in healthy plants and was two times heavier in the infected plants, with only mild damage compared to that observed for the non-SCS. Even after transplanting, SCS treatment contributed to a lower incidence of further infections and possibly to recovery of the seedlings to normal growth as compared to that observed in symptomatic plants. The active pathogenic macro-conidia and micro-conidia were considerably fewer in the soil, root, and seedling tissue of the SCS. In particular, the abnormality of macro-conidia with thick-walled, straight oblong shape, devoid of septum were retrieved in the SCS tissue; which is likely to be a comparative etiological disadvantage, compared to that of typical active macro-conidia, which are slightly sickle-shaped with 5-7 intact septa in non-SCS tissue. Active intact conidia with high inoculum potential were rarely observed in the tissue of the seedlings treated only in the SCS. We propose that promising result was achieved most likely via inhibition of the development of intact conidia, in concert with the aerobic, acidic conditions induced by the physiochemical characteristics associated with the air porosity of zeolite, alkalinity of silicate and the seed husk as a carbon source. In addition, the resistance of the healthy plants to pathogenic conidia was also an important factor. Therefore, it was concluded that the application of silicate coated seed (SCS) would be a feasible alternative to prevent the bakanae disease.

Keywords: silicate-coated rice seed (SCS), bakanae disease, direct wet seeding, raising seedling

Audience Take Away:

- Objectives of this research: The bird damage, poor germination and poor seedling establishment are obstructing the spreading of direct seeding technology in the rice paddy in Korea. Seed disinfection, sprouting and bakanae disease are problematic in the box seedlings for machinery transplanting. We have developed to solve these problems and to apply the silicate fertilizer and marketed the coating materials for making silicate coated rice seed (SCS).
- Coating materials and its action mechanism: Naturally infested rice seedlots not previously subjected to any fungicidal treatment were dressed with a mixture of 25% silicic acid at pH-11 and 300- mesh zeolite powder at a ratio of 50 g dry seed : 9 mL silicic acid: 25 g zeolite powder. We propose that promising result

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- Practical uses of this research: Farmers, who are the end users of this technology, can use or make seed coatings directly instead of chemical control and fertilizer application in seed disinfection and rice fields, thereby increasing friendly environmental control and silicate fertilizing effect and reducing production cost. In industry, it will be possible to develop seed coating materials and improve effective and friendly environmental products. In academia, it is necessary to research the fertilization effect and the principle of disease control by seed coating.
- Future project: The company is focusing on developing effective coating methods and materials for coating strength and multi-functionality of silicate coated seeds in rice cropping.

Biography

Education: Mar. 1980-Feb. 1985: Ph. D. in Agronomy, Dept. of Agronomy, Graduate School, Kyungpook National Univ.

Experience: Feb. 1971-Dec. 2003: Senior researcher (Director of Rice Physiology and Cultivation Division, National Institute of Crop Science, RDA)

May 2009-Present: Director of research institute, Saturn Bio. Tec. Co. Ltd.

Conference Attended

Sept. '99: A speaker at the 1st Silicon Conference in Agriculture, Florida, USA.

Aug. '02: A speaker at the 2nd Silicon Conference, Tsuruoka, Japan

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ABA-mediated stress response mechanism modulates stigmatic papillae development in *Arabidopsis thaliana*.

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Reproduction is an important process in the life cycle. Pollination is the first step in bringing together the male and female gametophytes for plant reproduction and starts when pollen grains land on the stigmatic papillae at the apex of gynoecium. While mechanism of pollination has been studied for many years, the development and elongation mechanisms of papillae remain largely unknown. In this study, we report developmental flexibility of papillae and their quick response mechanisms, in response to abiotic stress. There are many genes in the *A. thaliana* genome, and more than 15,000 genes are expressed in the stigmatic papillae for sustaining a reproduction and developmental functions, which includes a diversity of molecular players particularly those involved in metabolic, transcription and signaling processes. Through reverse genetic, in vitro, and transcriptome analyses, we found that the stigmatic papillae of *A. thaliana* changed their length rapidly in response to ambient conditions such as high humidity and salinity: NaCl treatment reduced the papillae length and ABA treatment induced papilla elongation, and that the key mechanism for the rapid response of papillae elongation is mediated by ABA pathway. The ABA-mediated response in papillae can be launched only when synthesized ABA precursor from the primary biosynthesis pathway is converted to an active form of ABA, by activation of the downstream biosynthesis pathway, enabling rapid response against ambient conditions. This is one of plant adaptations to the environment to maintain the chance of pollination for successful reproduction in Plants.

Biography

Keita Suwabe is Associate Professor in plant molecular genetics and breeding, at Mie University, Japan. He received his PhD in 2004 from the Department of Life Sciences, Mie University. He had postdoc experiments at John Innes Centre, working with Ian Bancroft. His research interest is the molecular dissection of pollination in higher plants, including pollen-pistil interaction.

Characterization of NBS-LRR type gene with altered expression in response to *Puccinia horiana*

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Chrysanthemum white rust is the most serious diseases of cut flower chrysanthemum. The best option to minimize damage caused by white rust is to develop cultivars resistant to chrysanthemum white rust. However, the mechanisms related to chrysanthemum resistance against this pathogen are studied very limitedly at molecular levels. We investigate the changes of gene expression of resistant wild type in response to *Puccinia horiana* during time course during a time course (1, 2, 4, 6, 24, 48 and 168 hours post-infection). We isolate several differential expressed genes by RNA seq. We can identify the genes of NBS-LRR type. The gene transcriptional profiles after infection showed that the response of NBS-LRR type gene was quicker and stronger in the resistance genotype than in the susceptible one during the early infection stage. This type gene is not existed in other resistant cultivars by PCR analysis. We will try to isolate the full length cDNA of NBS-LRR type gene, and characterize the gene.

Audience Take Away:

- The changes of gene expression of resistant wild type in response to *Puccinia horiana* during time course during a time course (1, 2, 4, 6, 24, 48 and 168 hours post-infection).
- Identification of differential expressed genes by RNA seq.
- The gene transcriptional profiles after infection showed that the response of NBS-LRR type gene was quicker and stronger in the resistance genotype than in the susceptible one during the early infection stage

Performance of *hylocerus* (cactaceae) hybrids under high temperature stress

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Hybridization, an effective method to obtain genetically improved agricultural crops, can be exploited to generate novel hybrids with desired traits, such as, enhanced growth, survival rate, and heat and disease tolerances. In this research, we studied two hybrids (i.e., the allotetraploid Z-10 and the allotriploid S-75) and their parent species (i.e., the diploids *Hylocerus monacanthus* and *H. undantus* and the tetraploid *H. megalanthus*) under short- and long-term heat stress. Short-term heat stress was applied by collecting leaf discs from mature stems and placing them in a water bath for 30 minutes at 35, 45, 55 or 65°C. Long-term heat stress was applied by exposing rooted cuttings placed in pots to day/night temperatures 45/35°C at 90% relative humidity for 14 days. Plants subjected to short- and long-term heat stress were compared with control plants exposed to day/night temperatures of 26/20°C. Assessments of electrolyte leakage levels and of the maximum efficiency of PS II photochemistry (Fv/Fm) after plant exposure to short- and long-term heat stress showed lower electrolyte leakage and more efficient PSII photochemistry in the two allopolyploids, i.e., Z-10 and S-75, than in their parent species. Our results suggest that the enhanced availability of carbohydrates (soluble sugars in the form of glucose) observed in the two hybrids relative to the parent species contributes to membrane integrity and photosynthetic activity under high temperature stress. Nocturnal acid accumulation was significantly lower in long-term heat-stressed plants compared to control plants, and hybrids showed higher nocturnal acid levels compared to parent species. Overall, the results presented here suggest that high temperatures could have significant effects on the physiological levels of vine cacti plants, among which the allopolyploid lines may be more tolerant to heat stress than their parent lines.

From the present study it is evident that the thermo-tolerance to high temperature can be efficiently altered and improved through hybridization. This study provides an insight to the researcher to be focused on new synthetic allopolyploid lines.

Biography

I am Divya Sravanthi Kumbha from India, and finished B.Sc in Agriculture at Acharya N.G.Ranga Agricultural University, India, which included a Rural Agricultural Work Experience Programme (RAWEP) for 4 months in a rural village. This programme gave me an opportunity to interact with farmers and gain knowledge regarding agriculture challenges and their solutions. I also participated in a few national conferences on food security. I am currently pursuing M.Sc degree at The Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Israel, studying high temperature stress in pitaya.

OsXRI5 gene confers resistance to bacterial blight and bakanae disease

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One of rice NPR1 homologous gene, OsXRI5 function was analysed related to bacterial blight and bakanae disease. Over-expression of OsXRI5 conferred disease resistance to bacterial blight and bakanae disease. OsXRI5-overexpressed transgenic lines were shown the higher level expression of several pathogenesis-related protein genes, OsPR4, OsPR10 and OsPAL, than wild type rice. The OsXRI5-green fluorescent protein (GFP) fusion protein was localized in the nucleus.

Audience Take Away:

- Construction and molecular biological analysis of transgenic rice
- Bioassay of bacterial blight and bakanae disease
- Analysis on localization with rice protoplast

Biography

B.S., M.S., Ph. D. in Agricultural Chemistry, Gyeongsang National Univ. Jinju, Korea Postdoc. BK21 in Gyeongsang National Univ., Jinju, Korea; Molecular Breeding Div. NAAS, RDA, Korea 2005. 04. ~ present. General Research Scientist, Gene Engineering Div. NIAS, RDA, Korea

De novo assembly and transcriptome characterization of Pineapple (*Ananascomosus*) flower induction in response to Ethephon

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Pineapple (*Ananascomosus*) is one of the most important fruit trees in tropical and subtropical areas. The flowering rate of pineapple is easy to be influenced by external environmental factors, and the induction of floral bud by application of ethephon (ETH) is widely used in commercial production to enhance flowering ratio and regulate the time to market of pineapple. In the induction of floral buds, ETH plays complex and variable roles in pineapple. However, lack of information hinders our understanding of the mechanisms of flower bud differentiation induced by ETH in pineapple. Here, high-throughput RNA sequencing (RNA-Seq) was employed for de novo assembly and transcriptome characterization of pineapple (*Ananascomosus*) flowering in response to ethephon. More than 80 million base pair-end reads were generated and assembled into 41287 unigenes with an average length of 802bp. These unigenes were annotated by query against various public databases. Approximately, 21,575 (52.26%) unigenes annotated by the Nr database and 15220 (36.86%) unigenes annotated based on known proteins in the Swiss-Prot database, 11543 (25.54%) unigenes were annotated based on Gene Ontology terms, and 7868 (19.06%) unigenes were assigned to Kyoto Encyclopedia of Genes and Genomes pathways, 13542 and 11213 unigenes were annotated by Pfam and String database respectively. In addition, Many known and novel ETH-induced and flowering-induced genes were found, in which 12 unigenes were randomly selected for more detailed expression comparison responding to ETH. These studies provide the global expression analysis of flowering-induced transcripts and a robust database for investigating the functions of genes induced by ETH in pineapple

Keywords: Pineapple, Ethephon, Flowering-Induction, RNA-Seq

COP9 signalosome 5A protein interacts with Flowering locus T (FT) and mediates ambient temperature-dependent degradation of FT protein

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COP9 signalosome 5A (CSN5A) plays an important role in the protein degradation by ubiquitination. In order to investigate the role of CSN5A in ambient temperature responsive flowering, we analyzed the flowering phenotype of *csn5a* mutants. The *csn5a-1* mutants, completely devoid of CSN5A expression, flowered early at 16°C under long-day conditions, but they showed a normal flowering time phenotype at 23°C under the same conditions. FLOWERING LOCUS T (FT) transcript levels were unaltered in *csn5a-1* mutants excluding a possibility that CSN5A regulates FT transcription. However, we found that FT protein abundance was increased in *csn5a-1* mutants at 16°C, comparing to wild-type plants, suggesting that FT protein stability is regulated by CSN5A at lower temperatures. A peptide array experiment and co-immunoprecipitation assays identified tyrosine 225 residue in CSN5A was important for the CSN5A-FT interaction. Taken together, we propose that CSN5A regulates the ambient temperature-dependent FT protein degradation.

DeBaser: An online tool for fast RNA-Seq data assembly and polymorphism discovery

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The advent of Next Generation Sequencing (NGS) represented a dynamic leap in the capacity to study the genomic basis of variation within and between species. Knowledge of this variation is not only important in understanding possible causes of phenotypic diversity but is also crucial for accurate design of many molecular research tools such as RNAi constructs. However, full scale de novo assembly of NGS generated transcriptomes can take many months and raw data sets are being accumulated faster than they can be processed into usable assemblies. In order to expedite sequence information from NGS raw data we have designed 'DeBaser'. This is a web based bioinformatic pipeline that aligns NGS raw data to a reference CDS set to produce a full transcriptome in just 48 -72 hours. Users can utilise DeBaser by uploading data and, if required, a reference genome. After assembly, the transcriptome is then stored permanently on the website and can be retrieved in full or the user can specify individual transcripts by entering gene identifiers. Polymorphisms between assembled transcriptomes can also be determined by selecting multiple varieties in the web interface. Users retrieve sequence information for each by entering selected gene identifiers or FASTA files. Multi-sequence alignment files showing polymorphisms between varieties are generated via MultiAlin or Muscle. The designers have also provided pre-assembled plant transcriptomes which can be utilised along with the user provided data. DeBaser is in the final stages of development and will be released in the second half of 2017.

Keywords: Next Generation Sequencing, polymorphism, multiple sequence alignment

Biography

Rod Eyles is a Post-Doctoral fellow at the International Institute of Tropical Agriculture and is based in Nairobi, Kenya. His PhD, completed in 2014, focused on profiling and functional analysis of microRNA involvement in root organogenesis in *Medicago truncatula*. He is currently working on a collaborative project, with DMSZ in Germany, on development of a VIGS system for cassava for the study of resistance to cassava brown streak disease and cassava mosaic disease. His research interests include plant physiology and disease and in particular the use of RNAi based approaches to plant research.

Complete plastid genome of the carnivorous plant *Drosera rotundifolia* reveals genome rearrangements and early stages of gene loss

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Chloroplasts of most plants are responsible for photosynthesis and contain a conserved set of about 110 genes that encode components of housekeeping gene expression machinery and photosynthesis-related functions. However, a number of plants in the process of evolution have developed the ability to receive nutrients not through photosynthesis, but as a result of parasitism or predation. Such plants are less dependent on photosynthesis, and some parasitic plants do not contain chlorophyll at all. To date, a number of chloroplast genomes of parasitic plants have been sequenced, the analysis of which has shown that the chloroplast genome undergoes rearrangements in hemiparasites, while in non-photosynthetic species the reduction of the genome and the loss of genes associated with photosynthesis was also observed. Much less is known about the structure of the chloroplast genomes of carnivorous plants, in which the selective pressure on the photosynthetic apparatus is also relaxed.

We determined the complete nucleotide sequence of the chloroplast genome (cpDNA) of the insectivorous plant *Drosera rotundifolia* (sundew). Sequencing of cpDNA was performed by pyrosequencing of the total plant genomic DNA. The cpDNA is a circular molecule of 192,912 bp containing a pair of 52,949 bp inverted repeat regions (IRa and IRb), which are separated by small (SSC) and large (LSC) single copy regions of 63,504 bp and 23,510 bp, respectively. The size of the chloroplast genome of *D. rotundifolia* is larger than that of most flowering plants due to the increase in the length of inverted repeats. Chloroplast genome of *D. rotundifolia* contains 88 unique genes, including the ribosomal protein genes, genes of the photosystems I and II, the cytochrome b / f complex, the subunits of ATP synthases, and RNA polymerase genes. The peculiarity of cpDNA is the absence of NADH dehydrogenase genes, which may reflect the weakened dependence of this plant on photosynthesis. Unusual is also the large number of rearrangements in *D. rotundifolia* cpDNA, although the structure of the chloroplast genome (the order of the genes) remains practically unchanged in almost all flowering plants. Genomic rearrangements have led to the duplication of fragments of some genes presented in the form of pseudogenes. The weakened selection pressure is also indicated by the increased rate of evolution of the sequences of certain protein-coding genes, accumulation of repeats and short insertions/deletions. However, the photosynthetic apparatus is completely preserved.

In general, the structure and gene content of the chloroplast genome of *D. rotundifolia* reflects the early stage of the plant's transition to heterotrophic nutrition. The next stage in the evolution in course of transition to heterotrophy is represented by the chloroplast genomes of parasitic plants, in which not only the rearrangements of the genome and the accelerated evolution of the coding sequences are observed, but also the loss of the genes of the photosynthetic apparatus.

Audience Take Away:

- Analysis of chloroplast genomes of plants is a useful tool for studying the evolution of plants. Plastid genomes of parasitic and carnivorous plants represent model systems in which to study the effects of relaxed selective pressure on photosynthetic function. Comparison of the chloroplast genomes of parasitic and carnivorous plants revealed common features of their evolution, in particular, the accelerated evolution of some genes, genome rearrangements and the loss of NADH dehydrogenase genes.

Biography

In 2015 I graduated from Moscow State University with a master's degree. At present I am a PhD student and researcher at the Research Center for Biotechnology of the Russian Academy of Sciences. The subject of my PhD thesis is related to the study of the evolution of genomes in parasitic and carnivorous plants.

Identification and characterization of an E3 ligase regulating the stability of BIN2

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Glycogen synthase kinase 3 (GSK3)-like kinase play crucial roles in cell signaling pathways in both animals and plants. Here we showed that the BRASSINOSTEROID INSENSITIVE 2 (BIN2)/GSK3 β -like kinase is controlled at the protein stability level in *Arabidopsis thaliana*, via a mechanism that involves an ubiquitin E3 ligase. Immunoprecipitation of the HA-tagged BIN2 protein complex followed by mass spectrometry identified BRASSINOSTEROID F-BOX 1 (BRF1) and BRF2 as interacting proteins. Validation in vitro by yeast two-hybrid analyses further confirmed the interacting complexes. These results, together with amino acid sequence alignment, suggest that BRF1 and BRF2 play redundant or overlapping roles in regulating BIN2 stability. Our results fill the gap in our understanding of the brassinosteroid signaling pathways, and elucidate a novel step of regulation that could integrate other signals, such as abiotic stress.

Key Words: GSK3-like kinase, BRASSINOSTEROID F-BOX 1

Identification of a new thermal mediator from various Arabidopsis accessions with genetics and Next Generation Sequencing analysis

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The timing of transition from vegetative to reproductive development is crucial for plant to maximize reproductive success. Plants synchronize this timing of transition by a complex network of flowering genetic pathways in response to internal and external stimuli such as GA, photoperiod, and temperature, etc. Since ambient temperature is one of the major environmental factors modulating plant development and due to global warming, the understanding of this ambient temperature mediated flowering time has been getting importance. *Arabidopsis thaliana* is one of the major model system to study wide aspects of from genetics to molecular biology in plants, but the classical study has been mainly performed by dissecting traits caused by mutations in a few laboratory *Arabidopsis* strains such as Col, Ler, and WS. To bypass the limitation of this traditional approach, an alternative approach using wild strains of *Arabidopsis* has been introduced since the plentiful source of genetic variations can be found within naturally occurring populations of wild *Arabidopsis* accessions as adaptation to environmental changes. To identify a novel gene which may be responsible for the ambient temperature responsive flowering, flowering time of wild *Arabidopsis* accessions were observed at the ambient temperature changes, 16°C and 23°C, respectively. To test whether the non-responsive flowering phenotype in these *Arabidopsis* accessions was caused by already identified thermal mediators such as *svp* and *flm*, flowering time of F1 between wild *Arabidopsis* accessions x *svp* and wild accessions x *flm* were measured. After isolating accessions exhibiting complemented flowering time (in other words, close to wild-type flowering time) in this F1 generation, early flowering plants among F2 *Arabidopsis* accessions x Col grown at 16°C were pooled, DNA extracted, whole genome sequenced and analyzed. Our hypothesis is that early flowering F2 plants at 16°C may have the homozygous gene for the non-responsive flowering phenotype in ambient temperature changes. To further narrow down a responsible gene, 6 backcrosses to Col have been performed by phenotypic selection for early flowering time.

Biography

Postdoc, 2015-Present, Department of Life Sciences, Korea University, Korea

Postdoc, 2014-2015, Department of MCDB, University of Michigan, USA

Ph.D., 2006-2014, Department of MCDB, University of Michigan, USA

M.S., 2002-2005, Department of Plant Science, Seoul National University, Korea

B.S., 1994-2001 Department of Life Sciences, Ajou University, Korea

Effect Of Drought Stress On Aquaporin Isoforms Expression Level And Lipid Peroxidation Changes In Leaves In Cv. Horozkarası Grapevine Grafted On Different Rootstocks

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Rootstocks play a major role in grapevine tolerance against water stress as well as phylloxera. In the present study, greenhouse grown grapevines of cv. Horozkarası (*Vitis vinifera* L.) grafted on different rootstocks (110R and 5BB) were subjected to two irrigation levels (well irrigated and non-irrigated) and subsequently they were screened for their aquaporin isoforms expression level and lipid peroxidation (MDA). In this context, the expression pattern of different PIPs group of aquaporin (PIP1-2, PIP1-3, PIP2-1, PIP2-2) and lipid peroxidation (MDA) were measured in leaves. The influence of rootstock/scion interaction on plant adaptation to stress is briefly discussed. The main conclusion of present study was that rootstock not only effected physiologically or biochemically but also regulated molecular levels.

Keywords: PIPs group of aquaporin, *Vitis vinifera* L., 110R, 5BB

Biography

He is a PhD candidate at University of Gaziosmanpasa University, Tokat, Turkey. He is also working as a research assistant at Department of Horticulture, University of Kilis 7 Aralık, Kilis. He had him master degree on the harwood cutting on blackmullberry (*Morus Nigra* L.). Now, He is doing my PhD but still in the courses period. He is specialized in the areas of plants stress physiology, hormonal regulation under stress conditions, horticultural plants, stress induced changes concerned with tolerant mechanisms against water constraints. He is a member of ISHS.

The ameliorative effects of silicon on salt -stressed Sorghum seedlings and its influence on the activities of Sucrose synthase and PEP carboxylase

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Under salt stress, Silicon is considered a beneficial element for the growth of higher plants as it alleviates the harmful effects caused by salt. In the present study, Sorghum bicolor L. seedlings were grown hydroponically in growth units, filled with continuously aerated half strength of Hoagland-nutrient solution. Different treatments were manipulated to examine the negative effects of NaCl and the combined effect of NaCl with Si on seedlings growth, chlorophyll content, soluble protein content, ion accumulation, phosphoenolpyruvate carboxylase (PEPCase) and sucrose synthase (SS) activities. The salt induced decrease in seedling growth was relieved upon treatment with Si. Meanwhile, the sucrose and glucose levels were significantly increased and there was a reduction in sodium concentrations in the salt-stressed plants treated with silicon. The PEPCase activity in sorghum seedlings subjected to salt-stress was higher in the treatment with Si than that without Si, but did not significantly differ from that of control.

Comparative morphological responses of Landrace Dwarf Common Bean (*Phaseolus vulgaris* L.) Genotypes Collected from Western Mediterranean Region of Turkey under salt stress

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Common bean (*Phaseolus vulgaris* L.) is an important crop in terms of both nutrition and sustainable agriculture, which can be grown anywhere except Antarctica. The most effective method to increase the tolerance level of common bean, which is a sensitive crop to salt stress, is to determine tolerant genotypes and use them in breeding studies. Landrace cultivars, which are extremely important genetic resources, must be evaluated and examined for breeding studies. In this study, plant growth parameters of 16 landrace dwarf bean genotypes collected from Western Mediterranean region of Turkey at different salt concentrations were investigated. As the threshold value for beans was 1.5 ds/m, the salt concentrations were applied 0.5 (regular irrigation water), 2, 4 and 6 ds/m. The study continued until the first flowering was observed in the plants. In the plants harvested after the first flowering; plant height (cm), root length (cm), plant fresh and dry weight (g), leaf width and length (cm) and stem diameter (cm). In addition, plants were evaluated according to scale 1-5. The data obtained that indicated a positively moderate statistically significant relationship between plant fresh weight and root length, plant dry weight and leaf length, leaf width and leaf length. Besides, the salt concentrations applied were not statistically significant on plant dry weight and stem diameter. However, plant height, plant fresh weight, leaf width and leaf length characteristics decreased with increasing salt concentrations. Genotypes gave different responses to salt stress and the ADY4 genotype gave the best results. Besides the ADY4 genotype, prominent genotypes were detected as BY24, ISGA1 and IYOZ10.

Using the plant development criteria examined in this study, researchers can perform pre-screening studies on stress tolerance studies. Since pre-screening allows for the separation of genotypes at the early stage of plant development, it will provide labour and financial savings for large-scale breeding programme.

Biography

Kamile Ulukapi. She is a Assistant Prof, Organic Agriculture Programme, Vocational School of Technical Science at Akdeniz University. She completed her PhD degree from department of Horticulture in Akdeniz University. She worked on molecular and morphological characterization of common bean (*Phaseolus vulgaris* L.) by SSR markers in PhD. Currently she is teaching and conducting researches on plant breeding and biotechnology. She is correspondence author of this manuscript.

Engineered disease resistance in cotton using gene silencing to knock down Cotton leaf curl Kokhran virus-Burewala and Cotton leaf curl Multan betasatellite

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Cotton leaf curl virus disease (CLCuD) is caused by a suite of whitefly-transmitted begomoviruses that infect cotton annually in Pakistan, resulting in extensive losses. RNA-interference (RNAi) is proven technology for knocking down gene expression in viral pathogens by targeting vital genes. In this study, a siRNA construct was designed, transformed into cotton plants, and plants were tested for efficacy to silence the expression of the Cotton leaf curl Khokran virus-Burewala (CLCuKoV-Bu) AC1 gene, essential for replication initiation, the Cotton leaf curl Multan betasatellite (CLCuMB) coding region, β C1, and non-coding satellite conserved region, having a role in suppression of plant host immunity. Results of the fluorescence in situ hybridization and karyotyping assays for six T1 plants indicated the transgene was present as a single copy on chromosome number six. Transgenic cotton plants (n=13) and non-transformed, positive control (n=13) were subjected to challenge-inoculation by whitefly transmission of CLCuKoV-Bu and CLCuMB using ten adult viruliferous whiteflies per plant. The absence of characteristically severe leaf curl symptoms on transgenic plants, accompanied by greatly reduced begomoviral-betasatellite accumulation (confirmed by real-time PCR analysis) in transgenic cotton plants, provided evidence of knock down indicative of abatement of CLCuKoV-Bu/CLCuMB biological activity.

Audience Take Away:

- The RNAi hairpin construct developed to engineer virus resistance in cotton is designed to silence multiple targets of Cotton leaf curl genome and associated betasatellite, simultaneously. The audience can take away the concept of targeting multiple targets inside the plant viruses
- The method to transform prepared constructs In Cotton.
- By targeting the conserved regions like Replication initiation gene Ac1, pathogenicity determinant β C1 gene and SCR non coding region can provide the practical approach to combat the devastating virus of cotton crop.
- Audience can use this strategy to control some other Leaf Curl Viruses like Tomato Yellow Leaf Curl Virus and Tobacco leaf curl virus.

Biography

I am Bioinformatics (4 years) Graduate from one of the best state university of the country, Government College University Faisalabad, Punjab, Pakistan. I have done research work of my M. Phil in Molecular from the Center of Excellence in Molecular Biology, University of The Punjab Lahore, Punjab, Pakistan. In parallel to my thesis work I have published research papers in the domain of fusion protein against Lepidopteron insects, color cotton and Universal drug development against influenza strains from which I got near about 13 Impact Factor. Now a days I am a Ph.D scholar and doing my research work in Plant Molecular Biotechnology field.

Molecular Characterization of Landrace Common Bean (*Phaseolus vulgaris* L.) Genotypes Collected from Western Mediterranean Region of Turkey

Kamile ULUKAPI*
Akdeniz University, Turkey

Common bean (*Phaseolus vulgaris* L.), one of the most grown vegetables in the world, is an important food source especially for underdeveloped and developing countries. Landrace cultivars are very important genetic resources. Landrace cultivars which are highly genetically adaptable to the area where they are grown are particularly hand-exchanged by seed exchange. This situation causes the mixture of cultivars. Molecular characterization is widely used in differentiating the cultivars which are hard to distinguish by morphologically characterization. In this study, a total of 124 common bean genotypes collected from Western Mediterranean Region of Turkey were characterized using SSR markers. Four markers (GATS11, PVat007, BM199 and BM201) of the 30 SSR markers used in the study were found to be monomorphic for both pole and dwarf genotypes. Five of the markers (SSR-IAC46, SSR-IAC11, BM209, BM114, PVat008) used in the study did not work on both the dwarf and the pole genotypes. 22 Markers in dwarf genotypes and 19 markers in pole genotypes gave polymorphic results for molecular characterization. Analyzes of SSR primer pairs were performed separately for the dwarf and pole genotypes. The dendrogram obtained for the pole genotypes was divided into two main groups. It has been determined that the genotypes with the highest similarity level are ISari1 and ISari4, and the similarity level is close to 100%. According to the results of dendrogram, dwarf genotypes were divided into 2 main groups. Dwarf genotypes with the highest similarity level were identified as BY-4 and BY-24. In the hybridization studies to be made considering the analysis result; The use of AGB-10, BKara-1A or AGB-5 genotypes, which are genetically most distant by BY-4 or BY-24, may have beneficial effects in increasing the genetic variation in landrace cultivars.

In the study, 30 SSR markers were tested and their discrimination for common bean genotypes was examined. The research includes informative data for future molecular characterization studies. It contains results that will be useful for plant breeders, molecular characterization studies and primer selection.

Biography

Kamile Ulukapi. She is a Assistant Prof, Organic Agriculture Programme, Vocational School of Technical Science at Akdeniz University. She completed her PhD degree from department of Horticulture in Akdeniz University. She worked on molecular and morphological characterization of common bean (*Phaseolus vulgaris* L.) by SSR markers in PhD. Currently she is teaching and conducting researches on plant breeding and biotechnology. She is correspondence author of this manuscript.

Tempe Lake Management Strategies as the Clean Water Source Society in Wajo District, South Sulawesi, Indonesia

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Lake Tempe as one of the water resources in Indonesia has permanent puddle problems in settlement area. This problem limits public access to clean water sources. This study reviews the society's limited access of clean water around Lake Tempe and the management strategy of Lake Tempe as a source of clean water for the society. The research method is descriptive quantitative with survey approach. Descriptive statistical methods describe the condition of the society water access and the method of Analytical Hierarchy Process. The results showed that society water access was very low in accordance with the three indicators, namely the quality of water sources, the location of the source of clean water and the sustainability of the clean water availability. The analysis result of tempe lake management strategy as a source of clean water showed that government plays an important role compared with private institutions and society institutions. The main strategy in clean water management is the provision of communal water treatment supported by participation of the society.

Keyword: Clean Water, Society and Lake

Biography

Andi Rumpang Yusuf, Man, Master of Environmental Engineering, graduated from the Department of Environmental Engineering, Bandung Institute of Technology, in 1998. as a Doctoral Program Student in 2016, Graduate Program of Makassar State University. Since 1991 as a lecturer of Faculty of Engineering, Department of Civil Engineering University of Bosowa Makassar. Chairman of the Civil Department 1993-1995 and 1999-2001 Universitas 45 Makassar, and as head of Hidrolika laboratory of Bosowa University Makassar, Indonesia. She has participated in several international and national seminars.

Genetic Diversity of Native Maize in North Mexico

Esther Adriana Cenicerros-Ojeda¹, Octavio Martínez de la Vega², Humberto Reyes-Valdes³, Francisco Zavala-Garcia⁴, Jesús Axayácatl Cuevas-Sánchez⁵, Oralia Antuna-Grijalva⁶, June Simpson⁷

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⁵PhD, Universidad Autónoma Chapingo, México

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Maize (*Zea mays*) was first domesticated around 9,000 years ago in Mexico. Local farmers have played an important role in both selection and conservation of specific genotypes adapted to particular environmental conditions and geographical locations. These maize varieties provide a reservoir of genes that could be exploited to develop new materials with specific adaptations. Therefore, it is very important to preserve these varieties of maize. Since the 1940s, maize germplasm resources obtained throughout Mexico have been collected and conserved ex-situ in a number institutions. But, which landraces maize have greater diversity?

The goals in this work were, (1) obtain a realistic image of the existing diversity in the north regions of the country where landraces are grown, and (2) identify within these samples the most uncommon or “rare” genotype combinations. The SSR-based strategy using bulked DNA samples allows rapid processing of large numbers of samples and can be set up in most laboratories equipped for basic molecular biology. We analyze 496 maize landrace accessions collected from the Mexican states of Chihuahua, Coahuila, Durango, Nuevo Leon, Nayarit, Sinaloa, Sonora, and Tamaulipas with the aim of identifying “rare” genotypes using 14 microsatellite loci distributed across the 10 maize chromosomes.

Audience Take Away:

- New methodology for study diversity
- They were identified rare genotypes and supporting decisions in conservation of maize germplasm. But, it can be used to any other crop.

Biography

Esther Adriana Cenicerros Ojeda has been a post-doctoral fellowship in Laboratory of Molecular Markers and Molecular Genetics in Department of Genetic Engineering, CINVESTAV-Unidad Irapuato, México. She received his Ph.D. from Centro de Investigación y de Estudios Avanzados (CINVESTAV, México).

Infection by the false root-knot nematode *Nacobbus aberrans* breakdown resistance to wilting of *Phytophthora capsici* in *Capsicum annuum*

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Interactions in which are involved phytoparasitic nematodes and soilborne plant pathogens that cause root rots and wilting might result in the phenomenon known as breakdown resistance, which occurs when a cultivar resistant to a particular soilborne pathogen becomes susceptible after being infected by certain species of phytonematodes. Our research group has been using the model *Nacobbus aberrans*-pepper (*Capsicum annuum* L) CM334 resistant to *Phytophthora capsici* Leoninan, to determine the biochemical changes induced by the nematode, that could be associated to the breakdown of resistance to *P. capsici* in CM334 chilli pepper plants. Resistance of CM334 to *P. capsici* is associated with the phenylpropanoid pathway. At 21 days after inoculation with *N. aberrans*, plants of CM334 were inoculated with *P. capsici* and six hours after were harvested and analyzed. Enzymatic activity (peroxidase and L-phenylalanine ammonia-lyase) and total soluble phenols (TSP) were determined in CM334 plants inoculated with either or both pathogens (Na-Pc). On the other hand, the root system was chemically analyzed for their phenylpropanoid profile and total lignin content by HPLC-ESI-MS/MS and quantitative lignin assay respectively. The highest peroxidase activity (POD) was observed in radical system without root tip while the major L-phenylalanine ammonia-lyase activity (PAL) and TSP were detected in root tip (2.7 and 0.3 fold, respectively). The highest peroxidase activity in radical system without root tip was registered in plants inoculated with *P. capsici* (13.7 mM of tetraguaiacol mg⁻¹ protein min⁻¹) (P≤0.05). However, in root tip the main POD activity was detected in plants inoculated with both pathogens (P≤0.05). On the other hand, in both strata of radical system the highest both PAL activity (38.7 nM trans-cinnamic acid μg⁻¹ protein min⁻¹) and TSP (11.3 mg tannic acid g⁻¹ dry matter) were detected in plants inoculated with *P. capsici* only, meanwhile treatments that involved plants inoculated with *N. aberrans* (only or in combination with *P. capsici*) showed a significant reduction of both (P≤0.05). Some phenolic acids (Hidroxibenzoic -pHBA-, gallic, caffeic, syringic, ferulic, vanillic and chlorogenic) and the flavonoid quercetin-3-O-rutinoside (rutin) were found in the root system. Quantification of phenylpropanoid compounds revealed that chlorogenic acid is the dominant phenolic acid in CM334 root (from 209 to 547 μg g⁻¹ of dry matter). Concentration of chlorogenic, pHBA and ferulic acids was lower in roots of plants inoculated with *N. aberrans* than control (P≤0.05). The lignin content was similar in all treatments (P≤0.05). Reduction in the enzymatic activity of peroxidase, PAL, total soluble phenolics and phenolic acids in plants inoculated with *N. aberrans* could be associated with the breakdown of resistance to *P. capsici* induced by the nematode. These results can help to understand the biochemical changes induced by the synergism of two pathogens that affect *Capsicum annuum* resistance to disease.

Audience Take Away:

- Try to understand the complex etiology of a particular root diseases influenced by associated microorganism.
- Results can help to understand the biochemical changes induced by the synergism of two pathogens that affect *Capsicum annuum* resistance to disease.
- Understand the etiology of root diseases because they can be influenced by associated microorganism

Biography

José María Quintero-Patiño and Jaime Mejía-Benítez are undergraduate students at Universidad Autónoma Chapingo. They have been working in nematode-plant interactions under supervision of Prof. Noé López-Martínez in the laboratory of plant biochemistry and crop physiology. They try to determine the biochemical changes induced by nematodes to create a favorable environment that let them to complete their life cycle.

DAY 3

Keynote Forum

Global Conference on
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September 11 - 13, 2017 | Valencia, Spain

GPMB 2017

Global Conference on Plant Science and Molecular Biology

September 11 - 13, 2017
Valencia, Spain

Applying combinatorial biotechnology in potato as an example of crop improvement

Elena Rakosy-Tican*

Babes-Bolyai University Cluj-Napoca Romania



The application of combinatorial biotechnology in potato improvement means to apply as many biotechnological tools and analytical methods as necessary in order to improve a crop. Potato is the most important vegetable in the world, being among the crops amenable for *in vitro* manipulation. Although, there are many cultivars obtained by classical breeding potato is still sensitive to many diseases and pests, which cause great yield losses each year. Climate change and population increase pose new challenges to potato breeders. Some examples of combinatorial schemes aimed at transferring resistance to late blight, Colorado potato beetle, potato virus Y (PVY) and drought are going to be discussed. The wild species *Solanum bulbocastanum*, which is sexually incompatible with the crop, was used as a source of resistance to late blight, Colorado potato beetle and drought. *S. chacoense*, another wild species which can be crossed with potato, was first transformed for inducing DNA mismatch repair (MMR) deficiency using *Agrobacterium tumefaciens* carrying two different constructs (*AtMSH2* gene as antisense – AS, or dominant negative-DN form). Both wild type and transgenic highest leptine producing accession of *S. chacoense* were used as a source of resistance to Colorado potato beetle and PVY. The initial accession was not tolerant to drought but after *in vitro* selection and phenotyping some of resulting somatic hybrid clones proved to be also tolerant to drought, a new trait caused by combining somatic hybridization and MMR deficiency. Some of the mechanisms involved in somatic hybridization, genetic stability and composition as well as biochemical signals involved in biotic or abiotic stress are also going to be discussed. The biotechnological tools used to produce pre-breeding clones and their analysis involved: transgenesis, somatic hybridization using protoplast electrofusion, selection of the somatic hybrid clones using molecular markers, back-crossing with potato crop and application of embryo rescue, analysis of the resistance traits, ploidy determination using direct and indirect methods, genome composition analysis with genome *in situ* hybridization (GISH), trichome types and density analysis, *in vitro* stress selection and phenotyping. The integration of those tools and analytical techniques allowed the selection of clones with multiple resistance traits representing a novel germplasm to be used in potato breeding programs.

Audience Take Away:

- The audience will learn that similar combinatorial biotechnological schemes might be applied to other important crops.
- The design of complex biotechnological approaches to integrate multiple genes and traits into crops will help improve productivity and yield as well as resistance to biotic and abiotic stresses in different crops. This is a very important objective of today's agriculture in the face of climate change and population exponential growth.
- This can help both researchers and teachers to expand their research and there is no limit how all new achievements in genetics and genome editing might be combined in the future for better crops to provide enough food to the next generations.

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Biography

Prof. Elena Rakosy-Tican is specialized in the field of plant biotechnology starting from 1985, she developed research on plant somatic hybridization and genetic transformation. In the last years the main subject of her research is potato improvement by biotechnological tools. She published many papers (145) and participated in numerous international conferences. Elena used to be an active member of Pannonian Plant Biotechnology Association, Romanian Plant Tissue, Cell and Organ Culture Association and other national and international organizations. As a teacher she developed the first MSc course in Plant genetic engineering (1998) in Romania (TEMPUS project). Elena was/is coordinating national and international projects and has developed successful cooperation with different universities and research institutions in Europe.

Global Conference on Plant Science and Molecular Biology

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Cascading effects of inbreeding on plant-herbivore interactions

Rupesh R. Kariyat*

*Biocommunication and Entomology, Swiss Federal Institute of Technology, Zurich,
Switzerland*



Inbreeding is common in flowering plants, and have been found to negatively affect plant fitness. Until recently the effects of inbreeding on plant-insect-pathogen interactions haven't been well explored. Using a weed species *Solanum carolinense*, and a Solanaceae specialist herbivore *Manduca sexta*, we had been investigating how inbreeding affects plant defenses and herbivore counter defenses- using a combination of lab and field experiments, and molecular, behavioral and genomic tools. Our results show that inbreeding in *S. carolinense* negatively affect structural and chemical plant defenses, affects pollinator choice and reward, and disrupt the expression of key genes in the defense pathways. In addition, inbreeding also affects the emission of both constitutive and herbivore feeding induced plant volatiles that affect herbivore feeding, oviposition, and the recruitment of predatory insects. As a consequence of impaired defenses due to inbreeding, herbivores tend to locate, feed, grow and develop better on inbred plants, and even have better flight and dispersal abilities. These interactions have consequences for multi-trophic interactions, and the evolution of plant mating systems.

Audience Take Away:

- Inbreeding is common in flowering plants. Our study is the first comprehensive examination on the effects of inbreeding on plant-insect interactions.
- We use a wide range of techniques in our research: lab and field ecological experiments, collection and analysis of plant volatiles using GC-MS, transcriptomic analyses, and insect behavior.
- Our work will help understand adaptive signaling in plants, and their effects on plant-insect interactions, and evolution of plant mating systems.

Biography

I am a scientist in Biocommunication and Entomology group at ETH Zurich. I am a plant Biologist with interest in the evolution of plant mating systems, and species interactions. I did my PhD from Pennsylvania State University examining how inbreeding affects plant-insect interactions. At ETH, I currently work on plant defense and herbivore counter defenses in native and invasive weeds. I am originally from India, and moved to USA in 2015 to do my MS in Plant breeding and Genetics at University of Wyoming.

Global Conference on Plant Science and Molecular Biology

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Aluminium and drought stress: Physiological basis and genetic tools to improve crop resistance

Ivica Djalovic*

Institute of Field and Vegetable Crops, Novi Sad, Serbia



Aluminium (Al) toxicity and drought stress are the two major constraints for crop production in the world. Aluminium toxicity is a major agronomic problem on acid soils due to increased Al solubility at low pH causing inhibition of root growth. Our understanding of the physiology and genetic basis of resistance to Al³⁺ (the dominant Al ionic species at low pH) in important crop plants has increased greatly over the past 20 years, largely due to the application of genetics and molecular biology. This review mainly focuses on the interaction of Al and drought regarding root development and crop growth and yield on acid soils. Furthermore, the review summarizes the possible physiological mechanisms and genetic strategies to improve Al resistance with examples from several case studies; it provides novel insights into breeding crops adapted to these combined abiotic stresses. The availability of genes associated with Al resistance provides new tools for QTL analyses and breeding aimed at improving Al resistance of cultivated plants. The better understanding of these mechanisms and strategies is essential for improving plant performance in Al-toxic soils.

Audience Take Away:

- Aluminium (Al) toxicity and drought stress are two major constraints to crop production in the world. Traditional plant breeding has been successful in improving crop resistance to Al toxicity and drought stress.
- However, further improvements in Al and drought resistance will require a deeper understanding of the underlying molecular and physiological mechanisms; this knowledge will open up new avenues of molecular/physiological inquiry that should greatly advance practical breeding outcomes to enhance resistance of elite cultivars to Al.
- Development of new cultivars adapted to soils with low fertility and Al toxicity is needed to improve global food production and environmental sustainability.

Biography

Dr Djalovic received his PhD at the University of Novi Sad, and has over 100 articles published in national and international journals. He participated in scientific meetings in the country and abroad. He received several national awards: the prof. dr. Lazar Stojkovic Award granted by Matica Srpska (2010) and the special award October Award of the City of Kraljevo, for outstanding results achieved in scientific research in the field of agriculture (2010). The main focus of his research includes crop rotation, root traits, nutrient uptake and ion toxicity in the soil-plant continuum, crop growth and physiology in stressed environments (drought, soil acidity), breeding crops for adaptation to environments with low nutrient availability, etc.

DAY 3

Speakers

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Sessions on: Trends in Plant Science

Session Chairs

Abdul Razaque Memon
Usak University
Turkey

Bernardo Gonzalez Ojeda
University Adolfo Ibanez
Chile

Session Introduction

Title: From seeds to roots: The role of seed-borne endophytes for the composition of the active microbiome of barley roots

Viviane Radl, Helmholtz Zentrum München, Germany

Title: Effect of copper on the plant-bacteria interaction between Arabidopsis thaliana and the metal resistant bacterium Cupriavidus metallidurans CH34

Bernardo Gonzalez Ojeda , University Adolfo Ibanez, Chile

Title: Gene expression of metal transporting P-type ATPases in Brassica nigra and Brassica juncea grown at different levels of Cu and Zn

Abdul Razaque Memon, Usak University, Turkey

Title: Oat beta-glucan – miracle or reality?

Havrlentova Michaela, Research Institute for Plant Productio, Slovakia

Title: Differences in sodium dependence in sodium-loving plants

Hideyasu Fujiyama, Tottori University, Japan

Title: Flow cytometry as a support tool for the identification of cryptic species?

Errol Vela, AMAP, Universite de Montpellier, France

Title: The effect of industrial aerosol emissions on the heavy metals content and distribution in herbaceous plants

Saglara Mandzhieva, Southern federal university, Russia

Title: Patterns of nucleotide diversity on the waxy locus linked to AAC of rice (Oryza sativa L.) in northeast India

Gayle Alisha Kharshiing, North Eastern Hill University, india

Title: Cucurbitacin-containing phytonematicides induce concentration-responses on selected nutrient elements in leaf tissues of green bean

Phatu William, University of Limpopo, South Africa

Title: Drought stress and air humidity provoke stomatal functioning

Peiman Zandi, Institute of Environment and Development in Sustainable Agriculture, China

Title: Cowpea potential, production constraints and utilization in South Africa

Maletsema Alina Mofokeng, Agricultural Research Council-Grain Crops, South Africa

Title: Impact of Elevated Ozone and Wounding on Foliage Stress Volatile Emissions and Gas Exchange of Tasmanian Blue Gum (Eucalyptus globulus)

Arooran Kanagendran, Estonian University of Life Sciences, Estonia

Title: Photosynthesis and Growth Responses of Mustard (Brassica juncea L. cv Pusa Bold) Plants to Free air carbon dioxide Enrichment (FACE)

Baishnab Tripathy, Jawaharlal Nehru University, India

Title: Recombinant glycinebetaine improves metabolic activities, ionic balance and salt tolerance in diazotrophic freshwater cyanobacteria

Prashant Swapnil, Banaras Hindu University, India

Title: DOF Affecting Germination 1: A tool to unravel how plants respond to drought stress in seeds

Ruta Veronica, University of Rome, Italy

Title: Improving faba bean for sustainable agriculture in dry areas

Fouad Maalouf, ICARDA, Lebanon

Title: Postulation of Rust Resistant Genes in High Yielding Wheat From Wild Species by Back-Cross Method

Khwaja Abdul Nayeem, College of Agriculture Khandala, India

Title: Sea buckthorn (Hippophae rhamnides L) A Magic Shrub for Socio Economic Development of Pakistan

Asad Hussain Shah. University of Kotli, Pakistan

Title: Efficient production of haploid durum wheat plant via maize pollination

AYED Sourour, Research Center of Agricultural and Development in Northwest Semi-arid regions of Tunisia, Tunisia

Title: The effects of beneficial nano-particles and nano-structured fertilizers on plants growth

Mohsen Janmohammadi, University of Maragheh, Iran

From seeds to roots: The role of seed-borne endophytes for the composition of the active microbiome of barley roots

Luhua Yang¹, Jasmin Danzberger¹, Yvonne Biggot¹, Prof. Michael Schloter¹, Prof. Peter Schroder¹, Viviane Radl^{#1}

¹Helmholtz Zentrum München, Research Unit Comparative Microbiome Analyses, Germany

Endophytes are microorganisms colonizing plant internal tissues. They are ubiquitously associated with plants and play a major role in plant growth and health. Among all endophytes, those found inside seeds are particularly interesting, as they are the first to colonize the tissue of the seedlings. Although significant efforts have been made to determine the composition of the endophytic bacterial communities, less is known about their activity. Therefore, we investigated the active bacteria communities residing in seeds and their relevance for composition of root tissues of barley in different growth stages, using an RNA-based approach. Moreover, metagenomic analyses of seed-borne root endophytes were carried out to obtain information about their genomes. We found out that members of the genera *Phyllobacterium*, *Paenibacillus* and *Trabusiella* were the most abundant active bacteria inside germinating seeds. The presence of the latest families was also confirmed by cultivation (e.g. *Panaenibacillus hordei* and *Pantoea agglomerans*). Though some of these populations were also found in the roots, we found a greater influence of soil microbes on the composition of the community, particularly at later growth stages. Metagenomic analysis corroborated the great dominance of *Enterobacteraceae* and *Pseudomonaceae* in roots of plants growing in axenic systems. In general, we detected genes related to functions assumed to be essential for bacteria colonizing plant tissue, such as antioxidative stress enzymes, osmoprotectants, biofilm formation, etc.. However, bacterial endophytes might possess different strategies to “communicate” with the host plant and evade their immune system, as we detected different pathways for the synthesis or regulation of plant signaling molecules, e.g. indole acetic acid and ACC deaminase. We hypothesize that the seed endophytes play a role during germination, but becomes less relevant as the plant develops, where endophytic bacterial populations most probably originates from the soil.

Audience Take Away:

- Our findings show that, although the diversity of bacteria communities colonizing seeds is relatively high, a few groups of organisms are particularly abundant among the active part of the community.
- Moreover, we observed they certain bacterial species, such as *Pantoea agglomerans* are frequently described to be present in plant tissues (other than barley), bringing to the idea that they might actually be selected by the host plant due to beneficial traits they possess.
- I observe an increasing interest of plant breeders on seed microbiome during a biological control of plant disease meeting of the “German Society for Phytomedicine”, as they might bring benefits to the host plant.
- Knowledge about: (i) the composition, (ii) but also in the stability and, even more important, (iii) the functions these bacteria are required in order to fully exploit their biotechnological applications.

Biography

Viviane Radl studied microbiology and immunology at the Federal University of Rio de Janeiro (2001) and got her PhD in microbial ecology at the Technische Universität München (2005), where she did a postdoc on the Influence of the cultivation of transgenic plants and soil microbial communities. Lately she went back to Brazil (Embrapa Agrobiologia-2010-11) where she started to work on the selection and characterization of rhizobial strains to be used as inoculant for cowpea, where she described a novel rhizobial strains. Since 2011 she is working as a research associate at the Helmholtz Zentrum München on plant-microbe interactions.

Effect of copper on the plant-bacteria interaction between *Arabidopsis thaliana* and the metal resistant bacterium *Cupriavidus metallidurans* CH34

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Chilean soils, as many other in the world, are rich in metals, most notably copper. As a result of the contamination leached from copper tailings, freshwater sources destined for irrigation of agricultural soils are compromised by excess of metallic pollutants. Although copper is a micronutrient for plants, at high concentrations it produces toxic effects, inducing chlorosis, growth inhibiting, and potentially altering plant root exudation thus affecting the signaling and nutrient network between microorganisms and plants, specially in the rhizosphere environment. Among other effects, the rhizomicrobiota can modify the metal stress plant response, increasing or decreasing metal mobility and availability. The soil borne bacterium *Cupriavidus metallidurans* CH34 is a multi-metal resistant microorganism that carries in its genome two mega-plasmids, pMOL28 and pMOL30, which encode several metal resistance genes, including at least 30 export and import metal pumps, chelating agents, and siderophores. These elements could result in changes in the availability of metals present in soil, and therefore, modify their effects on plants. The interaction of metal resistant strains such as *C. metallidurans* CH34 with plants has been scarcely addressed. The aim of this study was to characterize the interaction between the model plant *Arabidopsis thaliana* and *C. metallidurans*, when subjected to copper stress, to answer questions such as: is *C. metallidurans* capable of affecting plant growth, respond to plant exudates, or to differentially express metal resistance related genes? Plant and bacteria co-cultivation assays were performed to measure plant growth parameters and metal accumulation in whole plant tissue as well as shoot and root metal translocation and accumulation. The results showed that the presence of strain CH34 positively affected plant growth parameters at relatively low copper concentrations, but was detrimental for the plant at higher copper. This observation may be explained because this bacterium not only mobilizes Cu but also Zn, Co, Mo and B. In addition, root exudates from plants exposed to copper showed higher levels of sugars and aromatic compounds compared with those from non-copper stressed plants, thus significantly changing the rhizosphere environment, and therefore the *C. metallidurans* activity. Finally, the bacterium gene expression was tested by qRT-PCR in hydroponic plant-bacteria cultures. As expected, genes related to metal resistance (*copK*, *copC* y *copC* (CHR2)) were up regulated in the presence of the plant and the metal. Interestingly, plant colonization and rhizospheric adaptation functions (*phaC1* and *tonB* genes) were also up regulated in the presence of the plant, and the plant and the metal. Taken together, these results show that the plant – metal resistant bacteria interaction is clearly modified by the presence of metals, thus affecting the rhizosphere environment and plant's performance.

Audience Take Away:

- Metal resistant bacterial strains, presumably having “neutral effect” on plants, can modify plant's performance and rhizospheric environments when metals are present.
- Highlight the relevance of expanding plant-bacteria interaction research not only to known “plant growth promoting rhizobacteria”, but also to other soil-borne bacteria.
- Metals (trace or higher levels) effects must be carefully addressed when plants are cultivated in several contexts (agronomic use, phytoremediation procedures, etc.)

Biography

Bernardo González is a biochemist by profession and holds a degree in Biochemistry and a PhD in Biological Sciences. His academic and research career began at Universidad Católica de Chile, where he also held positions managing academic and postgraduate programs. At the same time, he has been a member of numerous committees and commissions, most notably his participation in MINEDUC; CONICYT; FONDECYT, in which he became Chairman of the Science Council, FONDEF, INACH, among others. His scientific contributions include 90 publications in international journals, 10 book chapters and non-WoS publications, and more than 200 communications to national and international scientific meetings.

Gene expression of metal transporting P-type ATPases in *Brassica nigra* and *Brassica juncea* grown at different levels of Cu and Zn

Abdul Razaque Memon*
Usak University, Turkey

Several hyperaccumulator plant species especially the species in Brassicaceae have been extensively investigated for their metal accumulation and detoxification. A number of regulatory mechanisms, including heavy metal absorption, transportation, chelation and detoxification have been developed by metal hyper accumulator plants for their survival in metal polluted environment. HMAs are particularly interesting and according to many recent studies they have been shown a key player in the metal hyperaccumulation. In this regard we have analyzed the gene expression data of model crop plants in Brassicaceae family by searching several databases available online. The criterion observed in this research is that the sequences of different metal induced genes have functional and evolutionary similarities among species. Our hypothesis is that the functionally related sequences of the genes from different species or organisms will be having conserved pattern or motif which will be possibly related to hyperaccumulation of heavy metals. Our qR-T PCR analysis showed that PAA1 and HMA4 play an important role in Zn and Cu accumulation in *B. nigra* and *B. juncea*. Interacome and 3D structural analysis showed the interaction of HMA4 with other metal transporters. This interaction is important to understand the role of these ATPases and their interacting molecules in detoxification of the toxic metals from the cells of accumulator plants.

Here, I will overview these findings and highlight their contribution to the field of plant metal homeostasis, and will discuss the emerging avenues of -omics technologies and their impact in understanding the mechanisms of metal accumulation and tolerance.

Audience Take Away:

- Heavy metal pollution of soil is a significant environmental problem with a negative potential impact on human health and agriculture and phytoremediation technology could be an effective and environmentally-friendly solution for cleaning heavy metal contaminated soils.
- Exploiting hyperaccumulating plant species and identifying metal accumulation genes is currently focal point for phytoremediation or phytomining.
- To understand the molecular mechanism for improving phytoremediation ability of accumulator plants we carried out heavy metal induced gene expression work by using microarray technology and R-T PCR experiments. Our data showed that the metal transporting P1B ATPases play an important role in metal accumulation in *B. nigra* and *B. juncea*.
- Additionally the Interacome and 3D structural analysis showed the interaction of HMA4 with other metal transporters. This interaction is important to understand the role of these ATPases and their interacting molecules in detoxification of the toxic metals from the cells of accumulator plants.
- Our research could provide some technical opportunities to the molecular biologists and agriculturists to engineer the plants with efficient metal uptake, transport, and high accumulation capacity in leaves or shoots of accumulator plants. This will surely help in enhancing the efficiency of phytoremediation of polluted areas.
- This research will also help the scientists to design better strategies to improve stress tolerance of crop plants.
- Is this abstract connected to an organized session? If yes, please provide full session title. Could be organized in Trends in Plant Science session

Global Conference on Plant Science and Molecular Biology

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Biography

Dr. Abdul Razaque Memon (BSc (Hons), MSc, PhD, DSc) is currently working as a Professor and Head of the Department of Molecular Biology and Genetics at Usak University, Usak, Turkey. He got his BSc (Hons) and MSc. in Agricultural Chemistry from the University of Sindh, Pakistan. He obtained one PhD. from Ege University, Izmir, Turkey in Agriculture and second one from Nagoya University, Nagoya, Japan in Biochemistry. He did 3 years postdoctoral fellowship in the Department of Botany, University of British Columbia, B.C., Canada and 1 year research fellowship in the Lund University, Sweden. He later joined the Department of Biology, Middle East Technical University, Ankara, as an Assistant Professor and then promoted to an Associate Professor in the same department. He moved to USA and worked as a visiting professor for one year at the University of North Carolina, Raleigh and then worked as a senior research scientist in Molecular Biology at the University of Texas, Austin (4 years), Texas A and M University, College Station (2 years) and Louisiana Cancer Research Center, Louisiana State University, Shreveport (1 year). He later joined Turkish Science Research Council (TUBITAK) in 1997 as a Principal Scientific Officer and Head of the Plant Molecular Biology and Genetics Laboratory. After 12 year of research at TUBITAK, he moved to Bosnia and Herzegovina and joined as a full professor and coordinator of the Department of Genetics and Bioengineering at the International University of Sarajevo, Sarajevo. After 6 years of teaching and research he moved back to Turkey and joined Usak University. He also worked as a visiting professor at the Biochemistry Center, Heidelberg University, Germany, in the Department of Plant Sciences, Oxford University, UK and CNRS, Institut de BiologieMoleculaire des Plantes (IBMP), Strassbourg, France and have still active research collaboration with Bielefeld University and Munich University, Germany. He authored 3 books and published around 200 papers in peer reviewed journals. His research work is mostly concentrated in two different areas of molecular biology and genetics. One is in the field of molecular cell biology and protein trafficking in plant cells and second one is on the heavy metal induced gene expression in plants. He supervised 20 PhD and MSc students in the area of stress induced gene expression and vesicular trafficking in plants. Currently 3 postgraduate students working on –omics technology under his supervision.

Oat beta-glucan – miracle or reality?

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¹NAFC – Research Institute of Plant Production, University of Ss. Cyril and Methodius, Slovakia

²Research and Breeding Station, Vigl'as-Pstrusa

Plants have evolved to live in environments where they are often exposed to different stress factors. Permanently changing climatic conditions in the environment as well as biotic and abiotic forms of stress can negatively affect the life cycle of crops what can result in reduced seeds quality and loss in yield. Being sessile, plants have developed specific mechanisms that allow them to detect precise environmental changes and respond to complex stress conditions, minimizing damage while conserving valuable resources for growth and reproduction and, on the other hand, human consumption. Oats have long been recognized as a cereal of superior nutritive value and its grain composition is very favorable for human nutrition and health-prevention. Currently, the demand for oat is increasing. Compared to other cereals, oat contains significantly higher amounts of essential amino and fatty acids, dietary fibre and its soluble fraction beta-glucan as well as other beneficial phytochemicals (tocopherols, avenanthramides and others). (1-3)(1-4)-beta-D-glucan works in the plant also as a tool of plant protection. In some cereals, especially seeds of oat and barley, beta-glucan is located in cell walls. Higher amounts of this polysaccharide have been detected in naked seeds compared to hulled, so there is an assumption of protecting role of the polysaccharide in the cell to resist the effect of stress factor to the intracellular space (especially the DNA). In heat stress, higher amounts of beta-glucan have been accumulated in the seeds of oat as a regulator of humidity in the plant, again, with the assumption of protecting role in heat stress conditions. In oat, plants with higher amount of beta-glucan were more resistant to biotic stresses caused by pathogens such as *Fusarium* or leaf-rust. Beta-glucan was observed only in some cereals, plants growing in broad-spectrum of regions, very often of extreme inhospitable conditions. On the other hand, the physical and physiological properties of cereal beta-glucans are of commercial and nutritional importance. Increasing interests during the last two decades are largely due to their acceptance as functional, bio-active ingredient. Among grasses, mature grains of barley and oat are suitable natural sources of health beneficial beta-glucans with the average amount 41.6 g.kg-1 and 34.9 g.kg-1, respectively. Naked seeds dispose of the highest amount of this cell wall polysaccharide. Genotype and environment are factors influencing the amount of beta-glucans, whereby genotype is superior. Higher temperature during grain maturation and lower precipitation increase its amount, also N and Se fertilization. On the other side, warehousing decrease the portion of soluble beta-glucans in grains, but cooling can slower it. Hydrogels prepared from cereal beta-glucans are one of possibilities to increase this component in food products and make foods healthier. Oat glucans in the amount 2% improve the total tastiness of bread and soften the acid taste of ketchup. The potential of beta-glucan in oat as a natural tool of plant protection and its adaptation as well as its uses in food industry are discussed in the contribution. This research was financially supported by the project: APVV-0398-12.

Audience Take Away:

- The audience will hear that *Avena sativa* is an excellent crop with multifunctional uses in agriculture, human nutrition and plant research, in general – it is promising to cultivate the plant and use them in many ways.
- Cereal beta-glucan located in the cell wall in oat seed is a natural protector against many stress forms and its consumption can be beneficial also for humans.
- Many beneficial substances are located in the plant – beta-glucans, dietary fibre, different polyphenols, avenanthramides... - all of them with different biological activity - can be used for human well-being and disease prevention.
- Oat is a natural crop cultivated in Slovakia, the presentation will show possibilities how the plant can help the Slovak agriculture, economy, environment and human health.

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Biography

Michaela Havrlentova was born in 1974. She lives with her family in Slovakia, in a small village. After graduating her study of biology at the Comenius University in Bratislava in 1997 she has been working at the Research Institute of Plant Production in Piešťany. Her activity is seeds quality (especially cereals and oilseeds) influenced by genotype and environment. Since 2012 she has been teaching at the Faculty of Natural Sciences of the University of Ss. Cyril and Methodius in Trnava. In her lectures she is oriented in general biology and plant biotechnology. She likes reading books, nature and discussing with people.

Differences in sodium dependence in sodium-loving plants

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Tottori University, Japan

Sodium (Na) is one of the most harmful elements to plants, and Na accumulation in soils is a serious problem in arid land agriculture. High Na concentrations in soil decrease plant growth by the following mechanisms. First, all Na salts are water-soluble and decrease the osmotic potential of soil solutions, which inhibits water absorption by plants. Second, Na competitively inhibits the absorption of macro-elements, such as potassium (K), calcium (Ca) and magnesium (Mg) by plants, resulting in deficiencies in these elements. Third, Na increases soil pH and inhibits the absorption of micro-nutrients, such as iron (Fe) and manganese (Mn), causing deficiencies in these elements. However, some plant species in the family Chenopodiaceae are Na-loving and require Na for growth. The response of Na-loving plant species to soil Na concentrations is completely different to that of highly Na-tolerant plant species. In most plant species, 100% relative growth can be obtained under Na-free conditions, even if they are highly Na tolerant. However, the growth of Na-loving plant species increases with an increase in soil Na concentration and reaches a maximum at certain Na concentrations. The Na concentration at maximum growth differs among Na-loving plant species. For example, under hydroponic conditions, *Salicornia bigelovii* exhibited maximum growth at 200 mmol kg⁻¹ Na (2/5 that of sea water) and could not survive under Na-free conditions. In Swiss chard that showed maximum growth at 80 mmol kg⁻¹ Na, we found that Na enhanced the absorption and transport of nitrate (NO₃⁻), increased NO₃-reductase activity, and played a role in stomatal opening. In most plant species, K plays a role in these functions. We therefore propose that Na plays a role similar to K in Na-loving plant species, and that differences in Na dependence among Na-loving plant species is related to their ability to substitute Na for K.

Flow cytometry as a support tool for the identification of cryptic species?

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²French botanical Society, France

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⁴EcoGozo Regional Development Directorate, Malta

⁵CNRS – I2BC, France

While floristics is the science that tries to elaborate tools for identifying plant biodiversity, taxonomy is the science that tries to distinguish biological entities, mainly genera, species, and infraspecific taxa (subspecies, etc.). Unfortunately a significant proportion of species or subspecies are not obvious to distinguish to the eye. Closely related species which do not bear evident macro-/micro-morphological criteria to discriminate them are classically termed ‘cryptic species’, and we used here ‘semi-cryptic’ when they only just bear a few subtle criteria. These semi-cryptic species are also very controversial within the scientific community because some (called lumpers) consider subtle characters only as part of the variability of the species and others (called splitters) consider them sufficient to circumscribe distinct species. A large part of these cryptic or semi-cryptic species or subspecies belongs to polyploid complexes, including hybridisation by allopolyploidy. Indeed, polyploidy is not only a major and rapid cause of speciation in vascular plants, it is also a major problem for the interpretation of phylogenies and their use in the delimitation of species. Thus, in polyploid complexes DNA phylogenies are hardly helpful and knowing the ploidy level of plants would be auspicious to help taxonomists identify semi-cryptic species and/or confirm the reliability of various prospective morphological criteria. Therein, even if it is not as accurate as chromosomal counting, flow cytometry is a relative cheap and rapid method to quantify the DNA content and consequently to estimate the ploidy level of a plant individual or organ. We have measured DNA content of hundreds of plant individuals and populations of several species and subspecies of various genera where polyploidy complexes are known, mainly Monocots as Amaryllidaceae (*Allium*, *Narcissus*), Asparagaceae (*Muscari*, *Prospero*, *Oncostema*) and Poaceae (*Avena*, *Avenula*, *Brachypodium*) but also Dicots as Araliaceae (*Hedera*) or Ferns as Aspleniaceae (*Asplenium*). In species-poor but overlooked complexes as *Avena*, *Brachypodium* or *Muscari*, we were able to confirm the presence of semi-cryptic species as new records for continental France. In another similar case as *Asplenium* and *Oncostema* we just initiated a reference database in order to explore cryptic biodiversity in understudied areas as Algeria. In the ivies (*Hedera*), introduced ornamental material is frequent in urban areas and cytometry helped us to confirm identification and consequently the probable geographical origin of the introduction. Finally, in species-rich and/or highly polyploidy complexes as *Allium*, *Avenula*, *Narcissus* or *Prospero*, ploidy levels help us to understand species delimitation and to achieve reliable criteria for clarifying synonymy and/or describing new taxa (classical species or natural hybrids).

Audience Take Away:

- In summary, flow cytometry is a modern tool that can successfully supplement, if not replace, the classical karyology.
- As a result, flow cytometry is an efficient support tool for the identification and/or description of semi-cryptic species of vascular plants, especially within polyploid complexes.
- It is why it should be developed in megadiverse but poorly known countries across the five continents.

Biography

Errol Vela is a field naturalist that obtained Ph.D. on plant ecology at Aix-Marseille University in 2002. After a 5-year period as biodiversity expert in a private company, he devoted himself to teaching and research at Aix-Marseille then Montpellier universities. His main lectures concern environmental expertise, functional ecology, climatology and mostly botany. His current researches are devoted to studying the Mediterranean hotspot biodiversity, particularly in terms of evolutionary biogeography, descriptive taxonomy and identification tools. He is particularly involved in cooperation with countries from southern and eastern Mediterranean (Algeria, Tunisia, Lebanon, Iraq...). He is the current Red List authority coordinator of the IUCN Mediterranean plant specialist group.

The effect of industrial aerosol emissions on the heavy metals content and distribution in herbaceous plants

Saglara S. Mandzhieva*, Victor A. Chaplygin, Tatiana M. Minkina, Tatiana V. Bauer, Marina V. Burachevskaya, Svetlana N. Sushkova, Inna V. Zamulina

Southern federal university, Russia

The territory of southern Russia warrants special attention, because this region is the largest producer of agricultural crops and a large industrial center. The close neighborhood of agriculture and industry poses some environmental problems, including the environmental pollution with heavy metals. Under increasing anthropogenic impact, the research of heavy metals content and distribution in plants is very important.

The aim of this study was the assessment of Cd, Pb, and Zn accumulation by different herbaceous species of the families Poaceae and Asteraceae and soils on the technogenic areas around Power station. The investigation has been carried out on the monitoring plots on the areas around Novochoerkassk Power Station (Rostov region, South of Russia). The long-term monitoring observations has been initiated in 2000. Soil and plant samples were taken annually in the second decade of June. *Ambrosia artemisiifolia* L., *Achillea nobilis* L., *Artemisia austriaca* Jaqc., *Tanacetum vulgare* L., *Elytrigia repens* L., and *Cichorium intybus* L. were studied.

The results of the 17-year-long monitoring studies showed that the high level of anthropogenic load related to the atmospheric emissions from the Power Station aggravates the accumulation of heavy metals in herbaceous plants. The increasing of all studied HM concentrations in the wild plants growing within 5 km from the Power Station along the predominant wind direction was investigated. Contamination with Pb, and Cd is revealed in plants growing near the Power Station. Correlation between the accumulation of metals in different herbaceous plant species and the distance from the emission source is revealed. The metals accumulation and distribution in the aboveground organs and roots vary among the herbaceous plants species. The main factor of the heavy metals distribution is the individual physiological features. *Ambrosia artemisiifolia*, *Artemisia austriaca*, *Achillea nobilis*, and *Tanacetum vulgare* have the highest amounts of metals in their aboveground organs under technogenic contamination.

Audience Take Away:

- Our results may help to solve fundamentally new problems in the field of biomonitoring and bioindication, biodiagnostics of ecosystems status.
- The results can be used in determining the permissible loads on the soil and plants, and in the forecast of the soil-plant system stability for pollution.
- The results of our investigation can be used in scientific, industrial and environmental organizations in the monitoring of plants and soil in order to identify the fact and their level of pollution, determining permissible loads on the plants and soil, the excess of which can lead to dangerous environmental effects, assessment of contaminated soil properties, prediction of soil resistance to contamination.
- The results presented here can be used for lectures and practical training courses on “Ecology”, “Chemical contamination of soil”, “Ecological soil functions”, “Environmental soil science.”

Global Conference on Plant Science and Molecular Biology

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Biography

Saglara S. Mandzhieva, Doctor of Soil Science

Leading Researcher and Head of laboratory in Academy of biology and biotechnology of Southern federal university

ORCID ID 0000-0001-6000-2209

Research interests: soil science, ecology, biogeochemistry, environmental chemistry.

Author of over 322 scientific publications, including 219 articles, 4 monographs.

Publications: Web of Science - 26, Scopus - 42

Citation indexes: Web of Science - 71, Scopus – 125.

H-index: Web of Science - 6, Scopus – 7.

Participant of academic exchange programs “Mevlana”, Turkey, 2014.

A graduate of Leadership Program “Open World” (USA) on the topic “Environmental Protection in the United States”.

Patterns of nucleotide diversity on the waxy locus linked to AAC of rice (*Oryza sativa* L.) in northeast India

Gayle Alisha Kharshiing^{*1}, Ph.D., Nikhil K. Chrungoo¹

¹North Eastern Hill University, India

North East India represents one of the world's biodiversity hotspots which harbours an enormous gene pool. Starch quality mainly controlled by the Waxy locus codes for GBSSI providing a unique model for elucidation of regulation at the molecular level. Sequence analysis of this region is expected to give novel insights into the structure, function and evolution of the different set of alleles encoding different levels of granule-bound starch synthases in rice varieties. A comprehensive comparative analysis of the genomic sequences targeting the 7.5 kb Wx locus on 35 rice accessions identified wx, Wxop, Wxb, Wxin alleles unique to waxy (0-5%), very low (6-10%), low (11-20%) and intermediate (21-25%) respectively. Further, investigations on the nucleotide sequences of rice germplasm have revealed the presence of two alleles (Wxa1 and Wxa2) that control accumulation of amylose content in rice endosperm. Wxa1 allele was found to be present in rice cultivars with apparent amylose content (AAC) ranging from 25-27% (High I) and Wxa2 allele was uniquely present in rice cultivars with AAC ranging from 27-33% (High II). A molecular phylogenetic tree constructed using the Wx gene sequence gave rise to six distinct clades corresponding to the allele wx, Wxop, Wxb, Wxin, Wxa1 and Wxa2. The Wxb, Wxin and wx allele joined the japonica lineage whereas allele Wxop, Wxa1 and Wxa2 were linked to indica lineage. These results strongly suggest that allelic diversification occurred after divergence of the two main varietal groups (indica and japonica) and molecular evidence supporting the single evolutionary origin of domesticated rice.

Audience Take Away:

- Although this paper surveyed the complete sequence of only one locus, its strength lies in the relatively broad sampling of both japonica and indica varietal groups harbouring all six Waxy (Wx) alleles which serve as identifiers for each class of rice based on the apparent amylose content. Furthermore, the specific genomic patterns of SNP's and INDEL's of the Wx gene unique to each Wx allele, has helped to determine the single evolutionary origin of domesticated rice. Also, a novel allele Wxa2 was revealed which distinguishes two sub-groups of high amylose class rice germplasm and a molecular marker was designed which will aid as a selection tool for breeding programs for rice based on their AAC content. The phylogenetic patterns detected in this study suggested two likely origins of domesticated rice, with indica originating in eastern India and japonica originating in southern China. The Wx gene, best described as a diversification gene, is selected in response to cultural preferences in some areas of the world but not uniformly favoured. My research findings will help elucidate the benefits of uncovering information in a highly polymorphic Wx locus in monocot plants which has been found to undergo multiple domestication processes followed by extensive introgression of strongly selected domestication alleles.
- Increasing demands of rice varieties with higher eating quality dictate the market value of the commodity particularly in rice consuming countries, hence playing a major role in development of new varieties. By targeting and sequencing larger regions of domestication genes, new and valuable information can be uncovered which will aid in the design of molecular markers to identify new varietal species or help understand. Variation found at the sequences of the Wx locus in landraces of rice, gives an opportunity to explore the effect of multiple alleles affecting different phenotypes relating to agronomic traits. The primary goal of this study was to assign phenotypic values to the different alleles at the Wx locus and to explore novel alleles which would help in distinguishing the large group of high amylose class. In the present study, we used 35 rice accessions distributed in different parts of north-east India and classified them into different categories based on their apparent amylose content. GBSS activity profiles of the Wx alleles provided valuable insights into the physiological mechanism underlying the allelic variation at the Wx locus. The degree of GBSS activity was in accordance with the AAC phenotype (wx < Wxop < Wxb < Wxin < Wxa1 < Wxa2) with wx allele having the lowest activity and the Wxa2 allele the highest supporting the classification of the six alleles.

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- The origin of Asian rice (*O. sativa*) has long been a puzzle to biologists and over the last two decades, independent origins domestication of japonica and indica has gained support largely from molecular data analysed by traditional phylogenetic methods. However in our study, sequence analyses of the Wx gene showed strong support for only a single origin of domesticated rice. Even with the inclusion of the annual ecotype (*O. nivara*) of *O. rufipogon* in the dataset that we have analysed reveal a closer relationship between the two ecotypes thereby establishing the fact that although both japonica and indica may have diverged into different separate groups they share single origin of domestication event. The finding that rice has a single origin was also supported by presence of selective sweeps shared by indica and japonica since the shared sweeps are related to domestication and that the same or different haplotypes may be fixed in the domesticated varieties. The shared sweeps were initially thought to arise from introgression between variety groups as a result of post domestication hybridization. Aside from the rc, sh4 and progl domestication genes, the starch biosynthetic (Wx) gene presents itself as one of the diversification gene with diverse alleles fixed in both variety groups all contributing to a phenotypic difference in rice cultivars. The polymorphic nature of Wx gene will help shine a light in uncovering information on other domestication genes which harbours potentially multiple alleles and such stable polymorphic regions can serve as aids in the study of evolutionary biology.

Biography

Gayle Alisha Kharshiing, a native to the north-eastern region of India is a region that is recognised as one of the biodiversity hotspot regions of the world. The potential of uncovering enormous amount information this region holds drove her into a career in research. She successfully completed her graduation and a master's degree program the field of Biotechnology during which she was trained in techniques such as High throughput sequencing, NGS, Real-time PCR etc. and acquired two publications. She is currently in her final year of Ph.D under the guidance of Prof. Nikhil K. Chrunghoo, under the Dept. of Botany.

Cucurbitacin-containing phytonematicides induce concentration-responses on selected nutrient elements in leaf tissues of green bean

Mashela, P.W.*¹, PhD., Pofu, K.M.², PhD, Mafeo¹, T.P., PhD.

¹University of Limpopo, South Africa

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Cucurbitacin-containing phytonematicides consistently reduce nematode population densities in various crops. However, there is no information on how these products affect the accumulation of essential nutrient elements in crops. The objective of this study was to determine the influence of Nemafric-BL and Nemarioc-AL phytonematicides on accumulation of essential nutrient elements in leaf tissues of green bean (*Phaseolus vulgaris*) under greenhouse conditions. Weekly application of phytonematicides each at 0, 2, 4, 8, 16 and 32%, were assessed on plant growth variables, nematode suppression and nutrient elements (Ca, K, Na, Fe, Zn) in leaf tissues of green bean at 56 days after initiating the treatments. Phytonematicide concentrations significantly affected nematode numbers and nutrient elements, without affecting plant growth. Calcium ($R^2 = 0.97$), K ($R^2 = 0.93$), Na ($R^2 = 0.94$) and Fe ($R^2 = 0.91$) each with increasing Nemafric-BL phytonematicide concentration exhibited positive quadratic relations. In contrast, K ($R^2 = 0.97$) and Fe ($R^2 = 0.98$) each with increasing Nemarioc-AL phytonematicide concentration exhibited positive quadratic relations, whereas Na ($R^2 = 0.92$) and Zn ($R^2 = 0.72$) each with increasing phytonematicide concentration exhibited negative quadratic relations. In conclusion, accumulation of essential nutrient elements in green bean leaf tissues and increasing phytonematicide concentrations exhibited concentration-dependent growth patterns prior to the eventual expression of plant growth responses.

Audience Take Away:

- The importance of lipoic acid for the plant, and in human health will be explained
- The identification and characterisation of several enzymes from tomato that are key in the synthesis of lipoic acid will be described
- The utility of over-expression techniques in bacteria and plants required for functional characterisation will be highlighted

Biography

Professor P.W. Mashela from South Africa is senior Professor of nematology at the University of Limpopo and specialises in research and development of phytopesticides, with special interest in cucurbitacin-containing phytopesticides.

Drought stress and air humidity provoke stomatal functioning

PeimanZandi*

Institute of Environment and sustainable development in Agriculture, Chinese Academy of Agricultural Sciences, China

To control water loss in plants they should encompass the ability to regulate the opening size of their available stomatal pores. This is important during water shortage, when water loss triggers their reduced growth, threatens their survival, and may lead to plant death. The negative impact of water stress in plants include poor growth pattern, expression of stress-related proteins and chaperones, overexpression/regulation of anti-oxidants, agglomeration of compatible solutes, enhancement of transporter quantity that account for water/ion acquisition and transportation and ABA-mediated stomatal closure. Stomatal closure is of the most rapid response in water conservation and maintaining turgidity in plants; being referred to as an avoidance mechanism. Acclimation and developments of plants in relatively high humidity promotes developing malfunctioning stomata incapable of increasing osmotic potential in guard cells leading to stomatal closure. Therefore, these plants in times of exposure to dryer conditions swiftly wilt and lose their commercial value. Exposing such plants to low atmospheric humidity or high temperature and ABA treatments during under-developing period; can avoid malfunctioning by producing more functional stomata.

Audience Take Away:

- The audience will be introduced to new findings in this area. Such information may be helpful prospering their undergoing research, providing practical solution to their impediments or even relevant teaching materials.

Biography

Peiman Zandi: Iran and China based researcher specializing in plant science, environment & conservation related themes: A scientific researcher from Islamic Azad University, Takestan, Iran, presently he is involving in a 3-year based research at Chinese Academy of Agricultural Sciences.

Cowpea potential, production constraints and utilization in South Africa

Shargie N¹, PhD., Nemadodzi E¹, Mofokeng MA^{*1}, PhD.

¹Agricultural Research Council-Grain Crops, South Africa.

Cowpea (*Vigna unguiculata*) is one of the most important pulses grown in South Africa. It grows in environments considered marginal for other crops. Its nutritional value and ability to withstand drought makes it an important crop for food and nutritional security in the sub-Saharan Africa. The objectives of the study were to evaluate cowpea genotypes for high yield potential under drought conditions and identify farmer's production constraints and variety preference. The experiments for yield potential were conducted over three seasons in cowpea production areas of South Africa. A survey on farmer's variety preference and production constraints was conducted using semi-structured interviews and questionnaires in four and five local municipalities of Mpumalanga and Limpopo Provinces, respectively. In each municipality, target villages were selected randomly. The yield data were analysed using analysis of variance and treatment means were separated by Least Significant Difference test in GenStat 17th version. Data on production constraints were analysed using cross tabulations in SPSS statistical software. The top twenty highest yielding cowpea lines were selected and tested in Potchefstroom, Taung and Casteel villages in 2014/15 season. The best five cowpea lines identified were 99K-494-6, 98K-476-6, ITOOK-1263, CH47 and Bechuana White. Data across locations showed ITOOK 1263 as the best for both grain and fodder yield. ITOOK 1263 can be recommended for farmers in cowpea production areas of South Africa for food and fodder. The major production constraints were insect pests and animals. The farmers also indicated that they prefer brown and cream cowpea cultivars with good yielding ability for both grain and leaves as well as resistance to insect pests. They also like to consume both fresh and dry grain and need canned cowpea. Cowpea can serve as the best pulse in farmer's fields for eradication of hunger and malnutrition in developing and under developed countries.

Keywords: Cowpea, production constraints, survey, yield potential, South Africa

Biography

Alina Mofokeng (Ph.D.) is a researcher at the Agricultural Research Council-Grain Crops in Potchefstroom, South Africa working on cowpea and soybean breeding and germplasm conservation. She has a PhD in Plant Breeding with her research on diversity analysis of sorghum using agronomic, SSR, and protein content and amino acid composition. Her MSc degree was on Plant Protection with her thesis entitled Host status of *Cucumis myriocarpus* to *Meloidogyne incognita* and her major subject was Plant Production during her BSc degree study. She was a Post-Doc at the Agricultural Research Council-Grain Crops breeding sorghum for improved yield and perenniality.

Impact of Elevated Ozone and Wounding on Foliage Stress Volatile Emissions and Gas Exchange of Tasmanian Blue Gum (*Eucalyptus globulus*)

Arooran Kanagendran^{*1}, Leila Pazouki¹, Ulo Niinemets¹

¹Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Estonia.

Ozone and wounding are two key abiotic stress factors significantly affecting plant eco-physiological activity, but there is a substantial lack of knowledge on their interactive effects on plant constitutive and stress-elicited volatile (VOC) emissions and time-dependent modifications during a combined stress recovery period. We studied the changes in photosynthetic characteristics and modifications of constitutive and stress-induced volatile emissions upon acute ozone (4-6 ppm) and wounding treatments through recovery (0.5-75 h) in *Eucalyptus globulus*. Application of acute ozone and wounding treatments showed impaired photosynthetic characteristics and increased emissions of constitutive and induced VOC through recovery period. Photosynthetic characteristics were surprisingly resistant to all ozone and wounding treatments with ca. 70 % reduction in net assimilation rate at 0.5 h since the stress across treatments and then substantial recovery to ca. 50 % of initial rate observed at 75 h. Constitutive isoprene emissions were significantly enhanced by ozone and combined ozone and wounding treatments and the enhanced emissions stayed at high level throughout the recovery phase, but wounding alone reduced isoprene emission. Furthermore, all stress treatments enhanced emissions of lipoxygenase pathway volatiles (LOX), mono- and sesquiterpenes. In contrast, LOX emissions, total monoterpene and sesquiterpene emissions decreased through recovery period. However, a secondary rise in total sesquiterpene emissions at 75 h and for monoterpene (*Z*)- α -ocimene at 10-25 h was observed. Through the treatments and recovery period, stomatal ozone uptake rate and volatile emission rates were poorly correlated, reflecting possible scavenging effect of volatile isoprenoids.

Audience Take Away:

- This is about plant stress studies and how emissions and reduction in maximum dark-adapted photosystem II (PSII) quantum yield estimated by chlorophyll fluorescence (F_v/F_m), net assimilation rate, and stomatal conductance to water vapor are regulated in response to single and combined elevated ozone and wounding through recovery.
- The outcome of this research can be used to extend the studies in plant stress modelling.
- Other faculty staff can use it for teaching and extension of research in plant stress studies.
- The outcome of this study can be used to atmospheric chemical studies.

Biography

Arooran Kanagendran is following his PhD in Plant Ecophysiology at the Estonian University of Life Sciences, Estonia under the supervision of Professor Ülo Niinemets. His main research interests are in terpene molecular biology and emission in higher plants. He did his masters in Molecular Biology at the University of Hertfordshire, UK.

Photosynthesis and Growth Responses of Mustard (*Brassica juncea* L. cv Pusa Bold) Plants to Free air carbon dioxide Enrichment (FACE)

Kamal Ruhil, Baishnab C. Tripathy*, PhD.

School of Life Sciences, Jawaharlal Nehru University, India

Increased atmospheric [CO₂] is likely to affect photosynthesis, plant growth and yield potential of plants. Mustard (*Brassica juncea* L.) is an important oil seed crop that is widely grown in India. Therefore, the impact of elevated [CO₂] (585 mol mol⁻¹) on pigment and protein content, chlorophyll a fluorescence, photosynthetic electron transport reactions, CO₂ assimilation, biomass production and seed yield potential was measured in *Brassica juncea* cv Pusa Bold, grown inside free air carbon dioxide enrichment (FACE) rings installed on the campus of Jawaharlal Nehru University, New Delhi, India. Plants were grown for three consecutive winter seasons (2010—2013), in ambient (385 mol mol⁻¹) or elevated [CO₂] (585 mol mol⁻¹), in open field conditions. Electron transport rate, photosystem I, photosystem II and whole chain electron transport rates increased by 3-5% in elevated [CO₂]. However, the net photosynthesis rate increased by ≈50% in 3 growing seasons under elevated [CO₂] condition. The stomatal conductance and transpiration rate decreased resulting in higher photosynthetic water use efficiency. The photosynthesizing surface, i.e. number of leaves per plant and leaf area index substantially increased leading to higher biomass and seed yield under elevated [CO₂] condition. The quantum yield of photosynthetic CO₂ assimilation measured at limiting light intensities, in ambient CO₂ was 0.058 and it increased to 0.745 in high [CO₂]. The A_{Ci} curve did not reveal any downregulation of Rubisco in mustard plants grown in elevated [CO₂]. Acclimatory downregulation of photosynthesis and plant productivity was not observed in 3 consecutive growing years suggesting that in the absence of nutrient limitation, *Brassica juncea* is highly responsive to elevated CO₂ whose yield potential shall increase in changing climatic conditions.

Recombinant glycinebetaine improves metabolic activities, ionic balance and salt tolerance in diazotrophic freshwater cyanobacteria

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To find out the physiologic mechanisms contributing to increased tolerance to salinity by glycinebetaine in diazotrophic cyanobacteria, methyl transferase gene ApGSMT-DMT catalyzing glycinebetaine synthesis in *Aphanothece halophytica* was transferred into N₂-fixing filamentous cyanobacteria *Anabaena PCC7120* and *Anabaena doliolum*. The transformants synthesized/accumulated significant amount of glycinebetaine. Under salt-stress (0.1 M NaCl), the transformants were more efficient in reducing nitrate and its incorporation into amino compounds compared to wild-types indicating that glycinebetaine not only shielded the enzymes from deleterious effect of salt but enhanced their activities. High photosynthetic rate of ApGSMT-DMT transformants under salt-stress exhibited haloprotection of the photosynthetic machinery, while reduced respiration revealed efficient use of photosynthates. Salinity reduced the electron flow activity of PS II causing damage to cytochrome b₆-f complex, which was overcome to an extent by glycinebetaine. The observed limited electrons transport from PSII to PSI under salinity favored additional excitation of PSI resulting in increased electron transport activity of PSI. Salinity reduced the intracellular K⁺/Na⁺ and Ca²⁺/Na⁺ ratios, while transformants showed the highest K⁺/Na⁺ ratio. This attempt to develop salt tolerant N₂-fixers can increase the nitrogen availability under saline conditions, and opens the way to transform symbiotic and free-living N₂-fixers to increase the salt tolerance and productivity.

Keywords: N₂-fixing cyanobacteria, Glycinebetaine, Intracellular cation, Nitrate assimilation, Photosynthesis, Respiration, Salinity

In natural ecosystems, organisms often grow under suboptimal growth conditions and face biotic and abiotic stresses. Salinity is one of the most deleterious factors that limit the growth and yield of the organisms. Salinity increases the intracellular levels of Na⁺ which competes with the transport of K⁺ and Ca²⁺ resulting in an ion imbalance, ion toxicity and nutrient deficiencies. Cyanobacteria, owing to their great evolutionary age and great adaptability are useful models for eukaryotic organisms. In a typical prokaryotic cell organization, they possess water-oxidizing photosynthesis of higher plants as well as nitrogen-fixing ability. The latter property makes cyanobacteria of agronomic importance. Salinization of cultivable land is a global concern. The deleterious effect of salinity on soil fertility and plant productivity has become a serious threat to the global food security culminating into various socio-economic problems. To address the problem, we reported the first successful transformation of nitrogen-fixing, filamentous and heterocyst forming cyanobacteria with ApGSMT-DMT genes. The transformants synthesized and accumulated GB. The

present study analyzes the effect of salinity on physiologic processes such as nitrate assimilation, photosynthesis and photosynthetic electron transport chain activities, respiration and intracellular cation concentrations (Na⁺, K⁺ and Ca²⁺) in transformed (with ApGSMT-DMT) cyanobacterial cells.

Audience Take Away:

- The level of GB synthesized in transgenic (*Anabaena PCC7120* and *A. doliolum* containing ApGSMT-DMT genes) compared to the native (*Aphanothece halophytica* from which the genes are transferred) is much low.
- Thus, it is suggested that the low level of GB cannot contribute to the osmotic potential, but may function as an osmoprotectant or chemical chaperone.
- As observed in the present experiments, development of salt tolerant N₂-fixers can increase the nitrogen availability to the crops, such as rice and sugarcane (being in the same habitat) under saline conditions and reduce the burden of chemical biofertilizers in soil.
- This attempt will open the way to transform symbiotic and free-living N₂-fixers to increase the salt tolerance and productivity.

Global Conference on Plant Science and Molecular Biology

September 11 - 13, 2017
Valencia, Spain

Biography

The author (Prashant Swapnil) did Ph.D. from Department of Botany, Institute of Science, Banaras Hindu University, Varanasi, India. My Ph.D. title was "Salt tolerance in recombinant glycinebetaine synthesizing fresh water cyanobacteria *Anabaena* PCC7120 and *Anabaena doliolum*, and a sodic soil cyanobacterium *Anabaena fertilissima*" and completed under the supervision of Prof. A. K. Rai, BHU. I am well versed with culture techniques and physiology of cyanobacteria. I am also well versed with various analytical tools relevant to cyanobacterial metabolism research.

DOF Affecting Germination1: A tool to unravel how plants respond to drought stress in seeds

Ruta Veronica^{*1}, Lorrari Riccardo, Gandolfi Francesco PhD., Lepore Rosalba PhD., Costantino Paolo, Vittorioso Paola PhD.

¹University of Rome, Italy

For most plants including crops, the seed is the starting point of the growth cycle. Seed germination ensures the survival of the next generation, and plants have evolved mechanisms that enable seed germination to be arrested under stress conditions and then resumed when conditions are favourable. Desiccation tolerance is an important trait of plant life, it is defined as the ability to reinduce seed germination after water loss without lethal damage. This capacity is established during maturation of seeds, in the same temporal window in which dormancy is established. The Arabidopsis DOF Affecting Germination 1 (DAG1) protein is a key player in the control of the developmental switch between seed dormancy and germination. Indeed, we proved that DAG1 functions in the establishment and maintenance of dormancy by controlling the hormonal balance between Gibberellins (GA) and Abscisic Acid (ABA). We have recently recently discovered that DAG1 also mediates drought tolerance in seeds. Although the molecular mechanisms underlying desiccation tolerance have not been completely elucidated, a number of seed-specific and stress-related proteins are known to be involved in this process as well, namely LEA proteins and the WRKY transcription factors. Interestingly, a genome-wide analysis (RNA-seq) allowed us to identify a number of LEA and WRKY genes as target genes of DAG1, since they are significantly deregulated in the *dag1* knock-out mutant. Analysis of the molecular and genetic epistatic relationships between DAG1 and these proteins is in progress. The results of this study will help in unveiling the molecular mechanisms of plant response to drought stress in seeds.

Audience Take Away:

- The audience will gain insight on the molecular responses of germinating seeds to environmental stress.
- It might be useful for the audience to learn how seed, arguably the most economically important plant organ as food source, senses and adapts to a changing environment. The results presented will elucidate common molecular mechanisms activated under abiotic stress to provide seeds complementary strategy to survive toward completing germination.
- Abiotic stresses, especially salinity and drought are responsible for reduced crop growth and the cause of important economic losses in agricultural production. Our data, on Arabidopsis as model plant, will contribute to find new molecular strategies to face up to this agronomic problem.

Biography

I hold a master degree in Genetics and Molecular Biology from Sapienza University of Rome in 2016, and I am currently a PhD student in Life Sciences in the same university. During my thesis project I had the opportunity to work on Arabidopsis thaliana and I was particularly interested in the molecular network underlying the seed germination process under optimal conditions and also under adverse environmental conditions. I am also quite interested in the theoretical development and the subsequent practical use of modern and cutting-edge technologies, especially proteomic and genomic analysis, which provide the means to unveil molecular networks and pathways in a way previously not possible.

Improving faba bean for sustainable agriculture in dry areas

Fouad Maalouf^{1*}, Ahmed Seid²

¹International Center for Agricultural Research in Dry Areas (ICARDA), Terbol, Lebanon

²International Center for Agricultural Research in Dry Areas (ICARDA), Rabat, Morocco

Faba bean (*Vicia faba*) is one of the oldest crops, originated in the Fertile Crescent and is now distributed around the world and produced under different agro-climatic conditions in Mediterranean and semi-arid conditions as a rainfed and in Nile Valley countries as irrigated crop. It is a good source of food, incomes to smallholder farmers and plays an important role as rotation and mixed crop in improving soil fertility that helps sustainable production of cereal crops and in conserving the ecosystem. Since the crop is partial allogamous benefits from the presence of insect pollinators. However, faba bean is threaten by diverse abiotic and biotic stresses. Among abiotic stresses heat, drought, salinity and soil acidity are the major constraints of the crop while *Orobanche crenata*, stem borer, aphids and fungal and virus diseases are key factors for high yield gaps. The International Centre for Agricultural Research in Dry Areas (ICARDA) holds the major and unique faba bean germplasm collection (10036 accessions), which has been used in gene mining that led to release of cultivars for high yield and tolerant to abiotic (heat and drought) and biotic stresses (fungal diseases and parasitic weeds) in many countries. Faba bean improvement program at ICARDA has generated many elite germplasm with high yield, low tannin content, market traits and resistant to diseases, parasitic weed and tolerant to heat and drought and shared with National agricultural systems (NARS) and many cultivars are developed and released. During the last 10 years 21 faba bean varieties were released by NARS from ICARDA International Public Goods (IPGs) and bringing impacts on the productivity and area increases in China, Ethiopia, Sudan and Egypt. In Ethiopia, various varieties (Gora, Gelbechu, Moti and Walki) are being scaled out in the wheat-based cropping system in Ethiopia. In Egypt, parasitic weed resistant cultivars (Giza843 and Misr3) helped in the rehabilitation of faba bean in Egypt leading to 25% area increase. In China, cultivar Yandoo147 covered 140,000 ha in Yunnan province. Besides the achievement made so far, the breeding efforts are relatively slow due to the nature and mechanism of resistance of key diseases, parasitic weeds and abiotic stresses. To accelerate breeding cycles, there is a need to use the emerging biotechnological tools, such as marker-assisted selection, which have not been widely adopted despite significant achievements on quantitative trait loci (QTL) studies and the development of consensus maps in faba bean. The progress made in tissue culture and genetic transformation of faba bean can help to the introgression of sources for multiple stress resistance/tolerance into high yielding and adapted cultivars.

Audience Take Away:

- The audience will be able to know the past research, the current situation of faba bean improvement and the trend in the future, especially on the advance in research and molecular tools and transgenic approach in faba bean.
- The researchers can have access of the Germplasm and they can also know the metrologies used for screening for biotic abiotic stresses and physiological and biological measures associated with heat and drought. This can be useful for other crops. It might be also materials for teaching.
- The presentation will be focusing on research for development and will show major outcomes and impact of the breeding program as the area covered of the released varieties.

Biography

Fouad Maaloufis a senior scientist working at ICARDA since 2007. He holds PhD and Post-doc on faba bean breeding at Cordoba University-Spain on the development synthetic varieties in faba bean under Drs. Jose Ignacio Cubero and Maria Jose Suso. He coordinated Lebanese component of EU project on "Durum wheat water use efficiency" at LARI and was teaching botany and Genetics at Saint Joseph (1997-2007) and Lebanese Universities (2003-2007). His current research focus is the faba bean Improvement. He has supervised 19 students, including 3 PhD, 10 Master and 6 undergraduate students on different aspects of faba bean breeding. He authored or co-authored more than 39 research publications, including 32 referenced journal articles. He contributed to the release of 12 faba bean varieties with NARS partners.

Postulation of rust resistant genes in high yielding wheat from wild species by back-cross method

K A Nayeem*, Ph.D., M Sivasamy, Ph.D

Bread wheat (*Triticum aestivum*) is the second most important food crop of the world. Improvement of yield beyond existing level and its stability will be possible through exploitation of hybrid vigour, introgression of novel genes for yield, biotic and abiotic stresses. Globally fungal diseases particularly rusts are major biotic constraints. The threats of epidemics of rusts disease always looms over wheat growing belts, and scientists should ensure our farming community that no such phenomenon occur again. The scientists world over exploiting effective alien genes for rusts resistance. The genes derived from *Agropyron*, *Aegilops* and rye are offering effectiveness against the prevalent races of stem, leaf and stripe rusts. At IARI R.S. Wellington judicious and meticulously planned back-cross technique was initiated to transfer effective dominant genes that governs The rust resistance resulted in development number of near isogenics lines of popular (released) Indian bread wheat cultivars. The present two pronged strategy i.e., sustain the yield level already achieved by replacing the rust susceptible wheat varieties using near isogenic lines of the same variety carrying specific rust resistant genes and developing high yielding rust resistant varieties using hybridization. At IARI Wellington large number of near isogenic wheat varieties of Indian bread wheat cultivars i.e., C306, HD 2402, HD 2285, HS 240, HD2329, Kalyansona, Sonolika, UP 262, WL 711, Lok 1, WH 147, HD 2687, RAJ 3077, PBW 343 and UP 2338 etc, by introgressing effective rust resistant genes like Lr 9, Lr 24, Lr 28, Lr 32, Lr 37, Lr 39, Lr 42 and Lr 48, for leaf rust, Sr 24, Sr 26, Sr 31, Sr 34, Sr 36, and Sr 38, for stem rust, and Yr 9, Yr 10, Yr 15 and Yr 17 for stripe rust using back cross method, Many of these lines developed by this method has become cultivar/ varieties in India in recent times. The various methods of Back Cross for Dominance, Recessive and multiple gene transfer has been discussed.

Audience Take Away:

- To educate regarding the gene transfer with low monetary involvement.
- Identification technique for three type of rusts under natural conditions
- Selection technique for pure line i.e., sister or isogenic line generation after generation.
- Specific gene markers know-how.
- This will be a major accomplishment if an aspirant transfer an alien rust
- Resistant gene in to susceptible strain.
- This is an important Chapter for teaching purpose.
- It is a practical solution for developing disease resistant varieties.
- Here it is an example for development of rust resistant in wheat, however this can be used for any crop for development of resistant varieties of disease and insects.

Global Conference on Plant Science and Molecular Biology

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Valencia, Spain

Biography

Fellow of ISGPB 1980

Born in Parbhani (Maharashtra) INDIA on 1st Feb. 1945

B SC (Agri) 1968, M Sc (Genetics and Plant Breeding) 1970 Ph D 1983

Head ICAR-IARI Welligton (TN) 2002-2007, Asso. Dir Seed and Wheat Specialist 1974-2002, Emeritus Scientist ICAR-IARI 2007,

Principal College of Agriculture Khandala Aurangabad

Research Areas and Contribution:

Hybrids and Varieties released: Sorghum CSH 7R & CSH8R, Wheat Ajantha, PBN 142, PBN51, MACS 6145 HD2285 CoW(W)1, Nilgiri dicoccum HW1098 and CoW (WS).

Maize Single Hybrid (PMH 19).

Developed Five Semi dwarf (NP 200) T. Dicoccums (Khapli) by mutation(gamma rays) and found two new PUSA Dwarfing genes Rht22pda and Rht 23pdb (complementary genes) . Identified the molecular markers.

4500 Pearl Millet lines 35-40 traits digitalized data generated.

Post Graduate guide (18 M Sci & % Ph D),Taught advance courses of Genetics Plant Breeding , Seed Science & Technology , Biotechnology Several Back Cross lines with rust resistant genes registered in NBPGR New Delhi'

Recipient of several awards and recently.

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Sea buckthorn (*Hippophaerhamnides L*): A magic shrub for socio economic development of Pakistan

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Sea buckthorn (*Hippophaerhamnoides L.*) is known for its multipurpose utility around the world. It is very popular for its nutritional, biochemical, industrial, environmental and agricultural value. The shrub has been populated in the mountain in Northern Pakistan. A comprehensive project has been launched in AJK, (Pakistan) for its genetic improvement and establishment in northern parts of the country. The extent of genetic variation on the basis of morphological attributes, biochemical constituents and molecular profile exhibited that wildy growing genotypes of Sea buckthorn have the considerable diversity. The studies based on AFLP were compared with morphological and biochemical markers to evolve a convincing picture of genetic variation among the Sea buckthorn plant populations. In addition this genetic variation and broad genetic base, Sea buckthorn improvement program with the exploitation of Sub Species Sinensis from China and wild Sea buckthorn germplasm in UK has been started. Sub species, Sinences articulated promising prospects for growth on the lower Himalayans of Azad Kashmir as compared to local genotypes which need genetic improvement. The genotype Sinensis was successful in micropropagation experiments which showed positive results to use soma-clonal variation in Sea buckthorn improvement. The presentation will show the prospects of this shrub for starting an economic activity on sustainable basis. This finding has shown the plant's potential to be used for industrial, environmental, nutritional and agriculture sectors successfully.

Keywords: Sea buckthorn, genetic diversity, biochemical analysis, Pakistan.

Audience Take Away:

- Sea buckthorn is an important multipurpose plant with tremendous characteristics for multiple aspects of agriculture, environment, health, industry and human nutrition. The presentation will ensure that the audience knows how to use three marker systems including morphological traits, Biochemical analysis and molecular estimations can lead to launch a genetic improvement of plants. The presentation will ensure to describe the steps of using the potential of plant for sustainable economic development in distant, mountain and deprived areas. This will be an excellent case study for the exploitation of natural resources to strengthen the resource base of mountain communities to sustain the livelihoods.
- The presentation will cover the used methodology and materials taken from diverse resources including, UK, Russia and China. This presentation will give a complete profile of Plant's analysis for future breeding programs. It will also cover the significance of germplasm to be utilized in international research.
- The presentation will add in to the efforts for Sea buckthorn research and development being carried out around the world. The use of AFLP for genetic profiling will be quite helpful for the audience to use this technique for other plants.

Biography

The author (Dr. Asad Hussain Shah) is assistant professor and chairman Department of Biotechnology, Faculty of Science, University of Kotli, Azad Jammu and Kashmir, Pakistan. He has been serving as Research Associate, Senior Scientific Officer, Lecturer in the Department of Plant Breeding and Molecular Genetics, Faculty of Agriculture, Rawalakot, University of Poonch. The author has published 40 peer reviewed papers, 30 conference papers and has published 2 books. Dr. Shah has been writing newspaper articles about plant research. He is the recipient of Productive Scientist of Pakistan Award with multiple certificates of excellence from three vice chancellors of Universities. He has been the Chief Organizer, secretary and coordinator of International Conferences in universities he served. He has earned multiple travel grants to present his research on international forum. He is teaching and supervising Ph.D and M.Phil students in his department.

Efficient production of haploid durum wheat plant via maize pollination

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Even though bread wheat haploids are being routinely produced by wheat × maize crosses, an efficient protocol for haploid production has been difficult to achieve in durum wheat. The objective of this study was to analyse the influence of various experimental factors on the production of embryos and haploid plants in durum wheat crossed with maize. Four Tunisian durum wheat genotypes (female parent), consisting of two local cultivars ('Jenah khotifa' and 'Biskri') and two improved varieties ('Karim' and 'Razzek'), were crossed with a maize genotype (Pioneer 37Y15) (male parent). After pollination, plant stems were either maintained in situ or cut 2-3 days after pollination near the base and kept in a solution of 2,4-dichlorophenoxyacetic acid (100 mg/l), sucrose (40 g/l) and sulphurous acid (8 ml/l). Twelve, 14, 16, 18, 20 and 22 days after pollination, embryos were excised from developed ovaries and cultured on either Murashige and Skoog (MS), MS/2 or Gamborg's (B5) media. The effect of different concentrations (0, 25, 50, 75, 100, 125, 150 and 175 mg/l) of 2,4-dichlorophenoxyacetic acid (2,4-D) and nitrate silver (AgNO₃) in sucrose solution and the combination of these two treatments (100 mg/l of 2,4-D and 75 mg/l of AgNO₃) were tested. Performance of durum wheat doubled haploids derived from durum wheat × maize crosses and their parents was evaluated on the basis of germination percentage and six morphological traits such as plant height, spikeless tillers/plant, spike tillers/plant, days from sowing to 50% ear emergence, kernels/spike and 1000-kernel weight.

The results showed that by cutting the plant stems after pollination, better results in terms of developed ovaries (65.55%), embryos (13.62%) and regenerated haploid plants (10.50%) were obtained than if in situ plants (46.65, 10.85 and 7.71%) were used. The optimal stage for embryo rescue was 18 days for haploid plant formation (14.4%) while B5 medium resulted in significantly better haploid plant (13.17%) production than MS and MS/2 (6.92, 10.87%) following embryo culture. The best results of embryo formation and haploid plants were obtained when the concentration of 2,4-D was 100 mg/l in combination with 75 mg/l of AgNO₃. Embryogenesis and the regeneration rates reached 26.01 and 22.22%, respectively. The results indicated that the doubled haploid (DH) lines Jenah Khotifa and Biskri showed greater germination percentage with 70% compared to their parent with 60%. However, DH lines derived from crosses of Rezzak and Karim genotypes hybrid with maize had the same behaviour as their parent respectively. Also, the results showed that the DH lines equalled to the control for average height of plants and spikeless tillers/plant. The difference in average days from sowing to 50% ear emergence between DH1 lines from Biskri and Rezzak and the control was reduced to 5 and 9 days. DHs lines showed 1000-kernel weight and spike tillers/plant greater in DH1 lines than in the control. However, kernels/spike was significantly greater in control compared with DH lines.

The effects of beneficial nano-particles and nano-structured fertilizers on plants growth

Mohsen Jamohammadi*, Naser Sabaghnia

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Soil of semi-arid Mediterranean regions are intensively tilled, they are low in organic matter content and consequently have weak structural stabilities. Furthermore water scarcity is one most limiting factor for plants growth in these areas. Although the conditions of soil and water are vastly different from place to place, all plants need permeable soils with high organic matter and sufficient concentrations of essential elements for an acceptable growth. Therefore a balanced fertilization strategy with macro and micronutrients in plant nutrition is very imperative for crop production in this areas. In this context, nano-technology can be one of the most powerful tools for improving the plant production in modern agriculture, and is estimated to become a driving economic force in the near future. It is predicted that nano-technology can boost agricultural production through the nano-formulations of agrochemicals and production of nano-fertilizers. During the last decade, some studies tried to examine the potential of nano-biotechnology to improve nutrients use efficiency and strategies that result in the design and development of efficient new nano-fertilizer delivery platforms for use at the farm level. Nano-formulated fertilizers presents unique physico-chemical properties, so that they can fulfil plant root requirements more efficiently in comparison with conventional fertilizers (in the form of salts or in bulk size). The gradual and regulated release of the nutrient could be through the process of dissolution and ion exchange reactions. Utilization of nano-fertilizers may increase solubility and dispersion of insoluble nutrients in soil, reduce nutrient immobilization (soil fixation) and increase their bio-availability. Besides, nanoparticles have unique physicochemical properties compared with bulk particles, so that their small size and propensity to cross barriers (cell wall and plasma membrane) facilitates effective absorption and their large specific surface can result in good level of interaction with intracellular structures. Consequently nano particles can be used to increase the supply of elements to plant shoots and foliage. Nano-silicon dioxide ($nSiO_2$) and nano-titanium dioxide (TiO_2) has exceptional optical and biological characteristics and has recently caught the attention of plant physiologists.

Audience Take Away:

- The importance of nano-fertilizer in sustainable plant production
- Major difference between modern fertilizer and conventional ones
- The effects of nano-chelated micronutrients on crop plants growth in semi-arid region

Biography

Mohsen Janmohammadi obtained his Ph.D. in Crop Physiology from Tehran University in 2008. His research is focused on the effects of environmental stress and nutrient managements on biochemical and physiological aspect of crop plants. He shows interest in improvements of the drought tolerance and nutrient use efficiency in pulse crop in semi-arid region. He is currently an assistant professor of crop physiology at Agriculture collage, University of Maragheh.

e-Poster Presentations

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GPMB 2017

Green spots in hot cities: Water economy through oriented root elongation of Mediterranean plants

Chrysanthi Chimona*, Ph.D., Sophia Rhizopoulou
National and Kapodistrian University of Athens, Greece

Young plants of Mediterranean species (i.e. *Ceratonia siliqua* L. - carob tree, *Myrtus communis* L. - myrtle, *Nerium oleander* L. - oleander) were developed in the laboratory and planted in plastic tubes (length: 100 cm and diameter: 10 cm) that contained soil. The same procedure was followed for plant species that are not resistant to drought conditions (i.e. *Rosmarinus officinalis* - rosemary, *Ligustrum japonicum* -Japanese privet, *Pittosporum tobira* - Japanese pittosporum) and are often used in urban plantations and parks. The tubes were cut along their length, which makes possible the observation of root development and sampling of tissues without destroying the plants. In addition, rhizotrons (i.e. rectangle boxes made of plexiglass) were used to study the development of above and below ground plant parts of well watered and unwatered plants. The results of the study show that the carob tree, myrtle and oleander plants are less affected by different watering conditions than rosemary, Japanese privet and Japanese pittosporum. More specifically, the above ground parts of the Mediterranean plant species exhibited growth in water deficit conditions. In addition, the Mediterranean examined species continued photosynthetic rates during the morning and evening hours every day, when gas exchange and transpiration took place. These results are supported by the fact that the root proline content, which indicates water stress of tissues, was lower in the Mediterranean species, in comparison with non-native species. The same holds true for leaf chlorophyll content; higher values were estimated in carob tree, myrtle and oleander. It is recommended to cultivate Mediterranean, resistant to drought plant species in urban landscapes where elevated temperatures (especially during summer) and water shortage are recognized problems for everyday life. Native, Mediterranean plant species, as natural part of the ecosystem, respond to summer drought by ecophysiological procedures and reveal a manner of public green spaces designing with less water usage. The study is funded by IKY Fellowships Of Excellence For Postgraduate Studies In Greece – Siemens Program.

Audience Take Away:

- The audience will understand that beautiful, ornamental plants are water consumers, a fact that creates problems in Mediterranean urban environments. People that live in cities are exposed to hot and dry climatic conditions and seek for green spots that will relieve their everyday lives. However, the conservation of green 'hot spots' also indicates the use of a lot of water amount, especially during drought. The preference towards plant species, typical of the Mediterranean ecosystem, is highly promoted through the present study; these species can be either native or endemic and usually consist of a root system capable for water uptake from deeper soil horizons.
- The results of the present study can be used for detailed comparison among Mediterranean, as well as other plant species. In addition, further studies could be planned for comparisons between Mediterranean species that may be more appropriate to specific urban environments.
- Designing green spots inside urban environment needs to consider practical issues like plants' ability to endure harsh climatic conditions and usage of water. Landscape designers should take in consideration the results of relevant studies.

Biography

Dr. Chrysanthi Chimona has obtained her degree of Biology in the National and Kapodistrian University of Athens. She immediately continued as a Ph.D. student in the same University, which she obtained with a scholarship co-financed by the European Union (European Social Fund – ESF) and Greek national funds (Research Funding Program: Heracleitus II). Her Ph.D. thesis is entitled 'Biomimetics and Water Status of Plant Tissues'. During her Ph.D. studies she participated in the CAREX Summer School on Life in Extreme Environments, which was attended by 40 selected students. She is currently working on a post-Doctorate research funded by IKY Fellowships Of Excellence For Postgraduate Studies In Greece – Siemens Program.

Dynamic of residue decomposition and effects on labile fractions of soil organic carbon

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Cover crop (CC) residues protect the soil from erosion and their permanence on the surface is largely influenced by their biochemical constituents. Cover crops (CC) are a necessary tool for the Pampas region to avoid soil degradation after summer crops grown on a year basis, leaving the soil naked during the mild winter (Rimski-Korsakov et al. 2015). In this way, CC may influence soil organic carbon (SOC) contents by providing additional residue carbon to soil (Wang et al. 2010). Nevertheless, reported effects of CC on SOC contents are inconsistent and range from losses (Mazzoncini et al. 2011) to gains (Duval et al. 2016).

In this study the dynamics of CC residues decomposition and their effects on soil labile organic carbon fractions were evaluated under controlled (incubation experiment) conditions. Three CC species (oats, *Avena sativa* L.; vetch, *Vicia sativa* L.; Persian clover, *Trifolium resupinatum* L.) and a no CC control (fallow) were evaluated. Shoot residues were applied on the soil surface and incubated for 362-days (with eight sampling times). Particulate organic carbon (POC), total and soluble carbohydrates (CHt and CHs, respectively) were determined in soil samples. Oats and vetch residues decomposed faster than clover, where k values were 1.3, 1.4 and 1.9 year⁻¹, respectively. At the end of the experiment, the POC concentration was the lower in vetch (1.83 g kg⁻¹) and clover (1.96 g kg⁻¹) than oats (2.21 g kg⁻¹) and fallow (3.00 g kg⁻¹), that's mean a loss between 45-64% of their initial values. Overall, the dynamics of residue decomposition were reflected in changes of CHt contents. The periods of greatest residue decomposition were 0 to 21 days and 130 to 201 days for vetch and oats, respectively which coincides with the greater soil CHt. Hence, this organic fraction is very sensitive to residue decomposition and can be indicators of changes in soil organic matter quality over short periods of time. Changes in soil labile carbon fractions were differentially influenced by residue quality over short periods of time. The lower POC concentrations in CC soils than in fallow soils indicated that despite extra carbon input, mineralization rate was much high in CC affecting also native organic pools.

Overall, the dynamics of residue decomposition were reflected in changes of CHt contents, where the periods of greatest residue decomposition corresponded to the higher soil CHt. Hence, this organic carbon fraction is very sensitive to residue decomposition and can be indicators of changes in soil organic matter quality over short periods of time.

Key Words: Particulate organic carbon, carbohydrates, cover crops, biochemical composition

Audience Take Away:

- The importance of lipoic acid for the plant, and in human health will be explained
- The identification and characterisation of several enzymes from tomato that are key in the synthesis of lipoic acid will be described
- The utility of over-expression techniques in bacteria and plants required for functional characterisation will be highlighted

Biography

He was born in Rosario, Provincia de Santa Fe, in 1961. He obtained his degree of Agricultural Engineer in the Facultad de Ciencias Agrarias de la Universidad Nacional de Rosario (UNR). He studied postgraduate studies at the Universidade Estadual Paulista (UNESP) - Faculdade de Ciências Agronômicas - Campus de Botucatu - Botucatu - Sao Paulo - Brasil, where he obtained a Master's degree in Plant Protection. He also obtained his Specialization in No Tillage System in the Facultad de Agronomía de la Universidad Nacional de Buenos Aires (UBA) where he obtained the Specialist of No Tillage System. He studied postgraduate studies at the Universidad Nacional del Sur (UNS) Departamento de Agronomía (CERZOS UNS-CONICET) - Bahía Blanca - Provincia de Buenos Aires where he obtained the Doctorate in Agronomy. He has numerous articles published in national and international magazines, has presented numerous works in National Congresses in the area of Crops and Soil Management.

He is in the area of Extension and Technology Transfer with Rural Extension Agency INTA (AER) Coronel Suárez - province of Buenos Aires as Jeff of Rural Extension Agency since 2012.

Use of a three-compartment model to evaluate the dynamics of cover crop residues

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Cover crop (CC) residues protect the soil from erosion and their permanence on the surface is largely influenced by their biochemical constituents. Simulation models have been proposed to evaluate the decomposition of residues in soil. Most of these models have taken in to account one or several compartments to describe the organic residues, each decomposing according to first or second order kinetics. In this study, the dynamics of CC residue decomposition by applying mathematical models was described. The kinetics of decomposition of residues was obtained from a laboratory incubation experiment. Three CC shoot residues were applied on the soil surface and incubated for 362 days (with eight sampling times). Total 72 samples (pots) were placed at random in a green house under controlled conditions of temperature ($25 \pm 1^\circ\text{C}$). The basic treatment design consisted of pots in which CC residue (24 pots for each specie), oven-dried, was covered. The residues of oats, vetch and clover cut into 2–3-cm particles and were added to pots at 5.4, 5.4 and 2.7 g dry matter, respectively, which corresponded to biomass rates of 6, 6 and 3 Mg ha⁻¹, respectively. This rate is equivalent to that observed in field experimental plots. Results from the application of the three-compartment model (LIG, C + H and NSC, with their decomposition rate constants) for simulating decomposition of different CC residues showed a better fit with the real data than the estimation from the negative exponential equation. Oats and vetch residues decomposed the most than clover, where k values were 3.6×10^{-3} , 3.7×10^{-3} and 5.3×10^{-3} day⁻¹, respectively. The three compartment model (non structural carbohydrates, cellulose–hemicellulose and lignin) to simulate residue decomposition presented a close fit between simulated and measured data. The decomposition rate constant (k) of CC can be used to estimate how long residues will remain in the field and how they could affect soil organic carbon. Vetch residues initially showed a fast decomposition rate. They lost over 40% in the first 21 days after being placed in incubation pots, which allowed high N-availability in the soil. Oats residues decomposed more slowly and caused temporary N-immobilization in the soil, with a late partial release between 3 and 4 months after the residues were placed in the pots. Decomposition rates for oats, vetch and clover residues were different, whereas the processes of mineralization and immobilization were enhanced by the C:N ratio of each CC. The decomposition dynamics of the CC can be described by a simple equation in the medium term, or else a three compartment model can be used for more accurate descriptions in the short term.

Keywords: Residue decomposition; oats; vetch; clover

Audience Take Away:

- The labors here front man you're perfectly repeatable in the wake of her methodologies itemized. It is a very arduous job since it requires the construction of a soil sampler of capacity for pots and adaptable to the three points of the tractor. Otherwise itself require of equipment special in order to her determination of the carbohydrates structural solvable and complete. This is a simple methodology easily usable by other researchers, in fact after this thesis were developed several theses in this Line of research in Universidad Nacional de la Pampa (UNLaP) and the Universidad Nacional del Sur (UNS).
- The models mathematics plain in order to the breakdown of the aftermath it can lend a helping hand in shape arterial in order to her obtainment of aftermath ma quickly. Otherwise the CHs and CHt you're one pointer of quality of ground at short times of tense.
- Any researcher of the sector of the science of the ground it can utilize this methodologic in order to lay on and expand to other studies which fringe this work of thesis.
- Yes, in as much as her methodology utilized taxpayer at the survey of the she contributes of MOP on the floor when utilized farming of coverage as improved of ground degraded by the monoculture and her abrasion.

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- She utilizes other methodology on the Science of the Ground in order to her obtainment of aftermath quick in the weather of the research of the other fractions of the organic matter of soil, demonstrable which is one methodology operative in order to the she broaches of the problematic of the trades in the operation of ground of the husbandry on the Argentina.
- In order to a lot of ground agriculture the farming of coverage they offer the not other than purport practical of provide her organic matter needful in order to keep the soil on a tall status of productivity. Her organic matter ago at the soil much friable, enhance her capacity of labors, and facilitation her penetration of the water. Her organic matter itself disperse and it can provide nitrogen and add nutrients tu the soil in order to the succeeding crops. The soil micro-organisms that benefited from such decomposition of the waste of the cover crops succulent, help provide greater at the ecosystem health. The cover crops coverage protects the soil of the officers degrading (precipitation an wind) while development her period vegetative. Once which itself suppress the growth, it may be methods mechanics (cut or crushed) or else chemists (glifosato) itself him SO It,s usually kept at surface without incorporate continuing her impact protector of the soil. As soon as at the balance sheet of water not interest lots of the lesser content of humidity at the discontinue the increase of the manure in as much as one ground with cover crops of coverage is further efficient at to roof-water harvestingof rain in the spring, as a result at relationship with the follow nude they don't exist differences on the availability of water (Cordone et. at the 1986). The agriculture continues of under de conditions of current agricultural practice, contributes of degradation of organic material in soil and consequently, at a accentuated degradation of the very.Given this situation, the development of technologies that restore fertility and reduce the physical deterioration of Pampas agricultural soils, and especially agricultural soils of Coronel Suárez (Province of Buenos Aires - Argentina) in the sub-humid Pampa region, is a priority. Began to suffer the negative effects of soy monoculture or wheat / soybeans.

Biography

He was born in Rosario, Provincia de Santa Fe, in 1961. He obtained his degree of Agricultural Engineer in the Facultad de CienciasAgrarias de la Universidad Nacional de Rosario (UNR). He studied postgraduate studies at the Universidade Estadual Paulista (UNESP) - Faculdade de Ciências Agronômicas - Campus de Botucatu - Botucatu - Sao Paulo - Brasil, where he obtained a Master's degree in Plant Protection. He also obtained his Specialization in No Tillage System in the Facultad de Agronomía de la Universidad Nacional de Buenos Aires (UBA)where he obtained the Specialist of No Tillage System. He studied postgraduate studies at the Universidad Nacional del Sur (UNS)Departamentode Agronomía (CERZOS UNS-CONICET) - Bahia Blanca – Provincia de Buenos Aires where he obtained the Doctorate in Agronomy.He has numerous articles published in national and international magazines, has presented numerous works in National Congresses in the area of Crops and Soil Management.

He is in the area of Extension and Technology Transfer with Rural Extension Agency INTA (AER) Coronel Suárez –province of Buenos Aires as Jefe of Rural Extension Agency since 2012.

Effects of Magnetic Field on Peroxidase Activity and Hardening of New Guinea Impatiens Explants

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In the present study, effects of an external magnetic field (MF) on peroxidase activity and hardening of New Guinea Impatiens (*Impatiens x hawkeri*) were investigated under controlled (in vitro) condition. To investigate the magnetosensitivity of plants, strong homogeneous magnetic fields (75, 150 and 200 mT) with exposure times of 10 and 60 min were employed for seven days and fourteen days after the explants hardening. In control and magnetic field treatments, shoot and root formation rates, fresh weights in hardened shoots and peroxidase activity in regenerated shoots were determined. The rate of shoot and root formation significantly increased. Results showed that the fresh weights of plantlets regenerated from treated explants increased, compared to controls. Peroxidase activity significantly increased in all treatments. It was shown that the level of peroxidase increased with the increase of shoot and root regeneration rate and fresh weights, as well as, MF. The present study also indicated the significant correlation between increased MF and increased level of peroxidase activity. Notably, the most significant difference in growth was observed in samples treated by 200 mT magnetic intensities for 60 min. Thus, it is suggested to use low-frequency homogenous magnetic fields in order to increase the efficiency and decrease the time of plants rooting.

Audience Take Away:

- The results showed that peroxidase activity significantly increased in all treatments which led to an increase in the fresh weights of plantlets regenerated from treated explants, as well as, the rate of shoot and root formation.
- It was also shown that there is a significant correlation between increased MF and increased level of peroxidase activity.
- It is suggested to use low-frequency homogenous magnetic fields in order to increase the efficiency and decrease the time of plants rooting in tissue culture.

Biography

Fardad Didaran is a senior student in Bachelor of Science Degree in Horticultural Sciences in the School of Agriculture, Shiraz University. He was graduated from Shahed high school in the major of Experimental Sciences in June of 2012. He was accepted to Shiraz University through an entrance exam in the same year. He has been working at Tissue Culture Lab of Shiraz University as a researcher for two years. Fardad Didaran was granted the third rank in Physics Olympiad. He is currently working on new projects in the mentioned fields and has an abstract accepted in VII International Symposium on Production and Establishment of Micropropagated Plants. Fardad Didaran lives in Shiraz, Fars Province, Iran.

Evaluation of some physiological characteristics of canola (*Brassica napus* L.) cultivars and Indian mustard (*B. juncea* L.) in response to salt stress.

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²Ferdowsi University of Mashhad, Iran

Salinity is one of the most important abiotic stresses and a serious constrain for crop production. Two oilseed amphidiploids Brassica species (canola) including rapeseed/canola (*Brassica napus* L.) and Indian mustard (*B. juncea* L.) which have common parent (*Brassica rapa* L.), are rather salt tolerant so can be used to grow on saline soils and soils affected by saline irrigation.

An experiment was conducted as factorial based on randomized complete block design with three replications in the Research Greenhouse of agriculture faculty, University of Birjand, Iran, in 2015. The first factor consisted of four salinity levels including 1.9 (Hoagland solution as control), 5, 10 and 15 dS/m (NaCl in Hoagland solution) and the second one was genotype consisting of two spring canola cultivars (Hyola401 and RGS003) and Indian mustard landrace. The medium was sand culture in pots. At three stages after starting salinity stress (approximately, stem elongation, flowering and filling pod stages) sampling was done from each treatment to determine photosynthetic pigments including chlorophyll a (CHLa), chlorophyll b (CHLb), total chlorophyll (CHL_t), carotenoids (CAR), relative water content (RWC), membrane electrolyte leakage and proline. Data analysis and statistical calculations were done using SPSS and EXCEL software.

Result showed that at second and third stages of sampling, salinity induced significant decrease in CHLa, CHLb, CHL_t and CAR but any decline trend didn't observe in these characteristics at stem elongation stage. With increasing the period of salinity stress, Indian mustard was impressed more than canola cultivars and had the least of mention traits at flowering and podding stages. Results showed membrane electrolyte leakage increased significantly by rising irrigation salinity up to 15 dS/m and the most of it observed at this level. Traits mean comparison illustrated Indian mustard had the highest amount of membrane electrolyte leakage at all stages that the amount of this trait in this genotype at flowering and stem elongation was 50 and 59.2 percent, respectively less than final sampling stage. Increased salinity level, resulted in a downward turn in RWC of canola cultivars that this trend was significant at second and third stages of sampling. Indian mustard had the highest amount of RWC at salinity level of 15dS/m at all stages. Also an upward trend was observed in proline in all genotypes at all stages by rising irrigation salinity. The highest proline in all genotypes was related to the highest salinity level relative to control and increase of this trait was more significant at flowering and podding stages in comparison to stem elongation stage. The least of proline at all stages related to Hyola401. The highest amount of proline at stem elongation and two other stages was related to Indian mustard and RGS003, respectively.

Photosynthetic pigments and RWC of All genotypes at first phenological stage were not affected significantly by salinity but by increasing duration of salt stress significant declines were appeared. There were not significant differences in traits of proline and membrane electrolyte leakage between genotypes at all times of sampling at control level related to salinity levels.

Audience Take Away:

- As I mentioned above, salinity is a big problem for crop production, especially in arid and semiarid areas. In these regions we need good information about physiology of resistance to salinity in crops. This research and other research in this field help us to reach this goal.
- Results of this research useful for agricultural students and top farmers.

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Biography

First Name: Gholam Reza Last Name: Zamani Birth Date: 1/07/1964

Gender: Male Marital: married Number of Children: two

Sep. 1999-Present Ph.D., Crop Physiology, Ferdowsi University, Mashhad, Iran,

Ph.D project: Study on physiological aspects of wheat- wild oat competition under salinity stress.

Feb. 90-Feb.93, M.Sc., Agronomy, Ferdowsi University of Mashhad, Iran.

M.Sc. Project: Effects of planting pattern and plant density on radiation absorption, yield and yield components of Maize (*Zea mays* L.).

Sep. 1986 – Feb 1990, B. Sc., Agronomy and Plant Breeding, Ferdowsi University of Mashhad, Iran

B.Sc.Project:Study of Growth and development of *Berberis vulgaris*. Supervisor: Dr.M. Nasirri Mohalati.

Now is working as an academic staff (Associate professor) at University of Birjand, Iran

Seasonal sap-flow dynamics in *Larix sibirica* trees growing in the Krasnoyarsk forest-steppe

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²Siberian Federal University, Krasnoyarsk, Russia

We measured and analyzed seasonal dynamics of sap flow in the stems of Siberian larch trees (*Larix sibirica* Ledeb.) characterized by different radial growth rates. The investigated site of growth was located nearby the research station of the Institute of Forest "Pogorelsky Bor" (Krasnoyarsk forest-steppe, 56.36°N, 92.95°E). Continuous measurements of sap flow intensity with 30 min resolution were carried out using the Energy-balance (THB) method during the growing seasons 2014 and 2015. The studied even-aged trees characterized by approximately the same heights but various diameters at DBH. They grew at 3 m from each other, so that its growth was not markedly affected by competition. Nevertheless, data of start and finish of the vegetation period of the trees with different diameters was shifted in several days. It occurred that seasonal sap flow intensity through the stems were characterized by high correlation ($R = 0.77-0.94$) within overlapping interval of the vegetation period, while the absolute diurnal amplitudes occurred highly different. Eco-physiological BS-model developed earlier by the authors Anna Benkova and Alexander Shashkin, verified for the site and trees investigated by the data of sap flow measurement, allowed to calculate daily and seasonal dynamics of transpiration, photosynthesis, stomata conductance and soil moisture. We revealed that seasonal dynamics of sap flow and calculated transpiration as well as seasonal variations of vapor pressure deficit (VPD) were synchronous. Seasonal precipitation was correlated with the values mentioned quite well also. We analyzed the seasonal dynamics of stomata conductance in relation to soil moisture variations and concluded that the trees did not suffer from prolonged water stress in the vegetation seasons of 2014-2015. We supposed that soil moisture could not be the main factor responsible for sap flow intensity in the studied growth conditions, but most likely VPD could. The data obtained in the seasons of 2014 and 2015 were illustrated that continuous automatic measurements of sap flow intensity allow to study phenocycles of individual trees characterized by various growth rates and to fix quite exactly the data of start and finish of vegetation periods.

Biography

Born in Artemovsk, Russia, August, 12, 1951. Graduated from Krasnoyarsk State University, Faculty of Physics, Ph.D. (a dissertation "Dielectric Relaxation of Bound Water in Wood" was defended in 1987, degree in Wood Science & Technology), Doctor of Science (a dissertation was defended in 2005, degree in Wood anatomy). Senior Researcher at the Institute of Forest, Siberian Branch, Russian Academy of Sciences. Author of the papers on wood science, wood anatomy, dendroecology. Responsible for Creation of Russian version in Multilingual Glossary of Dendrochronology by Kaennel M. & Schweingruber F.H. (Compilers), 1995. Co-author of "Anatomy of Russian woods: an atlas for identification of trees, shrubs, dwarf shrubs and woody lianas from Russia" by Vera E. Benkova & Fritz H. Schweingruber. 2004. The Fellow of International Academy of Wood Science since 2013.

Effect of potato defense responses on development of *Globodera rostochiensis* juveniles

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Monoculture of potato as an important and widely distributed food crop is very sensitive to diseases. One of the most serious potato pest is potato cyst-forming nematode *Globodera rostochiensis* Woll., a subject for strict quarantine regulations over the world. The immune system of plant-host has significant influence on plant-parasite interactions (compatible or incompatible) and, accordingly, on plant resistance/susceptibility to diseases. Phytoimmunity is based on the effective detection of parasite effectors and rapid induction of defense responses. In this study the effect of immunity system of resistant (cv. Krepysh), susceptible (cv. Nevsky) varieties and plants pre-treated with temperature (temperature drop from 23 to 5°C for 2 h at the end of the night period during 6 days before nematode infestation) on juvenile development inside the potato roots was investigated. Results have shown that resistant plants accumulated transcripts of R-genes (H1, Gro1-4) at pre-invasion stage. During the nematode invasion levels of R- (H1, Gro1-4) and PR-genes (PR1, PR2, PR3, PR6) transcripts were up-regulated. These plants have possibilities for rapid activation of defense responses to juvenile's penetration into the roots. As a consequence, females of *G. rostochiensis* have a reduced multiplication rate. The situation was different in a case with susceptible potato plants, which have inactive R-genes (H1, Gro1-4) and low transcript level of PR-genes (PR1, PR2, PR3, PR6) prior and during nematode invasion. The lack of possibility of plants timely recognize the nematode attack lead to very slow formation of defense responses to subsequent juvenile's parasitism. So, nematodes had favorable conditions to developing and complete their life-cycle, and reproductive capacity of *G. rostochiensis* was maximal. Susceptible plants pre-treated by temperature had the similar traits with resistant ones. R-genes were expressed at pre-invasion stage that allows recognizing nematode effectorson time, rapidly generating strong signal for enhanced transcript abundance of PR-genes. At the same time transcripts level of Pel-1, Eng-1.4, Cle, SPRYSEC-1, VAP1, Tpx, Gpx in nematode tissues were down-regulated. These juveniles were limited in formation of syncytium and exposed to the defense responses of the plant-host. Development of the juveniles occurred in unfavorable conditions and was accompanied by a disruption in the reproductive function of females: the number of eggs and juveniles, and egg's viability were reduced. Thus, resistant, susceptible and temperature-treated susceptible plants have differences in transcription profile of R- and PR-genes that is reflected on the timing of defense responses. This allows identifying the main mechanisms of plant resistance and susceptibility. Pre-treatment (daily short-term temperature drop) modulated the expression of genes in susceptible plants and enhanced their resistance to the invasion and suppressed nematode development. The relationships between nematodes and temperature-treated susceptible plants are defined as incompatible. The study was carried out under state order (№ 0221-2014-0030) and supported by RFBR (№16-34-00650).

Biography

Victoria Lavrova is a researcher at laboratory for Animal and Plant Parasitology in Institute of Biology, Karelian Research Centre of Russian Academy of Sciences. Research interests are interactions between cyst-forming nematodes (*Globodera rostochiensis*, *Globodera pallida*) / root-knot nematode (*Meloidogyne incognita*) and their host plants: phytonematode biology and development, plant responses and resistance/susceptibility to the nematodes (morphology, physiology, defense-and resistance genes expression); Innate and induced resistance of plants; Priming of plant immunity. Technical skills in Plant Biology and Nematology. Participation in professional development courses and training seminars.

Role of Jasmonic acid in regulating tomato susceptibility to root-knot nematodes

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²Centre of Parasitology, A. N. Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia

The root-knot nematodes (RKNs) *Meloidogyne* spp. are obligate sedentary endoparasites of root system of many plant species. *M. incognita* is widespread and economically important pest. There were investigated the expression of resistance Mi1.2 gene (encoding receptor proteins with the function of recognizing effectors secreted by nematode into plant tissue), PR1 and PR6 genes (markers of induced systemic plant resistance) in the roots of tomato plants pre-treated with Jasmonic acid (JA) during *M. incognita* invasion. It has been established that resistant and susceptible tomato plants have a similar level in transcripts accumulation of Mi1.2 and PR-genes at pre-invasion stage. However, differences between plants in the dynamics of the expression level of these genes were revealed during subsequent nematode invasion. In resistant plants it was accompanied by increased transcripts accumulation of Mi1.2 and PR-genes. In the roots of infested susceptible plants transcription of Mi1.2 gene was unchanged and of PR1 and PR6 genes was slightly induced. In the roots of JA-treated tomato plants transcription of Mi1.2 and PR6 genes were up-regulated prior and during nematode invasion. Increased expression of the Mi-1.2 gene at early stage of host-parasite relationships in combination with the high transcription of PR6 gene at the late stage of nematode parasitism promoted recognition of nematode attack and suppression of the possibility of their normal feeding and development. Thus, results have indicated exogenous treatments of tomato by JA modulate the accumulation of transcripts of resistance and defense genes that contribute to the formation of induced resistance to root-knot nematodes in the susceptible plants. The study was supported by RFBR (№15-04-04625).

Biography

Victoria Lavrova is a researcher at laboratory for Animal and Plant Parasitology in Institute of Biology, Karelian Research Centre of Russian Academy of Sciences. Research interests are interactions between cyst-forming nematodes (*Globodera rostochiensis*, *Globodera pallida*) / root-knot nematode (*Meloidogyne incognita*) and their host plants: phytonematode biology and development, plant responses and resistance/susceptibility to the nematodes (morphology, physiology, defense-and resistance genes expression); Innate and induced resistance of plants; Priming of plant immunity. Technical skills in Plant Biology and Nematology. Participation in professional development courses and training seminars.

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