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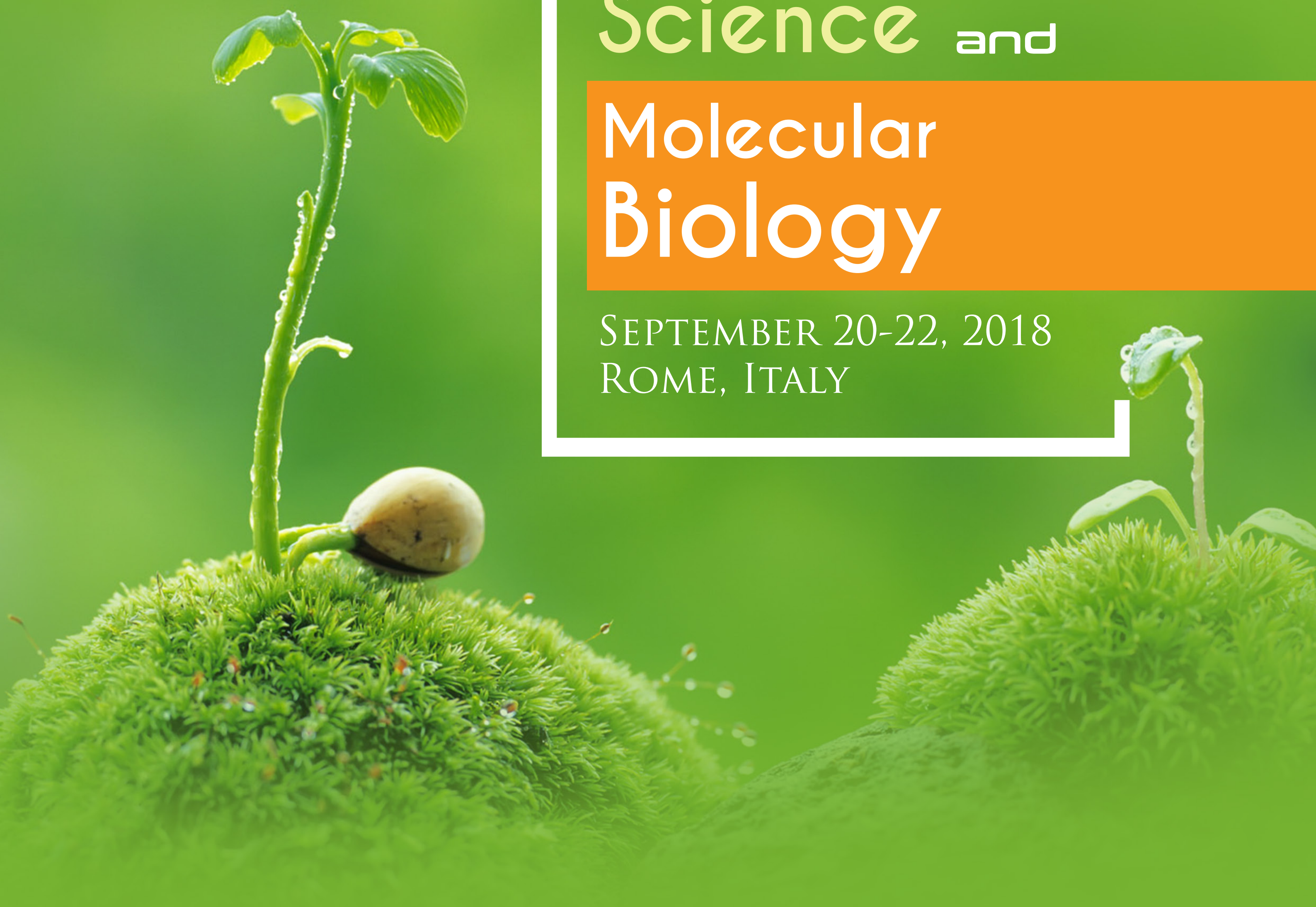
Group

2nd Global Conference on

Plant Science and Molecular Biology

SEPTEMBER 20-22, 2018
ROME, ITALY



Theme: Accentuate Innovations and
Emerging Novel Research in Plant Sciences

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2018

BOOK OF ABSTRACTS

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

Theme:
Accentuate Innovations and
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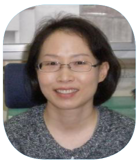

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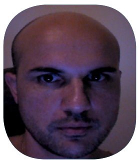

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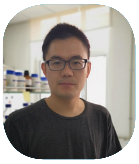

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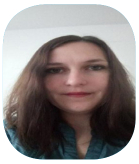

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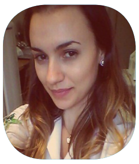

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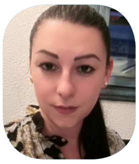

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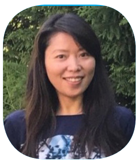

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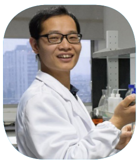

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Thank You
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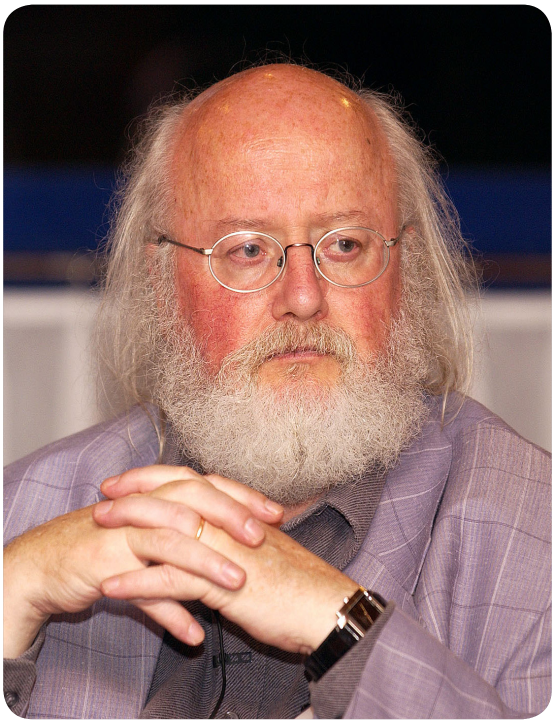
Welcome Message



It is an honor and pleasure to write a welcome note. Biotechnology today makes unprecedented progress, every year new, truly innovative methods for faster and more precise plant breeding. This opens new opportunities to adapt modern breeds to climate change, especially drought impact, but also to achieve higher productivity and to introduce intelligent, differentiated and easier methods to work against crop pests, and even organo-transgenics can be planned properly. It is not a coincidence that most mass crops in modern agriculture originate from ancestral species with natural monodominant stands.

Despite those advantages of modern breeding, many people are fearful about modern agriculture, so we need also better communication methods, contradicting straightforward the often-cheap propaganda of GM opponents. We will have to build our learning processes on different kinds of knowledge, covering all aspects of food production. This is why this conference, inviting on a broad spectrum in age and institutions, will guarantee a professional and well-planned information platform for all ages of speakers, poster writers and listeners.

We look forward to seeing you in Rome, Italy!

Klaus Ammann

Prof. Dr. Klaus Ammann
University of Bern
Switzerland

Welcome Message

On Behalf of the Magnus Group and organizing committee, I cordially invite you to participate and enjoy the 2nd Global Conference on Plant Science and Molecular Biology (GPMB 2018) during September 20-22, 2018 at Rome, Italy. This meeting and city provides a unique opportunity to share cutting edge research and ideas, while surveying the most impressive of historical locations.

Too many times, we become isolated in our individual perspective, and we thus narrow our focus on how to best address the significant challenges of our world and planet. GPMB 2018 is an opportunity to visit with people from diverse cultures and viewpoints and to share ideas for the common good of all. I encourage you to be open to possible collaborations that begin at this conference, but may persist and grow into long term friendships and collaborations.

I look forward to meeting you in Italy.

Thomas C Mueller

Thomas C Mueller, Ph.D.
Professor of Plant Sciences
University of Tennessee, Knoxville, TN, USA

Welcome Message

Dear Participants of GPMB 2018

On behalf of the Planning Committee, we warmly welcome you to Rome to participate in the second edition of the Global Conference on Plant Sciences and Molecular Biology. This conference provides us with the opportunity to celebrate what we have achieved as a professional community of plant scientists to create greater value to all corners of the globe. This conference also provides a platform for us to share and exchange ideas. The conference discusses innovative research spanning the entire spectrum of plant molecular biology, genetics, development, evolution, physiology, biochemistry and related areas. It demonstrates the importance of multidisciplinary approaches to face the challenges of addressing the needs of an ever-increasing world population in a changing climate.

We have an exciting program at the conference that will allow participants to reflect upon scientific advances in the field of plant sciences, renew friendships and establish new networks, and explore future research directions and collaborations. We hope that you will have a productive and fun-filled time at this very special conference.

To put a global conference of this magnitude together is not a small task. To that end, we want to thank the Magnus group and organizing committee for the tremendous efforts to organize all sessions and tracks. We also would like to thank all presenters and participants for their contributions, which are the foundation of this conference.

Enjoy the conference!

Ali M. Missaoui, Ph.D
Institute of Plant Breeding Genetics and Genomics
University of Georgia, USA

Welcome Message

Dear participants of the GPMB 2018,

Welcome to Rome to participate to the 2nd Edition of Global Conference on Plant Science and Molecular Biology. The GPMB 2018 is an opportunity for researchers of academia and industry to share their work and to discuss critical issues in the field of Plant Sciences. This conference should serve to develop new interactions between researchers of different scientific fields and to establish fruitful collaborations to develop innovative approaches. This conference is also expected to allow discussion between senior scientists and young researchers to exchange on their research development and scientific life.

The conference takes place in Rome, one of the famous world cities, a great site for both science and cultural activities.

With our warmest regards, the Organizing Committee wishes you the most productive work and a very pleasant stay in Rome.

Professor Pierre Frendo
University of Nice Sophia Antipolis
France

Keynote speakers

Klaus Ammann
University of Bern
Switzerland

Thomas C Mueller
University of Tennessee
USA

Ali M. Missaoui
The University of Georgia
USA

Frendo Pierre
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About
MAGNUS GROUP

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

Participation from 80 different countries and 688 different Universities have contributed to the success of our conferences. Our first International Conference was organized on Oncology and Radiology (ICOR) in Dubai, UAE. Our conferences usually run for 2-3 days completely covering Keynote & Oral sessions along with workshops and poster presentations. Our organization runs promptly with dedicated and proficient employees' managing different conferences throughout the world, without compromising service and quality.

About GPMB 2018

GPMB 2018 will provide a dedicated platform to peer researchers, young inspired scientists, academicians, and industrialists to meet, discuss and share the knowledge that's still more to be revealed in the field of plant science and molecular biology.

Plant Science and Molecular Biology conference explores the entire breadth of plant science with earlier and contemporary work and provides a critical review of the present state of the subject. GPMB 2018 provides an international forum to intensify the information exchange and is an excellent opportunity for researchers and scientists in the domain of plant science from around the world and to promote/present innovative ideas that will influence and foster continued research.

DAY 1

KEYNOTE FORUM

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

SEPTEMBER 20-22, 2018
ROME, ITALY

Biography

Prof. Emeritus hon. Bern University Switzerland. Born Dec. 6, 1940 in Bern, thesis: vegetation and glacier history, summa cum laude in 1972 Bern University. Research topics: Biodiversity, Vegetation Ecology, Lichens and Mosses, Biomonitoring of Air Pollution, Plant Biotechnology: Biosafety, Gene Flow and Ecology of Transgenic Crops. Guest lecturing in Delft, Netherlands, Istanbul, Turkey, research in Jamaica, at Duke University and Missouri Botanical Garden. Member of the steering committee of www.prri.net. Scientific activities: maintaining 500 reference bibliographies on plant biotechnology and biodiversity, over 320 publications under Klaus Ammann in journals, blogs, newspapers, books on biosafety research and ca. 190 slide presentations, many literature references with full text links. Editor, Co-Editor in journals from Elsevier, Springer and Landes. Member of scientific committees in Switzerland and Europe on biodiversity and biosafety. Fellow of the Royal Society of Biology, external member of the European Academy Details see http://www.ask-force.org/Curriculum/Links2.pdf

How to structure the debate on modern breeding in agriculture?

Klaus Ammann, Prof. hon. Emeritus

University of Bern, Switzerland

We need to introduce a new way of Discourse of difficult topics which are debated since many years in Science, Governments, Institutions and the Public without real progress made and consensus solutions still far away. This means that we have to follow innovative Discourse methods with respect to a diversity of knowledge, from Science to many other transdisciplinary fields of thinking. These discursive methods, coming from Churchman and Rittel, are not easy to apply and need much more work than just done in a happy weekend. The professional discursive work will take months and needs a careful planning of the zero-hypothesis about topics and participants. The debates must be free of ideological constraints and need to commit all participants to a fair amount of factual knowledge, well imbedded in to social sciences. Solutions need to include traditional, modern and organic farming as well.

Take Away Notes:

- The broad audience will be interested in a new vision of the ardent debate on modern breeding, often denounced as dangerous, new concepts will be presented in order to avoid sterile ideologically minded debates on the subject.
- Since the debate will include a great variety of professional views reaching over most faculties in the university teaching, the speaker hopes to present many eye openers in knowledge and practical professional work.
- It will open the way to innovative organo-transgenic agriculture, which is the future of food production world-wide.
- The visions offered in this presentation will ease up a narrow view of ideological constraint and will be a door opener for innovation in agriculture.

Biography

Thomas C. Mueller is a Professor in the Department of Plant Sciences at the University of Tennessee. He received his BS from the University of Illinois in Agronomy, his MS from the University of Kentucky in Crop Science, and his PhD from the University of Georgia in Crop Science. His primary research areas are environmental fate of pesticides (especially herbicides) in soils, water systems, and in the air (via drift), and the confirmation and subsequent control of herbicide-resistant weeds. He has published > 120 refereed articles in > 20 different journals. Dr. Mueller has served on an US-EPA Scientific Advisory Board, has served as an associate editor for Weed Science and Weed Technology, has served on the executive board for the Weed Science Society of America as Secretary, and was named a fellow of the WSSA in 2014.

Why is the mid-southern United States an epicenter for the development of herbicide resistant weeds?

Thomas C Mueller

University of Tennessee, USA

The intensity of agriculture varies across the globe. This report discusses one aspect of plant biology as it relates to the control of unwanted vegetation in a highly managed, intensively farmed area within the United States. While the biological principles apply in all environments, a combination of factors has resulted in a rapid development of herbicide resistant weeds based upon the selection pressure applied. The general area I'm describing is the mid-southern United States approximately 500 km in a circle drawn around Memphis Tennessee.The list of currently confirmed glyphosate resistant weeds in this area is lengthy, and includes Conyza canadensis, Palmer amaranth, Ambrosia trifida, Amaranthus tuberculatus, Lolium multiflorum, Sorghum halepense, Poa annua, Eleusine indica and Echinochloa species. Many of these also have resistance to other different modes of action. Why are there so many weeds that develop resistance in this area?

While no meta-analysis has been performed to identify the most important causal agent, a listing of the factors would include 1. A long growing season, 2. Intensive agricultural production 3. Imperfect crop rotation sequences, 4. No tillage systems being commonplace, 5. A warm climate, 6. Rapid adoption of new technology, and other factors. A long growing season is important because there are multiple niches available for different crops to grow and thus develop and complete their lifecycles. More days of plant growth allow more opportunities for different species to thrive here. Intensive agriculture implies that there is no grazing and no perennial crop such as grass that would provide long-term competition for the various weeds. It is rare to have major herbicide resistant issues within grazed systems. The agriculture in this area is cotton, corn, soybeans and some rice. The frequency of farmers changing what crops they are growing, or rotating their crops, is variable among the different operations. Some farmers grow soybeans each year due to annual river flooding of bottom land fields. Unfortunately, some farmers will grow the same crop multiple years in a row which leads to the situation to select a given weed given a specific herbicide regime. The loess-based rolling topography of this area coupled with intense thunderstorms in the early summer impart the propensity for massive soil erosion losses, so many of the fields are under no tillage production systems. This removes tillage, both before and after planting, as a viable weed control strategy. This puts even more pressure on the herbicides to provide effective weed control. A warm climate has several factors besides having more crops growing here. Crops can germinate earlier in the year and later in the year. Additionally, herbicides that may last and persist to provide greater residual control under cooler environments may degrade more rapidly and thus provide less residual control in a warm climate such as this area. Given the combination of all the above aforementioned aspects of this region, many growers rapidly adopt new herbicides and new herbicide technologies. Thus they are the first ones to begin using them and as such are the first where resistance may develop. As the colloquial phrase goes, "the pioneers take all the arrows". That being said, even though they may rapidly adapt the new technology, there is still a culture where there is some resistance to change. Thus, the attitude, "I will continue to use my identical herbicide program as long as it works" is a prevalent attitude.

Another aspect of why so many herbicides have been confirmed with resistance in this area has to do with scientific discovery. In this region there are several highly active weed science research communities or groups. These diligent and dedicated scientists pursue the weed populations that are not adequately controlled and conduct research upon them to confirm and provide alternate control strategies to the producers. In the absence of this research activity, the existence of some of these populations would only be known in a very small local area.

Take Away Notes:

- There is a perspective that we rely too heavily on herbicides for weed control, and that very well may be correct. The same research groups are actively pursuing non-herbicidal control strategies including cover crops, crop rotations, crop seeding times and rates, and a host of other options. The goal is to have weed control systems that are effective, economical and environmentally sustainable to maintain our production of food and fiber in this region.

Breeding for climate change: Dissecting key adaptation traits in *Medicago sativa* through QTL mapping

Ali Missaoui, PhD

The University of Georgia, USA

Biography

Ali is leading research in forage and bioenergy breeding and genetics at the University of Georgia and teaches advanced plant breeding at the Institute of Plant Breeding Genetics and Genomics. Prior to this role, he worked as Discovery Breeding scientist with Monsanto for 7 years focusing on developing molecular approaches for capturing genetic diversity and maximizing the efficiency of germplasm enhancement. His research interests are focused primarily on applied genetic research of perennial cool season grasses and legumes in addition to perennial grasses as feedstocks with improved suitability as biofuel. He works toward integrating molecular technologies into crop improvement.

With the erratic changes in weather patterns, development of adapted cultivars is becoming a challenge to breeders because of the pseudo-GXE. This implies a clear understanding of key adaptation traits in order to package as many as possible in a cultivar for broad adaptation. This presentation will focus on understanding the genetic basis of cold tolerance and seasonal dormancy in the perennial Medicago sativa (alfalfa) and the association between the two traits, using genotyping by sequencing of a bi-parental population. Developing non-dormant winter hardy alfalfa cultivars allows for extending the production season that would benefit growers and contribute to economic sustainability. QTL analysis was conducted in a pseudo testcross F1 bi-parental mapping population developed by crossing two cultivars contrasting in fall dormancy (3010 with FD = 2, and CW1010 with FD=10). The mapping population along with the two parents, and standard checks were evaluated in three replications at two locations (Athens and Blairsville, GA). Fall dormancy (FD) was measured as plant regrowth height 28 days after clipping on 21st September and in mid-winter to confirm the dormancy level of the segregating genotypes. FD levels were assigned based on a regression equation derived from check cultivars. Cold tolerance and freezing sensitivity of the segregating population was evaluated using indoor screening in a cold chamber at -8 . Frost damage in the field was scored visually from 1-5, with higher numbers indicating more damage. The mapping population was genotyped by using Genotyping-by-sequencing (GBS). The GBS library was constructed using a single digestion with ApeKI enzyme followed by annealing of adapters and amplification. The 96-multiplexed library sequenced at the Georgia Genomics Facility on an Illumina NextSeq PE75 High Output Flow Cell platform. Out of 2032 million raw reads received from sequencing, 1008 million paired reads were usable. The sequence data was processed with the Tassel Uneak pipeline using the R1 reads of the pair-end data. The loci that were present in at least 80% of the total population were considered for the genotyping. Single dose alleles were used for constructing the parental genetic maps resulting in maternal map (CW1010) of 645 and a paternal map (3010) of 1028 SNPs mapped into 8 linkage groups. The average density of markers in the CW1010 linkage map was one marker per 1.9 cM and the average density of markers in the female map was one marker per 1.34 cM. The markers were subsequently used for QTL mapping of fall dormancy and cold tolerance, resulting in 13 major QTL and showing a weak correlation between FD and frost damage.

Take Away Notes:

- The audience should be able to extrapolate the information provided in this presentation to other perennial herbaceous crops.

- With the enormous efforts being made to increase crop yields to meet the needs of a growing global population in food, fiber, and energy, the need for expanding the growing area of crop species beyond their adaptation area is becoming a necessity.
- Climate changes and erratic weather conditions are also imposing different growing conditions on cultivars developed for specific environments.
- Understanding the genetic basis of adaptation traits like cold tolerance, drought and heat will enable breeders to quickly tweak cultivars to cope with these stresses.
- The procedures used in this research will help researchers implement mapping studies in perennial outcrossing species and in crops that do not have reference genome sequences and no available genomic resources.

DAY 1

SPEAKERS

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

September 20-22, 2018
Rome, Italy

Effects of Dicamba Micro-Rates on sensitive crops

Stevan Z. Knezevic
University of Nebraska-Lincoln, Concord, NE, USA

In order to control glyphosate resistant weeds, Dicamba-Tolerant (DT) Soybeans were plated at about 20 million US acres in 2017. It is believed that the number of acres will increase in 2018 season, which created a concern that the widespread use of dicamba-based herbicides in DT soybeans can result in un-intended drift due to windy conditions in USA. Therefore, the objective of this study was to establish some baseline indicators on the injury of potentially sensitive crops (eg. non-dicamba-tolerant soybeans, grapes and tomato) to six rates of three dicamba-based herbicides (Clarity, Engenia and XtendiMax.Field study was conducted in 2016and 2017 as a split-plot design with 6dicamba rates, 3 application times and 4replications. Dicamba rates were: 0; 1/10; 1/100; 1/500; 1/1000; 1/1500 of the label rate of three dicambaherbicides (560 g ai/ha). Plots had four rows of each soybean type (conventional,organic, Roundup-Ready,Liberty-Link),and Dicamba-tolerant soybeans(as a check) as well as pot-grown grape plants (2nd year of growth) and tomato seedlings.There were three application times of dicamba (eg. V2 (soybean 2ndtrifoliate), beginning flower (R1) and R2 (full flower) and corresponding size of grapes and tomato.As micro-rates increased, the crop growth parameters were significantly impacted, including: reductions in plant height, alterations in branching pattern, delayed days to canopy closure and delayed dates of flowering, reductions in flower number, delayed dates of physiological maturity, and most importantly reductions in soybean yield. The foregoing negative impacts were dependent on correspondence of application date with the soybean growth stage; with V7/R1 stage being the most dicamba sensitive. The 1/10 rate killed grapes (1st timing) and severely injured tomato (80%). However, there was only temporary injury in the 2nd timing in grapes. The 1/100 (and 1/1000) rate provided only transient symptoms in grapes and tomato (both timings). This is suggesting that grapes and tomato are not as sensitive to dicamba as the non-dicamba soybeans. These results clearly showed that non-DT soybeans were sensitive to even very low micro-rates of Clarity, Engenia and XtendiMax, hence, efforts should be made to avoid drift of dicamba onto non-DT soybeans.

Take Away Notes:

- Audience will have a chance to learn about one of the most important production issue in US soybean production.
- Members of the audience that are involved with soybean production will learn the level of soybean sensitivity to micro rates of Dicamba based products.
- Our data will provide information needed for educational materials about the critical need for proper herbicide application procedures and sprayer cleaning in order to reduce dicamba's off-target movement.

Biography

Stevan Knezevic teaches graduate level internet based class on "Integrated Weed Management". He published 146 manuscripts, 10 book chapters, 19 extension publications, including an annual Guide for Weed, Diseases and Insect Management in Nebraska, of which he is a senior editor. Stevan has supervised 3 postdoctoral fellows, 28 graduate and 14 undergraduate students. He also hosted 31 international visiting scientists in his lab. Stevanhas received total of 22 awards for his research, publications, or presentation style.

A genomic analysis of interactions between a vector-borne phyotpathogen and cotton

Enrique G. Medrano*, Ph. D., USDA/ARS/SPARC, James Glover, Ph. D. Graduate Student, Texas A&M University, and Michael Brewer, Ph. D., Texas A&M University

Cotton (*Gossypium hirsutum* L.) is grown globally and of significant economic value. Polyploids of several G. hirsutum have been sequenced. Bacteria transmitted by piercing-sucking pests of cotton bolls can cause major yield losses due to resulting seed and lint necrosis. We recovered Serratia marcescens bacterial representatives from rotted bolls fed upon by verde plant bugs (Creontiades signatus) in Texas that is a major US cotton producing state. Here, we present a draft whole genome sequence generated using high-throughput sequencing technology of a S. marcescens strain called CC118 that is capable of causing a comparable cotton boll infection. A focus of the project was to mine for virulence genes and respective host avirluence genes from published cotton genomes. A chromosome (4.4 Mb) and plasmid DNA (>100 kb) were identified. Bacterial genome annotation revealed homologies with pathogenicity determinants including a type IV secretion system and invasins that are known to be involved in the infection process of other pathogens. Further, putative avirulence genes in the allotetrapliod G. hirsutum acc. TM-1 have been potentially identified. This work assists in developing techniques to minimize damages associated with S. marcescens infections.

Take Away Notes:

- Presentation attendants shall be informed of vector-borne plant infections, bacterial biology, and disease agents identified genetically in a novel S. marcescens strain vectored by a significant insect cotton pest.
- The information presented could likely be broadly applicable to other phytopathogenic bacterial infection paradigms for use by researchers and incorporated into plant pathogen courses. Generally, the whole genome sequence data could be used in comparative genomics work toward differentiating between plant pathogenic bacteria and non-pathogenic strains based on the presence/absence of disease determinant genes; thus, bypassing the time consuming and costly process of identifying genus and species followed by testing for pathogenicity capacity.

Biography

Dr. Medrano has 15 years research experience with the United States Department of Agriculture-Agricultural Research Service. He was the first to show that rotting of immature green cotton bolls is caused by infective microbes and demonstrated that these pathogens are vectored by boll-piercing insects such as stink bugs. He has authored 44 scientific publications and is known and respected by colleagues for conducting innovative and superior quality research. He has presented more than 64 papers, posters, and seminars at scientific conferences, many by invitation including 7 international conferences.

Genetic breeding as a tool to control the pine wilt disease

Raquel Díaz*, PhD, Margarita Alonso, graduate degree, María Menéndez-Gutiérrez, PhD
Lourizán ForestResearch Centre, Spain

Pine wilt disease (PWD) is caused by the pine wood nematode (PWN), Bursaphelenchusxylophilus, which is transmitted by a vector of the Monochamus genus. This nematode is an invasive pest that nowadays constitutes the greatest menace to conifer forests, mainly pine forests, worldwide. It is native to North America, where it´s non-pathogenic; it has been introduced to East Asia and Portugal and has caused severe environmental and economic losses. In Spain five outbreaks have been declared, three of which are still active.The forecasted losses for Spain are higher than 11 billion euros for 2008-2030. The main host species in Europe is maritime pine (Pinuspinaster), however radiata pine (P. radiata) and Austrian pine (P. nigra) have also been affected.

Breeding for resistance or tolerance is presented here as one of the main strategies to fight against this disease.Resistance or tolerance to this nematode has been included in the Galician P. pinaster and P. radiata breeding programs. Since 2013 we have performed several inoculation assays under greenhouse conditions with the aim of findingresistant or tolerant genetic materials which could be included in the Spanish National List of Basic Materials to produce Forest Reproductive Materials for new plantations. We performed inoculation assays on different genetic materials (species, provenances and families). We found significant differences at the three genetic levels. When working with P. pinaster and P. radiata families, the character resistance or tolerance to PWN was found to be genetically controlled, since some families of both species were less susceptible to this nematode than the other evaluated ones. Moreover,some individuals of both species were inoculated more than once and they remained asymptomatic. All of these indicate that genetic breeding could be a possible strategy to control the terrible disease caused by the PWN.

Additionally we studied different constitutive chemical compounds trying to find if any of them could be related to theB. xylophilus resistance or tolerance. Our results show that it is possible that some of the studied compounds could be related to it, as a good relationship was found at species level. If this relationship also worked at family level, these constitutive chemical compounds could be used as a proxy for resistance or tolerance.

Take Away Notes:

- Start similar works with other pathogens and/or diseases which are affecting different plant species and are causing a big impact in forest and/or agricultural sectors.
- Learn how to design and work in a plant breeding program and highlight the importance of genetic breeding as a useful tool to fight against pathogens and/or diseases.
- To be aware of the threat that pine wilt disease constitutes to pine forests and adopt prevention measures in countries at risk of pine wilt disease entrance. Give information about the susceptibility of species and provenances which had not been tested before to B. xylophilus.
- Provide information about the use of constitutive chemical compounds as a proxy of tree tolerance.
- Give confidence to the forest sector (industries, owners and researchers) that the genetic breeding can be one of the solutions to pine wilt disease.

Biography

Raquel Díaz (PhD, Forest Engineer) graduated in Forest Engineering (Madrid Polytechnic University – Universidad Politécnica de Madrid) in 1996. Since 1997 she has been working at the Lourizán Forest Research Centre (Pontevedra, Spain) on quantitative genetics of forest trees. She presented her thesis ("Genetic Breeding of Juglansregia") in 2001. Since 2010 she has been in charge of the Galician genetic and silviculturalbreeding programs of Pinuspinaster and Pinusradiata; and since 2013 her main objective has been to study resistance or tolerance mechanism of pine trees against pine wood nematode and find resistant or tolerant individuals as a strategy to control pine wilt disease.

High diluted solution of *Thuya occidentalis* changes photosynthetic response curves in tomato plants infected with *Meloidogyne incognita*

Jose Renato Stangarlin* (PhD, Western Parana State University, Brazil)
Thaisa Muriel Mioranza (PhD student, Maringa State University, Brazil)
Adriano Mitio Inagaki (PhD, Western Parana State University, Brazil)
Monica Anghinoni Müller (PhD student, Parana Federal University, Brazil)
Odair Jose Kuhn (PhD, Western Parana State University, Brazil)
Vandeir Francisco Guimaraes (PhD, Western Parana State University, Brazil)

The use of high dilutions on plants may cause changes in plant metabolism and result in disease control by inducing resistance. This work aimed to study the physiological responses of tomato plants (Solanum lycopersicum L.) infected with the root-knot nematode Meloidogyne incognita and treated with highly diluted preparations of Thuya occidentalis. The treatments included: T. occidentalis 6CH, 24CH, and 50CH (CH: centesimal Hahnemanian) prepared according Pharmacopoeia; a water control (with nematode and without treatment); and an absolute control (no treatment and no nematode). At the time of transplanting, the root system of the tomato seedlings was dipped in 0.1% of treatment solution (1 mL of solution diluted in 1 L of distilled water) before seedlings were planted in the pots. Seven days after planting, seedlings were inoculated with pathogen. Gas exchange was measured on full sun days, between 9:00 am and 11:00 am, using an infrared gas analyzer (IRGA) portable photosynthetic system (Li-6400XT, LI-COR, Lincoln, Nebraska, USA). Gas exchange measurements were done prior to nematode inoculation and five, eight, and 13 days after inoculation. Measurements were performed in 6 cm² of the second fully expanded leaf that was exposed to sunlight. Photosynthetic rate, stomatal conductance, transpiration, leaf internal CO2 concentration, and leaf temperature were measured at various photosynthetic photon flux densities, varying from 1800 µmol m-2 s-1 to zero and measurements started at 400 µmol mol-1 of CO2. Experiments were conducted in a greenhouse using a randomized block design with four replications. No significant difference was found in the different gas exchange specific measure parameters between the treatments. Untreated infected plants showed an increase in net photosynthesis and in the carboxylation capacity, as shown by the light response curve. Treatment with T. occidentalis 24CH inhibited the increase in CO2 fixation in tomato plants inoculated with the pathogen M. incognita, leading to a similar behavior as healthy plants, independently of the photon density.

Take Away Notes:

- The use of homeopathy for controlling plant diseases, and even in other fields of science, requires assays with experimental and statistical designs to ensure its efficiency. I think with these data, other researchers would be interested in use the homeopathy in their biological systems. Homeopathy is an eco-friendly tool very useful for agriculture in spite to solve phytosanitary problems.

Biography

The presenter author is professor in a public university since 2000. I got my PhD working with plant pathology, specifically the development of alternative methods for controlling plant diseases caused by fungi, bacteria and nematodes. To reach this purpose, we use extracts obtained from medicinal plants and fungi, as well as high diluted solutions (homeopathy), in spite to induce resistance defense mechanisms in treated plants against the pathogens. Some of plant defense mechanisms we study are pathogenesis related proteins like chitinases, beta-1.3 glucanases and peroxidases, phenolic compounds and their key enzyme phenylalanine ammonia-lyase, and reactive oxygen species as hydrogen peroxide and superoxide anion.

Transfer of chromatin of wild goatgrasses (*Aegilopssp.*) carrying leaf rust resistance genes into triticale (× *Triticosecale* Wittmack) using chromosome engineering

Michał Tomasz Kwiatek*, Ph.D., Jolanta Belter, M.Sc.,Halina Wiśniewska, Prof.
Institute of Plant Genetics of the Polish Academy of Sciences, Poland

In cereal breeding, precise chromosome engineering using homologous recombination is a method harnessed for controlled introduction of chromatin fragments with desirable genes or loci into nuclear genome of crop plants. Alternatively, this practice can be employed for induction of changes in chromosome structure, which increase the value of crops. This study focuses on introduction of chromosomes (and chromosome segments in further stages) of goatgrasses (Aegilops sp.) carrying leaf rust and yellow rust resistance genes into cultivated triticale using chromosome engineering. In this purpose we have developed three types of monosomic substitution lines of hexaploid triticale (× TriticosecaleWittmack) carrying 2DAe.tauschii or 2SAe. kotschyior 2SAe. variabilis instead of chromosome 2R. At the same time, we have produced triticale DH lines carrying telosomic 2R chromosomes and 5BS-5BL.5RL translocation (lack of Ph1 loci). The aim of this work is to develop three types of translocation plants carrying Lr22a+Lr39 (from Aegilopstauschii), Lr54+Yr37 (from Ae. kotschyi) and Lr59 (from Ae. variabilis). The primary recombinants carrying Robertsonian translocations were produced using induced hybridizations between triticale monosomic plants carrying a donor Aegilopschromosome and triticale (lacking Ph1 loci) bearing 2R telosomic chromosome as an acceptor. The future aims involves the production of secondary recombinants, carrying reduced segment of Aegliops chromatin and the consolidation of the resistance genes loci.

Take Away Notes:

- The term "chromosome engineering" describes technologies in which chromosomes are manipulated to change their mode of genetic inheritance. This study shows recent innovations in chromosome engineering of triticale that promise to greatly increase the leaf rust resistance of this crop. This kind of technology enables to introduce into triticale newly discovered and effective resistance genes in short period of time. It allows to omit the time-consuming classical breeding programs, that mainly are basing on the cross-hybridization rounds with resistant forms of wheat followed by subsequent backcrossing and multi-year selection.

Biography

Michał T. Kwiatek was born in Poznań, Poland in 1985. He did his M.Sc. at the Poznań University of Life Sciences and joined the Laboratory of Distant Hybrids at the Institute of Plant Genetics of the Polish Academy of Sciences in Poznań. His Ph.D. thesis was considering the cytogenetic analysis of Aegilops-triticale hybrids. As a Ph. D. candidate and later as a post-doc, he was a head of two National Science Centre projects and co-executor in nine scientific projects. Now he is an academic teacher and holds a prestigious scientific project – LIDER, granted by National Centre of Research and Development.

ATTRACAP: An innovative attract-and-kill strategy for the control of wireworms

Beitzen-Heineke W*[1]., CEO, Beitzen-Heineke E[1]., M. Sc., Przyklenk M[1]., Ph.D., Patel A[2]., Prof., Vidal S[3]., Prof.,
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[2]University of Applied Sciences Bielefeld, Germany
[3]Georg-August University Goettingen, Germany

Wireworms, the polyphagous soil-dwelling larvae of click beetles (Coleoptera: Elateridae), are a major insect pest of worldwide relevance causing tremendous yield losses in several crop production systems, like potatoes. The entomopathogenic fungus Metarhizium brunneum is already known as an efficient biocontrol agent against wireworms. However, applications of unformulated M. brunneum are too expensive due to a required high dose per ha. Besides, the fungus is poorly storable for months and has a low rhizosphere competence. Therefore, an innovative attract and kill formulation based on solely biological components was developed: ATTRACAP®. The granulate contains baker's yeast as an attract component, an isolate of M. brunneum as a kill component and a substrate as a nutrient source and drying aid. The granulate emits CO2 after contact with soil humidity over a period of several weeks to attract the wireworms. Simultaneously, M. brunneum is growing out of the beads and forming new conidia infecting the attracted wireworms. The attract and kill formulation enables a lower application dose per hectare, thus, making the granulate cost-effective and eco-friendly. In 2018, ATTRACAP® obtained for the third time the emergency registration in Germany and Austria. The future aims are to improve the efficacy of ATTRACAP® and to transfer this technology to other pests. These aims will be investigated in a new research project called ATTRACAP and the project is founded by the Bundesministerium für Ernährung und Landwirtschaft (BMEL).

Take Away Notes:

- A smart an innovative formulation
- The use of biomaterials as nutrient source and as drying agent
- The synergistic use of two microorganisms in one product
- How can an innovative formulation reduce the dose/ha

Biography

Wilhelm Beitzen Heineke studied agricultural sciences at the Georg-August University D- Goettingen. Afterwards he worked for the company KWS located in Einbeck, he was responsible for the distribution of seeds, at least especially in Russia. At the KWS he firstly came in contact with the beneficial organism Trichogramma brassicae in 1982. In 1995 Wilhelm Beitzen-Heineke founded his company BIOCARE for the production of TRICHOSAFE® (Trichogramma brassicae) as beneficial against the corn borer. In 2003 BIOCARE enter the European market and produced over 100.000 ha TRICHOSAFE® products in 2018. In 2016 BIOCARE expanding the production line by introducing a newly developed biological product ATTRACAP® which is used to fight wireworms in potato farming.

Seagrass (*Zostera marina*) population genetics in a spatially-structured natural system

Nahaa M. Alotaibi [1, 2]*, Emma J. Kenyon [3], Kevan J. Cook [4], Luca Börger 1, and James C. Bull [1]

[1] Department of Biosciences, Swansea University, Wales, United Kingdom.
[2] Princess Nourah bint Abdulrahman University, Kingdom of Saudi Arabia.
[3] School of Life Sciences, University of Sussex, Brighton, England, UK.
[4] Natural England, Truro, England, UK.

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 important sources of coastal primary production and it provides a critical habitat for juvenile reef fish and commercial fisheries. However, seagrass experiences numerous local and broader scale threats and is seen to be declining globally. 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 over-arching goal of this study is to gain an understanding of the spatial population genetics of eelgrass, Zostera marina, in the Isles of Scilly, UK.

The Isles of Scilly includes the largest continuous expanse of seagrass in England and Wales and is reported to be amongst the best condition in the UK. However, long term monitoring has revealed worrying declines there. Using an existing panel of 15 microsatellites, we estimated genetic variation in Zostera marina at five sites around the Isles of Scilly and compared this to long term ecological monitoring. We tested hypotheses on how long term declines in local seagrass populations are predicted to result in restricted genetic diversity and departure from Hardy-Weinberg equilibrium.

As predicted, the level of genetic variation was found to be substantially lower at the two sites observed to be in long term decline. However, while all sites had less observed heterozygosity than expected under Hardy-Weinberg equilibrium, observed heterozygosity was greatest at the two declining sites, and inbreeding lowest at these two sites. This is contrary to the widely held assumption that low heterozygosity and high inbreeding are signs of poor population health and viability. We propose that the explanation for this is a shift in the relative contributions of sexual and asexual reproduction, likely resulting from the underlying causes of population decline. A collapse in vegetative reproduction through rhizome extension, leaving flowering as the main source of productivity could result in these observations. This not only has implications for understanding seagrass population viability but also wider implications for assessing numerous plant species with similar reproductive strategies.

Take Away Notes:

- The audience will be able to understand more about the population genetic structure, evolution of the population, and measures of genetic distance between sites.
- The presentation will provide an in-depth understanding to adapt experimental protocols presented for other important plant species.

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 Prof. Luca Borger in the Department of Biosciences, Swansea University, UK.

I have gotten Masters of Science degree in plant ecology from Princess Nourah 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. In 2011, I have been working in Princess Nourah bint Abdulrahman University, Riyadh, Saudi Arabia.

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.

Genomic analysis of lipid-related genes showed insight to the high oil content in sesame

Linhai Wang* Ph.D., Xin Wei Ph.D., Yanxin Zhang Ph.D., Prof. Xiurong Zhang
Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture, P. R. China, Oil crops Research Institute, Chinese Academy of Agricultural Sciences, Wuhan 430062, China

Sesame is considered the queen of oilseeds for its high oil content and quality, and is grown widely in tropical and subtropical areas as an important source of oil and protein. The completion of sesame genome assembly provides novel insight into its genomic structure and gene composition, which offered us the chance to study the genes associated with lipid biosynthesis. Sesame genome was predicted to contain 27,148 gene models, and 708 were expected to be lipid-related genes. The number was lower than other plants, in spite of the higher oil content. In comparison to soybean, sesame was found to have more lipid transfer protein type 1 (LTP1), but less copies in the two cytosolic lipoxygenase (LOX) and lipid acyl hydrolase-like (LAH) families, which suggested the expansion of some lipid gene families, and the contraction of lipid degradation-related families may lead to higher oil content in sesame than soybean. Genome-wide association study for the genes related to lipid by resequencing 705 diverse sesame varieties showed a total of 13 significant associated peaks in different environments, and the two SiPPO and SiNST1 were interestingly included in the candidate causative genes, but they were not predicted to have direct involvement in oil biosynthesis. Comparative transcriptome profiling of developing sesame seeds and capsules showed a list of lipid-related genes may responsible for the oil content difference in different sesames, including the genes encoding lipid transfer protein. In addition, some new genes that may contribute to lipid biosynthesis were also figured out for future study.

Take Away Notes:

- The research advance of the special oil crop sesame.
- Why sesame seed is high in oil content?
- What happened to LTP genes during the evolution of sesame?
- The gene expression profiles of high and low oil content sesame in seed development.
- Which genes will act to shape the high and low oil content sesame?
- A comprehensive database including sesame genetic and genomic informations.

Biography

Linhai Wang is a vice professor of Oil Crops Research Institute, Chinese Academy of Agricultural Sciences (OCRI, CAAS), and leads a group study on sesame and special oil crops. He earned his PhD in wheat genetics and breeding from the Graduate School of Chinese Academy of Agricultural Sciences (GSCAAS) in 2009. Then, he was recruited to study sesame molecular genetics by OCRI, CAAS. He is mainly focusing to study sesame plant type and quality traits such as oil content based on genetics and genomics at present. In 2014, he published the first sesame genome sequence in Genome Biology, and updated it to a better level in 2016.

Breeding of rice in the agricultural research center “Donskoy”

Kostylev PI
Agricultural Research Center “Donskoy”, Russian Federation

In the process of selection work in the rice laboratory a number of intensive varieties were created with different vegetation period and grain form. In the Register of breeding of the Russian Federation achievements made rice varieties: early maturing Contact (1994), mid-ripening Boyarin (2002), long Svetly (2006), mid-ripening Commandor (2008), salt tolerance Uzhanin (2011), high-yield Kuboyar (2014), bushy Acoustic (2018).

The starting material 900-samples the personal collection from the International Rice Institute (IRRI), All-Russia Research Institute of Plant (VIR), Rice Research Institute Rice (Krasnodar) and its (ARC “Donskoy’) are used for selection.

Of great importance is the resistance to blast. In this regard, the use of disease-resistant plants in the selection process is necessary. In our collection there are samples with resistance to blast, which is controlled by the genes Pi-1, 2, 33, 40, b, ta. With their participation a large number of hybrids have been obtained, combining all these genes and possessing a set of economically valuable traits.

At the first stage of work in 2003, we crossed the varieties Boyarin and Virage with donors of genes for resistance to blast Pi-1, Pi-2, Pi-33 in 6 combinations. In the second generation, in each combination, plants selected combining early maturity, short stature, nonshatter and fertility of the spikelets. They were analyzed for the presence of dominant alleles of resistance in them. PCR analysis allowed to isolate forms homozygous for Pi-1 Pi-2 and Pi-33. The electrophoregrams of DNA showed the spectra of stable and unstable forms. As a result, the work was created by middle-grade blast resistant and Mogul carrying genes Pi-1 and Pi-2 and Pirouette having 3 gene: Pi-1, Pi-2 and Pi-33. They form a grain yield of more than 10 tons per hectare. At the second stage of the work, when the donor genes Pi-b and Pi-ta, in 2010 took place hybridisation with them the forms, combining genes in genotype Pi-1, Pi-2, Pi-33. F2 hybrid plants in 2012 were analyzed using one a marker for each gene. 12 lines are identified, with all 5 dominant genes. An intermediate-variety Pentagen with five genes was created. The period before maturation is 120 days, height of the plants is 100 cm, length of the panicle is 22 cm.

To select salt-tolerant forms, natural provocative backgrounds are used - salted checks and laboratory tests. The salt tolerance was determined from the ratio of the length of germs and rootlets in the test to the percentage control. Seeds were germinated in a 1.5% solution of NaCl (experiment) and in distilled water (control) by a roll method in triplicate at 25°C for 10 days. Hybrids were analyzed from the crossing of Asian salt-resistant samples of NSIC Rc 106, IR 74099 and others with the Russian variety Novator. At the same time, the DNA of best plants was analyzed for the presence of Saltol gene markers. The best samples are selected.

In the world, large areas of the earth are prone to flooding, with a duration of more than two weeks, rice dies. The Sub1 gene, which regulates the reaction to ethylene and gibberellin, leads to a restriction in the consumption of carbohydrates and the calmness of shoots under water, which contributes to tolerance to immersion. In Russia, this gene can be used to create varieties resistant to the phase of germination to a large layer of water, during which perches die, which will be an effective way to protect rice from weeds without herbicides. Donors of the gene for resistance to prolonged flooding of Sub 1A were varieties: BR-11, CR-1009, TDK-1, Inbara-3. Homozygous lines F5 carrying this gene and adapted to the conditions of northern rice growing are isolated.

Biography

Kostylev Pavel Ivanovich - Doctor of Agricultural Sciences, Professor, Head of laboratory breeding and seed production of rice Agrarian Science Center “Donskoy”, Zernograd, Russia.

From 1972 to 1977 he studied at the Rostov State University in the Biological Faculty, specialization - genetics. Upon graduation in 1977 working in the laboratory of rice All-Russian Scientific Research Institute of Crops. Since 2000, the head of the laboratory work.

In 1986 he defended his thesis on “The prospect of selective use of wild species of rice” on the specialty 05.01.04 - plant breeding and seed. In 1999 he became a doctor of agricultural sciences. He received his Ph.D. at the Kuban State Agrarian University, Krasnodar, on the topic: “Breeding of rice and sorghum using distant hybridization conditions in the North Caucasus”, majoring in plant breeding and seed. In 2007 he received the title of professor.

Conducted research on the genetics and breeding of rice. First held in Russia interspecific hybridization and got distant hybrids of rice with 15 wild species.

Together with the Laboratory of Biotechnology Research Institute leading rice breeding resistant varieties of rice blast disease using DNA markers and PCR analysis. With his graduate students spent a large amount of research in the field of genetics of quantitative traits not only in rice but also in sorghum, soybeans, peas, barley and wheat.

Scientific experience - 40 years experience of pedagogical work - 17 years; personally and co-authored published 340 scientific, 8 educational works and 19 inventions. Of scientific publications: Sorghum (breeding, seed, technology, economics), 2003, Recommendations for growing rice varieties in the Rostov region, 2004, North Rice, 2004, Catalog donors and sources of rice ARSRIC, 2008, Guidelines for rice cultivation technology, 2008, Agrotechnological passport Don rice varieties, 2010, Methods breeding, seed production and quality agrotechnics rice, 2011, Wild species of rice, 2011, Weeds, diseases and pests of rice agrocenosis Southern Russia, 2011.

Spend with rice breeding work to create productive varieties resistant to blast disease, salinity, flooding, cold, lodging. Working with coarse samples the genetic collection of 900 samples.

I am one of the authors of the twelve rice varieties: Budennovsky, Privolny, Razdolny, Contact, Virage, Boyarin, Svetly, Volgogradsky, Comandor, Uzhanin, Austral, Kuboyar, Akustik and four varieties and three hybrids of sugar and grain sorghum: Sever 2 , Sever 44, Kazachy 2, Zersil, Darcil, Picador, Sazhen who entered into the State register of breeding achievements of the Russian Federation.

Member of the editorial board of the journal "Rice-growing," a member of the Dissertation Council, Don State Agrarian University. Carry out scientific management in 20 post-graduate students who have defended their dissertations.

Nucleolar iron impacts rDNA organization and expression in *A. thaliana*

Montacié C.[1, 2*], Wei L.[3], Escande M.L.[4, 5], Jobet E.[1, 2], Barbarossa A.[1, 2], DeBures A.[1, 2], Laudié M.[1, 2], Pontvianne F.[1, 2], Mari S.[3] andSáez-Vásquez J.[1, 2]

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[5]BioPIC Platform of the OOB, 66650 Banyuls-sur-mer, France.

The biogenesis and structure of the nucleolus are directly linked to ribosomesynthesis. Remarkably, plant nucleoli contain a major pool iron. Interestingly, accumulation of iron in animal cells induces rDNAhypermethylation and oxidation of pre-rRNA, and is linked to neurodegenerative diseases. In this context, it would be important to study the structural and functional relationship between iron andplant nucleolus.Here, we studied the functional rDNA organization in Arabidopsismutant plants with reduced amount of iron in the nucleolus:nas (nicotianamine synthase) plants.

In A. thaliana (Col-0), hundreds of 45S rRNA genes (45S rDNA) units are located on chromosomes 2 and 4, in regions called Nucleolar Organizer Region (NOR 2 and 4). Each 45S rDNA contains the 18S, 5.8S and 25S rRNA sequences separated by internal transcribed spacer (ITS1 and ITS2) and flanked by 5' and 3' external transcribed spacer (5'ETS and 3'ETS). Three major classes of 45S rDNA, referred as rDNA variants 1 to 4 (VAR1-4), can be identified in Arabidopsis. The rDNA VAR1 (~50% of the copies) is expressed only during seed germination and localizes in the NOR2 (inactive/silenced) while rDNA VAR2 and 3 are constitutively transcribed and localize mainly in the NOR4 (active).

We observed that in nasplants,reduced amount of iron seems to not affect rRNA processing or assembly with ribosomal proteins. In contrast, we showed that rRNAVAR1 genes are expressed, indicatingthe activation of the normally silenced NOR2. De-repressionof NOR2 is correlated with itsassociation to nucleolus and with rDNA methylation changes. Interestingly,hypomethylationof the 3'ETS, rather than the 5'ETS (hypermethylated), is correlated with activation of NOR2 in the nas plants. These results, associated to other observations, suggest that NOR2 activation in nas mutant correspond to a failed-silencing of NOR2 during early stage of plant development. Altogether, these data will be presented and discussed.

This work is supported by the CNRS, the UPVD (fellowship to CM) and by an ANR grant SVSE2_SUBCELIF 087217.

Take Away Notes:

- This work addresses fundamental question concerning gene regulation in plants. More precisely how iron, which is major issue in plant agriculture, affect DNA functional organization and expression. We provides evidences that iron in plants affect rDNA NOR2 repression/de-repression in A. thaliana. Nevertheless, this high pool of iron in the nucleoli should have other effects on cell processes that need to be study. Since, NOR silencing is controlled by epigenetic mechanism we can expect that RNA silencing pathways as RdDM activities might be controlled by iron. Another major issue could beto determine the absence/presence of Reactive Oxygen Species in nucleolus.

Biography

Charlotte Montacié is a Ph.Dsudent in third year of thesis under the direction of J. Sáez-Vásquez, at the "LaboratoireGénome et Développement des Plantes" Perpignan, France (http://lgdp.univ-perp.fr/index.php?page=equipe-4).

She published an article demonstrating a link between proteasome and nucleolus functional structure (Montacié et al., 2017, Frontiers in Plant Science).

Before doing her thesis, she did training courses in applied biology:

- Bachelor degree (6 months): Detection of Citrus roots stock diplo / tetra – ploidy by phenotyping analysis, an helpful tool for citrus breeders and producers.
- Master degree (4 months): Mangiferin quantification, using HPLC method, in leaves of Coffea species.

Breeding for the ensure the good quality of the Hungarian Persian walnut industry

Geza Bujdoso*, Ph.D, Ferenc Izsepi, Ph.D student, Krisztina Bartha-Szügyi, Ph.D student, Virag Varjas research fellow, National Agricultural Research and Innovation Centre – Fruitculture Research Institute, Budapest, Hungary
Anita Vegh, Szent István University, Budapest, Hungary
Nóra Adányi, Ph.D, Éva Kónya, Ph.D, National Agricultural Research and Innovation Centre – Food Science Research Institute, Budapest, Hungary

The Persian walnut (Juglans regia L.) is the most important shell fruit species in Hungary. Growing of this species became very popular in the past 10-15 years. Pomological evaluation of a double selected walnut population was done to select new promising genotypes at the National Agricultural Research and Innovation Centre – Fruitculture Research Institute. The experimental orchard was established in 1997, and it contains around 100 double selected different genotypes. The examined genotypes originated from the following combinations: 'Milotai 10' x 'Pedro', 'Pedro' x 'Alsószentiváni 117', 'Alsószentiváni 117 x Pedro'. During the examination period the most important characteristics of the genotypes were examined, such as leafing-out time, blooming time, ripening time and physical parameters of the walnut fruits. Based on our results five genotypes had late leafing-out time. Significant difference was observed during the examination of blooming time and ripening time compared to the standard Hungarian variety. Based on the results of the measurement of physical parameters all genotypes reached 32 mm fruit size in diameter, which is the requirement of the first grade fruits on the market. The fruit weight and fruit volume values of most hybrids exceeded the results of the control variety 'Alsószentiváni 117'. Only two genotypes reached 50% in kernel rate. 11 genotypes reached the ideal 70% cracking ratio (ratio of halves and whole). Based on the results of this study three genotypes (tree no. V/2/28-30, tree no. V/3/30-31 and tree no. BD6) were found which had excellent values. Further studies are required to investigate this three promising walnut hybrids. As these genotypes characteristics analyses carried out, also the compositional data of the walnuts was started to determine in the National Agricultural Research and Innovation Centre – Food Science Research Institute. Nuts and particularly walnut are recommended, important parts of human daily diet, because of their advantageous composition and nutritional value. Walnut is a good source of edible oil, fatty acids, tocopherols (vitamin E), phenolic compounds, and minerals (calcium, iron, magnesium, potassium). The composition of walnut (fatty acids, vitamin E, protein content) is affected by the cultivars, geographical origin, climate, storage.

Walnut is a good source of oil (50-73 g/100 g) and rich in polyunsaturated fatty acids (PUFA). According to the composition of fatty acids walnut consumption has protective effect against cardiovascular diseases. The major fatty acids found in walnut oil are oleic acid (16-31 g/100 g), linoleic acid (50-63 g/100 g) and linolenic acid (8-14g/100 g).

Gamma-tocopherol (164-295 mg/kg) is in ten times higher concentration than alfa- (8-21 mg/kg), and delta tocopherol (9-16 mg/kg), and tocopherols show antioxidant activity. Alfa-tocopherols presents the highest biological potential. Besides tocopherols the phenolic compounds (total polyphenols 1326-2175 mg/100 g) also have important role in protection against lipid oxidation.

The research was supported by National Research, Development and Innovation Office in the frame of "Walnut breeding in order to release new late leafing and lateral bearing cultivar(s) project (project no. 123311).

Take Away Notes:

- The audience could lead how different to evaluate a Persian walnut population using classical methods.
- Message of the presentation is to have some information about the Persian walnut breeding aims.
- Furthermore, some information / characteristics / traits about the novel bred cultivars will be provided to the audience during the presentation.

Biography

Géza Bujdosó finished the University of Horticulture and Food Industry in Budapest in 1999, he received his PhD degree at Doctoral School of Corvinus University of Budapest in 2007. In 2017 dr. Bujdosó finished his habilitation at Széchényi István University in Győr (Hungary). He is head of Nut Tree Working Group of EUFRIN (European Fruit Research Institute Network).

He started to work at National Agricultural Research and Innovation Center Fruitculture Research Institute and its processors in 1999. One is his research topics is evaluation of a double selected Persian walnut population.

Ex situ conservation and in vitro multiplication of potential cactus species resistant to cochineal and productive of fruits consumable in Morocco

Youssef El Kharrassi* Ph.D., Mouna Lamaoui Ph.D., Mohamed El Gharous, Ph.D., Ahmed Lebrihi, Ph.D., Faouzi Bekkaoui, Ph.D.

University of Mohammed VI Polytechnic (UM6P), AgroBioSciences Division, Lot 660 – Hay Moulay Rachid, 43150 Ben Guérir, Morocco.

Cactus pear genus Opuntia spp is a very important fruit crop in Moroccan agriculture, and especially resistant to droughts. This succulent plant contributes to guarantee the sustainability and remediation of an ecosystem with much degraded vegetation. It is very rich in biomolecules with high therapeutic and medicinal potential especially (β-Sitosterol, α-tocopherol, betalains and polyphenols). Currently this plant is threatened with extinction by cochineal Dactylopius coccus since 2014. However, measures to struggle this scourge remain ineffective in the face of the propagation of this insect. In Morocco, Rhamna region is the more infested. Our study is based on three objectives: Ex situ conservation of cactus genetic resources in Rhamna area, by creation a collection of different genotype, and more precisely the species sensitive to cochineal, and which have a socio-economic interest. The phenotypical aspect and morphological traits allowed classifying the ecotypes collected in fourteen species. Each species has its own chemical and nutritional phenological characteristics. The second goal is the characterization resistant cochineal species productive a good quality of fruit and seed oil with a high yield, based on farmers surveys and bioassays. Then, intensive multiplication the cochineal resistant cactus by innovative biotechnological method superior to classical method. Our observations showed that four species are putatively resistant to cochineal. These species have the particularity to be Xoconostles or acidic cactus pears, are fruits prized for their fleshy and acidic mesocarp. In perspective, the plants derived from tissue culture must be confirmed they are resistance to cochineal in the field prior to providing plants to clients. In addition, we will limit the genetic erosion of cactus species in Morocco.

Take Away Notes:

- The importance of nutritional value of succulent plants for example: cactus opuntia genus, benefit the main nutrients, exploit the different mode of use and the genetic diversity
- The public will be able to knowledge the cactus species which are a socio-economic interest and to target the ecotypes resistant to cochineal.Our research will be benefit for the farmers on the choice of cultivars. To know the importance of the daily consumption of the cactus and precisely the different parts of the plant (fruit, juice, cladodes, flower), and to sensitize the farmers on the importance of exploiting this succulent plant in the arid areas.
- Several information cited in this work may lead several research professors to think about the selective study of the cactus by species and by variety.
- The role of tissue culture on germoplasm biodiversity conservation.

Biography

Youssef El Kharrassi was obtained his Ph. D in life of sciences specialty Biochemistry, molecular and cell biology at University of Burgundy Faculty of Gabriel Sciences Dijon France and University of Hassan 1st Faculty of Science and Technology of Settat, Morocco. Currently, he is a Postdoctoral researcher in University of Mohammed VI Polytechnic (UM6P), AgroBioSciences Division at Ben Guerir, Morocco.He has published more than eight papers in reputed journals.These research works are focused on the valorization of the cactus. Among the studied aspects, there is the conservation, identification of the biomolecules and the genetic diversity.

The effect of BC204, a plant bio-stimulant, on the growth of *A. thaliana* and *S. lycopersicon*

J. Loubser*, J Kossmann (PhD), P.N Hills (PhD)
Stellenbosch University, South Africa

BC204, an agricultural product of a local company in South Africa, is a biostimulant consisting of a citrus extract and certain organic acids. The plant growth-promoting effect of BC204 has been demonstrated previously and is currently used in agriculture to promote plant growth in a variety of crops, increase yield and stimulate plants to improve resistance against abiotic and biotic stress. Although the physiological effects have been seen in practice, very little molecular or biochemical data has been collected. The aim of this study was to gain a deeper understanding of the biochemical and genetic changes occurring in A. thaliana and S. lycopersicon following the application of BC204. Wild-type Arabidopsis (Col-0) plants were treated weekly with three different concentrations of BC204 or a water control for three weeks, after which the fresh weight, dry weight, leaf number, and leaf surface area were measured. The growth experiments were repeated using only the optimal BC204 concentration (0.01% v/v) and the same physiological measurements were recorded, with the addition of photosynthesis rates. Control and BC204-treated A. thaliana plants were harvested, RNA extracted and analysed for transcriptomic changes via an RNA-sequencing approach. Additionally, a hydroponic system was established for S. lycopersicon to analyse changes in root exudates via LC-MS following treatment with BC204. Furthermore, plants of both species were subjected to NaCl as a biotic stress and treated with BC204. Basic physiological measurements were recorded, as well as established osmotic stress markers. The expression of certain genes responsive to salt-stress were evaluated via RT-qPCR.

Take Away Notes:

- Plant growth promotion in recent years has been focused on creating genetically modified organisms or breeding for valuable traits. Although these routes do deliver positive results, they are lengthy and expensive. Using a biostimulant is not only a rapid way of improving plant growth, but it can also be used to investigate novel ways of plant growth and development.
- Data generated from the transcriptomic analysis could provide other researchers with novel information about lesser explored genes and pathways.
- The hydroponic system established for tomato plants can be used by other researchers to analyse root exudates.

Biography

J. Loubser is currently finishing his PhD at Stellenbosch University and aims to further this research as a Postdoctoral fellow at the same institution. He currently holds a Scarce Skills Doctoral Scholarship from the National Research Foundation (NRF) of South Africa. His research interests include growth promotion via the application of plant growth promoting substances (PGPS).

Regulatory divergence in wound-responsive gene expression in domesticated and wild tomato

Ming-Jung Liu*, Koichi Sugimoto, SahraUygun, Nicholas Panchy, Michael S. Campbelle, Mark Yandell, Gregg A. Howe, and Shin-Han Shiu
Academia Sinica, Taiwan

The evolution of transcriptional regulatory mechanism is central to how stress response and tolerance differ between species. However, it remains largely unknown how divergence in cis-regulatory sites and, subsequently, transcription factor (TF) binding specificity contribute to stress-responsive expression divergence, particularly between wild and domesticated species. By profiling wound-responsive gene transcriptomes in wild Solanumpennellii and domesticated S. lycopersicum, we found extensive wound-response divergence and identified 493 S. lycopersicum and 278 S. pennellii putative cis-regulatory elements (pCREs) that were predictive of wound-responsive gene expression. Only 24-52% of these wound response pCREs (depending on wound-response patterns) were consistently enriched in the putative promoter regions of would-responsive genes. In addition, between these two species, their differences in pCRE site sequences were significantly and positively correlated with differences in wound-responsive gene expression. Furthermore, ~11-39% of pCREs are specific to only one of the species and likely bound by TFs from different families. These findings indicate substantially regulatory divergence in these two plant species diverged ~3-7 million years ago. Our study provides new insights into the mechanistic basis of how the transcriptional response to wounding is regulated and, importantly, the contribution of cis-regulatory components to variation in wound-responsive gene expression between a wild and a domesticated plant species.

Take Away Notes:

- Gene expression variation is one of the key contributing factors to the phenotypic diversity in crops. This research provides information of how domesticated and wild (stress-tolerant) tomato differentially mediate gene expressions in response to stress and the underlying regulatory mechanisms.
- Precise control of where and when gene products are made is an important issue for minimizing the trade-off between defense response and plant growth. From a synthetic biology standpoint, knowledge gained will guide the design of synthetic sequences for the control of gene expression in plants and thus has the potential in agro-biotechnological applications.

Biography

I am a plant molecular and computational biologist with strong interest in stress biology. After completing the postdoctoral research at MSU, USA, I started my own lab in May 2016 and currently am an Assistant Research Fellow in Academia Sinica, Taiwan. Our research directions are currently focusing to (1) develop the combining experimental and mathematical modeling methods for genome-wide annotation and quantification of translated genes and (2) systematically identify the transcriptional/translational control in response to stress in crops.

Biosafety on reliable bacteria application

Vílchez, J.I.[1, 2*] and Manzanera, M.[2]
[1] Shanghai Center for Plant Stress Biology, Chinese Academy of Sciences, China.
[2] Department of Microbiology, Institute for Water Research, University of Granada, Granada, Spain.

The use of microorganism-based products in agriculture has been raising for the las two decades. Bioinoculant products has been calculated to produce around 2 billion USD in 2017, and economic analysts estimate they will produce 2-3.29 billion USD profit by 2022. This growing trend means that research into new strains and their application is greater year after year. However, the isolation of new candidate strains has not gone hand in hand with a deep characterization of them. Although every day we know more about the mechanisms of growth promotion, protection against pests and pathogens, as well as improvement of the tolerance to abiotic stress mediated by these strains, very little progress has been made in the potential or real impact that they are causing after application. Conventionally, it is accepted that said strains beneficial for the plants and therefore harmless in their application. However, the application of new techniques for population description (metagenomics), as well as the increasing awareness about ecological networks and their balance, are bringing to light situations of potential risk not initially planned. Far from causing skepticism or reticence in the use of biofertilizers, the application of biosafety criteria will allow us to use them more efficiently, controlled and reliably, guaranteeing their sustainability. In this sense, we proposed the Environmental and Human Safety Index (EHSI) in 2016 as a first alternative modulated and adaptable to different ecosystems as a starting point to assess application risks and precautionary or monitoring measures.

Take Away Notes:

- The audience will be able to realize an underlying problem, generate new evaluation criteria in their research and improve their ecosystem perspective. In the same way, the audience will be able to use new risk assessment formulas.
- Control changes and risk by use microorganisms, understand application side effects.
- Apply new tools to evaluate safety of plant-beneficial microorganisms.
- Audience will open the frame of effects and conditions to take into account at time to use microoganisms in plants. This will let them to improve their skills in protocols design and the way the teach knowledge about new biotechnologies application management.
- New insights provided will give the audience tools to afford new perspectives in biosafety during their research of product management. New criteria and knowledge in sustainability and environmental-friendly science application will be also adquired.

Biography

Dr. Juan Ignacio Vilchez was licensed in Environmental Sciences degree at University of Granada (Spain) in 2009, he was recognized by Final Degree Research Project based on the use of Actinobacteria strains to promote growth and enhance drought-tolerance in pepper and tomato plants. By 2010, he coursed master studies in Research and Advances in Microbiology at University of Granada to characterize bacterial-symbiotic relations to alleviate abiotic stresses in crop plants and thereafter he obtained Spanish National Pre-Doctoral Fellowship FPU to continue this work. In 2016 he got his PhD title in Systems and Fundamental Biology, in branch of Environmental Microbiology, by University of Granada. During this time, he performed several doctoral stays in other Spanish (Madrid, Malaga and Granada) and European (CeBiTec-Universität Bielefeld, Germany; IT Carlow, Ireland) groups, working in biosafety, proteo-metabolomic and transcriptomic fields. His work in PGPR biosafety assessment was published as a new reference index and is under consideration to new Biofertilizers Regulation in EU. Nowadays, he is in second year of a postdoctoral stay at Shanghai Plant Center for Stress Biology (PSC) by CAS President's International Fellowship Initiative (PIFI).

Exploring key cellular processes and candidate genes regulating the primary thickening growth of Moso underground shoots

Qiang Wei[1]*, Chen Jiao[2], Lin Guo[1], Yulong Ding[1], Junjie Cao[1], Jianyuan Feng[1], Xiaobo Dong[1], Linyong Mao[2], Honghe Sun[2], Fen Yu[3], Guangyao Yang[3], Peijian Shi[1], Guodong Ren[4], Zhangjun Fei[2]

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[4]State Key Laboratory of Genetic Engineering, Institute of Plant Biology, School of Life Sciences, Fudan University, Shanghai, 200433, China

The primary thickening growth of Moso (Phyllostachys edulis) underground shoots largely determines the culm circumference. However, its developmental mechanisms remain largely unknown. Using an integrated anatomy, mathematics and genomics approach, we systematically studied cellular and molecular mechanisms underlying the growth of Moso underground shoots. We discovered that the growth displayed a spiral pattern and pith played an important role in promoting the primary thickening process of Moso underground shoots and driving the evolution of culms with different sizes among different bamboo species. Different with model plants, the shoot apical meristem (SAM) of Moso is composed of six layers of cells. Comparative transcriptome analysis identified a large number of genes related to the vascular tissue formation that were significantly upregulated in a thick wall variant with narrow pith cavity, mildly spiral growth, and flat and enlarged SAM, including those related to plant hormones and those involved in cell wall development. These results provide a systematic perspective on the primary thickening growth of Moso underground shoots, and support a plausible mechanism resulting in the narrow pith cavity, weak spiral growth but increased vascular bundle of the thick wall Moso.

Take Away Notes:

- In this presentation, audience will get the new knowledge of the special characteristics of bamboo underground shoot and the responding molecular basis such as the spiral growth, and will discover the importance of pith tissue on promoting the primary growth of bamboo shoot.
- Beside this, audience will learn the mathematical method to precisely describe the morphology of plant shoot apical meristem.
- This work combines mathematic, anatomic, physiological, bioinformatic and molecular methods to successfully explore the biological question of non-model plants. We believe researchers working in non-model plant development field will have interest on it.

Biography

Qiang Wei, Graduated from Fudan University, Doctor of Biochemistry and Molecular Biology, now is an associate professor at Nanjing Forestry University. Wei's lab employs a combination of anatomy, mathematics, genomics, genetic, biochemical and other approaches to disclose the molecular mechanisms underlying the distinguish developmental process of bamboowith special interests in the development of bamboo wood.

DAY 2

KEYNOTE FORUM

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

SEPTEMBER 20-22, 2018
ROME, ITALY

Biography

Professor Pierre Frendo has studied the physiology and the molecular regulation of nitrogen-fixing symbiosis between Rhizobia and leguminous plants for more than 20 years. He has published more than 50 articles in international peer-reviewed journals and books. He is the group leader of a team of ten researchers/lecturers, working on the redox regulation of the plant-bacteria interaction during nitrogen-fixing symbiosis. After 17 years of work in the French CNRS, he has been recruited as a Professor in the Nice-Sophia Antipolis University. He is a member of the French Society of Plant Biology and elected member of the French National Council of Universities.

Redox state components controls the nitrogen-fixing symbiosis between *Medicago truncatula* and *Sinorhizobium meliloti*

Pierre Frendo

University of Nice-Sophia Antipolis, France

The world population growth associated with the shortage of fossil resources and global climate change create a strong socio-economic demand for the development of plant production systems requiring less natural resources and more respectful of the environment. Legume plants provide an answer to these issues, thanks to their capacity to establish a symbiotic relationship with nitrogen-fixing rhizobia. In fact, legume crops have the unique ability to grow efficiently without nitrogen fertilizers, which are notorious for their negative environmental impact in terms of fossil energy consumption, greenhouse gas emission and water pollution. Nitrogen-fixing symbiosis leads to the formation of a new organ, the root nodule. Inside the plant nodule cells, the bacteria differentiate into bacteroids, able to reduce atmospheric nitrogen in ammonia which is then supplied to the plant in exchange of carbon sources. The cellular redox state regulates root nodule development and functioning. More precisely, redox signals are involved in the regulation of the early steps of the interaction, in the differentiation of the two symbiotic partners and in the efficiency of the nitrogen fixation. This presentation will address the importance of redox control through the production of reactive nitrogen and oxygen species and the presence of an efficient antioxidant defence in the two symbiotic partners. On one hand, the lecture will present the involvement of nitric oxide and hydrogen peroxide in the crosstalk between the two symbiotic partners and in the regulation of the biological nitrogen fixation during the interaction between M. truncatula and S. meliloti. On the other hand, the importance of glutathione and other molecular components of the antioxidant defence in the redox state equilibrium and the efficiency of symbiotic nitrogen fixation will also be addressed. This lecture will provide an overview of the involvement of redox equilibrium in the regulation of the symbiotic nitrogen fixation.

Take Away Notes:

- In the general context of sustainable development and agriculture, the presentation will help the audience to have a general view of different players involved in redox state equilibrium and their different roles in the nitrogen fixing symbiosis.
- The presentation will help the audience to better understand the nitrogen-fixing symbiosis and to see that redox state regulates in this symbiotic interaction.
- This presentation will be interesting for researchers and lectures for a better understanding of the nitrogen fixation set up and the regulation of its efficiency by the redox state during the nodule formation and functioning.

Biography

Dr. Aiming Wang is a Senior Research Scientist at the London Research and Development Centre, Agriculture and Agri-Food Canada (AAFC) and an Adjunct Professor of Dept of Biology, Western University. Dr. Wang has worked for more than 20 years in the field of crop genetics/breeding and plant virology. He has been the principal investigator of many funded studies. Dr. Wang edited five books, and authored 23 book chapters, over 100 peer-reviewed papers and over 200 other articles. Dr. Wang is the recipient of various awards, such as Queen Elisabeth II Diamond Jubilee Medal from Government of Canada in 2013, and a Gold Harvest award from AAFC in 2010. Dr. Wang has been instrumental in developing novel strategies against potyviruses. Dr. Wang currently holds editorial positions of major journals in his research area including PLoS Pathogens, Molecular Plant-Microbe Interactions, Journal of Virology, Molecular Plant Pathology, Virology and Scientific Reports. He is an ad hoc manuscript reviewer for many decent journals and proposal reviewer for major funding agencies of many countries. Dr. Wang received his BSc from Yangzhou University in 1983, M.Sc. from Nanjing Agricultural University in 1988 and Ph.D. from the University of British Columbia (Vancouver, Canada) in 1999.

Understanding defense and counter-defense in plant-virus co-evolutionary arms race and developing next generation antiviral resistance

Aiming Wang, PhD

London Research and Development Centre, Agriculture and Agri-Food Canada, Canada

Plants are constantly attacked by diverse pathogens including viruses. They have evolved sophisticated defense mechanisms to protect themselves from pathogen infections. For viral pathogens, nucleotide-based RNA silencing and receptor-based innate immunity that comprises PAMP (pathogen-associated molecular patterns)-triggered immunity (PTI) and effector-triggered immunity (ETI) are the primary antiviral strategies. In response, viruses have also evolved virulence strategies to suppress host defenses. RNA silencing and viral suppression of RNA silencing have been extensively investigated in the past twenty years. A number of viral suppressors of RNA silencing have been identified and their functional mechanisms have been elucidated. Although PTI- and ETI-based immunity concepts were initially developed based on molecular interactions between plants and no-viral pathogens, recent evidence has suggested that these also apply to virus-plant interactions. It has been revealed that most antiviral R gene products share structural similarity with antibacterial and antifungal R proteins and elicit typical ETI response. Viral resistance breaking isolates may evade ETI to overcome R-mediated resistance through introduction of mutations into the viral elicitor. Viral replication-associated dsRNA can trigger PTI-like responses. Recent data have shown that viruses do encode and deploy Avr factors to suppress PTI. Furthermore, viruses have ability to inhibit the NPR1 pathway, part of both PTI and ETI signaling pathways. Emerging evidence also reveals that the autophagy and unfolded protein response pathways are interlinked with the receptor-based innate immunity and play essential roles in viral infection. Thus, the co-evolutionary arms race between plants and viruses is extremely complex and aggregative. These recent findings will assist in the development of next generation antiviral resistance.

Biography

Hong-Wei Xue was issued the Bachelor and Doctorial degree in 1991 and 1996, from East-China Normal University and Shanghai Institute of Plant Physiology, Chinese Academy of Sciences, respectively; then went to the Max-Planck-Institute of Molecular Plant Physiology, Germany for postdoctoral research (1996-1998).

Dr. Xue was back Shanghai Institute of Plant Physiology and Ecology, SIBS, CAS in 1999. He has served as the deputy Director (2005-2009) and Director (2009-2014) of the Shanghai Institute of Plant Physiology and Ecology, and Director of the National Key Laboratory of Plant Molecular Genetics (2006-2017).

Currently Dr. Xue is the principal investigator and serves as the member of the editorial board of Plant Physiology (2011-present); Molecular Plant (2008-present); Cell Research (2006-present).

The main interests of Xue's group include: 1) functional mechanisms of auxin and protein phosphorylation in hormone effects, and 2) genetics and epigenetics regulation of rice seed development. He has published more than 40 papers in Nature Communications, EMBO J, Plant Cell, Cell Research, Cell Reports, etc. and was invited for review articles in Current Opinion of Plant Biology and Biochemical J.

Proteasome regulation in plant development

Hong-Wei Xue

Chinese Academy of Sciences, China

The ubiquitin/26S proteasome proteolytic pathway selectively removes regulatory proteins, providing an efficient and rapid strategy to control many cellular processes and plays critical roles in protein removal in mammalian and plant cells. The proteasome is highly conserved and it has been shown that the bovine proteasome inhibitor 31 (PI31) and its homologues in mouse and humans diminish the activity of purified 20S proteasome; however, still little is known how proteasome activity is regulated in either mammals or plants.

Through systemic genetics studies, we showed that an Arabidopsis homologue of the proteasome inhibitor PI31, which was designated as PROTEASOME REGULATOR1 (PTRE1), is a positive regulator of the 26S proteasome. Loss-of-function ptre1 mutant presents growth defect in multiple processes, and interesting, ptre1 is insensitive to auxin-mediated suppression of proteasome activity. Further studies showed that auxin alters the subcellular localization of PTRE1, indicating this may be part of the mechanism by which it reduces proteasome activity and auxin regulates proteasome activity via PTRE1 to fine-tune the homoeostasis of Aux/IAA repressor proteins thus modifying auxin activity.

Our further studies indicated that various factors modulate PTRE1 activity to involve the regulation of hormone signaling including gibberrllin and brassinotgeroids, and plant thermotolerance, which will be presented.

As proteasome and whose activity control are involved in various developmental and stress-related processes, there should be possible links with the researches at different fields.

DAY 2

WORKSHOP

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

SEPTEMBER 20-22, 2018
ROME, ITALY

Using new media tools to connect micropropagation scientists, propagators and hobbyists

Avihai Ilan, PhD

Private consultant, Israel

New media tools such as internet chat, photo and video transfer, video-conference and disciussion groups developed in recent years. The discussion groups that address plant tissue culture include groups covering a wide range of plant species or groups dedicated to a specific group of plants (for example: carnivorous plants) or a specific family (example: orchids). Some groups are limited to scienentists while others combine scientific, commercial and hobby backhrounds. The size of the discussion groups vary between a few hundreds up to a few thousands members. These groups discuss a wide range of relevant issues. Among the topics discussed at Micropropag, a facebook group that I established on 2016, are: micropropagation stages (0 to 4), culture vessels, propagation protocols for various plants, medium and gaseous phase, temporary immersion, somatic embryogenesis, synthetic seeds, microbial contamination, micropropagation tools, sterilization of vessels and tools, nurse cultures, culture conditions (various illumination sources, effect of temperatures, etc.) plants' conservation in vitro, etc. The means for discussing the above were posts, photos, videos and video conference. Contests of best photo and video encouraged members' participation. Recommendations for relevant bibliography as well as professional scientific meetings are mentioned from time to time. Direct advertisement was rear. Commercial issues were discussed between members using their private Messengers. With the aid of the host (Facebook, LinkedIn, etc.) the group administrators can obtain group insights such as groups growth info, number of publications, popular days and hours for posting, active members, members' countries and cities. New Media tools provide additional ways for discussion and information transfer that can be used by scientists and professionals. Understanding its opportunities and limitations of using is, therefore, important.

Take Away Notes:

- The information and ideas provided in this lecture can assist others in establishing and managing New Media groups dealing with micropropagation and other plant science and technology topics.

Biography

Dr. Avihai Ilan is a consultant on plant propagation and Agriculture development. He worked for many year in a large plant propagation company (micropropagation and fruit tree nurseries) in various roles including managing director. His advisory work spans a diverse range of countries including Israel, Egypt, Nepal, India, Ethiopia, Uganda and others. In recent years Dr. Ilan was involved micropropagation consulting (Israel, Uganda and Madagascar). Dr. Ilan teach plant propagation to international students at Agro Studies, Israel and consult private companies on micropropagation. Dr. Ilan has BSc and MSc degrees from the Hebrew University of Jerusalem, Israel and PhD from The University of Tennessee, USA.

DAY 2

SPEAKERS

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

SEPTEMBER 20-22, 2018
ROME, ITALY

The critical role of silicon in alleviating drought stress and mineral nutrient deficiencies in different crop plants

Dr. Nusrat Ali, Dr. Jean-Claude Yvin, Dr. Adrian Schwarzenberg and Dr. Seyed Abdollah Hosseini*
Agro Innovation International Roullier Saint Malo, France

Recently, researchers have been more focused on silicon (Si)topic andwide-ranging benefits of Si for stressed plants are exploited for agricultural gain. In this context, Sihas been widely reported to alleviatesthe response of drought stress and plant nutrient deficiencies. However, the mechanism (s) by which Si mitigates abiotic stresses has not yet been fully discovered. In GPMB 2018, our recent investigations on the role of Si supplement on different crops under different indivitual mineral deffciensies and drought stress will be discussed. The results will be emphasized on the role of Si on drought-induced metabolite and hormonal changes using combined metabolite and transcriptional approaches.

By this way, participantswill be gained:

1) What is the the new mechanisms by which Si mitigates abiotic stresses in plants.

2) Whether and what is the genotipic difference in response to Si supply under drought condition and

3) Finally scientists will be encouraged to work more on Si topic as an importance nutrition alleviating stress responses.

Biography

Dr. Seyed Abdollah Hosseini has 16 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 and Pos-doc at Leibniz Institute of Plant Genetics and Crop Plant Research (IPK).Since 2016, he is working as independent scietist and project managerin plant nutrition group at Agro Innovation International Roullier. All his scientific works and research contributed in 9published papers in different outstanding international journals.

Regulatory circuits connect early leaf development and senescence in *Arabidopsis thaliana*

Bresson, J., Saile, S., Doll, J., Riester, L., Kleinhempel, C., Xie, Y., Wenkel, S., Zentgraf, U*.
University of Tübingen, Germany

Plant senescence is a highly regulated processthat aims at breakdown and subsequent remobilization of macromolecule components of mature leaves, either for further growth or for deposition in developing fruits and seeds. Senescence is governed by endogenous cues like leaf or plant age; however, stress conditions can induce premature senescence. While developmental senescence tends to maximize seed quality and quantity, premature senescence describes an exit strategy, often resulting in severely decreased yields. Despite the agricultural importance of senescence, our knowledge on its regulatory mechanisms is still limited. In contrast to system biology approaches which characterize overall and genome-wide changes, we want to decipher the molecular mechanisms of this regulatory network starting from one point, namely the transcription factor WRKY53, which is tightly regulated by diverse mechanisms and is a convergence node between senescence and biotic and abiotic stress responses. WRKY53 is part of a complex regulatory network between many different WRKY factors but also many other proteins which built up several layers of regulatory feedback loops which fine-tune this network. Salicylic and jasmonic acid as well as reactive oxygen species (ROS)appear to be the most important signals that trigger this network. In contrast to calcium signaling, which is executed by storage and release of Ca2+, ROS signaling is controlled by production and scavenging.By scavenging H_2O_2 specifically in different compartments, we could show that the cytoplasmic H_2O_2 appears to be more effective in senescence signalling than the chloroplastic or peroxisomal ROS.

Furthermore, we have already identified a connection between early leaf development and senescence. Class III homeodomain leucine zipper (HD-ZIPIII)transcription factors, which are involved in basicpattern formation, have an additional role in controlling the onset ofleaf senescence in Arabidopsis. REVOLUTA (REV) acts as a redox-sensitive transcription factor, and directly andpositively regulates the expression of WRKY53. HD-ZIPIII proteins are required for thefull induction of WRKY53 expressionin response to H_2O_2as signalling molecule.Consequently, mutations in HD-ZIPIII genes strongly delayed the onset of senescence.Thus, a crosstalk between early and late stages of leaf developmentappears to contribute to reproductive success.Moreover, the antagonist of REV in early leaf development, KANADI, appears to antagonize REV also in senescence. Here,KANADI does not antagonistically regulate WRKY53 expression but regulates the expression of the antagonist of WRKY53, namely WRKY18.

Take Away Notes:

- Early leaf developmental defects have an impact on the later fade of the leaf.
- Transcriptional networks act different in different developmental contexts.
- Antagonistic proteins regulate not only the same target genes in opposite direction but also regulate the expression of other antagonistic gene pairs.
- Breeders can possibly exploit this to improve e.g. seed quality by precisely regulating leaf senescence and remobilization processes.

Biography

Ulrike Zentgraf graduated on RNA polymerase I transcription in the Department of General Genetics at the University of Tübingen, Germany. As a postdoc, she was involved in the Arabidopsis genome project for a short time at the University of Tübingen, then, she built-up her own research group working on regulatory mechanisms of plant senescence. She was a founder member of the Centre of Plant Molecular biology (ZMBP) in Tübingen where she is now working as a professor, still on the same topic.

New compounds and their application as innovative approach to plant protection against pathogens

Rafal Kukawka*[1,2] **MSc. Judyta Strakowska**[1], **Ph.D. Patrycja Czerwoniec**[1,2], **MSc. P. Kaczynski**[3], **Marcin Smiglak**[1], **Prof**

[1] Poznan Science and Technology Park

[2] Adam Mickiewicz University in Poznan

[3] Institute of Plant Protection National Research Institute

Crop protection in modern agricultural industry is still a field that requires new and more efficient methods, which can improve quantity and quality of crops due to exposure of plants to factors such as fungi, bacteria and insects. Excessive consumption of Plant Protection Products, especially fungicides and, related to it, negative impact on human health and environment (through for example phenomenon called Colony Collapse Disorder (CCD) of bees) is becoming an increasing problem that requires a comprehensive and effective solutions.

Since 1990 popularity of room temperature quaternary ammonium salts (major class of ionic liquids) is still raising, due to the fact that both ions in ionic liquid can be independently modified and thus properties of ions may separately be incorporated into the final IL salt. In recent years, dual functional ionic liquids with biological functions started to be investigated in fields of plant protection products as herbicidal and antifungal agents or inducers of plant resistance.

In addition, ionic liquids containing long alkyl chains have a significant effect on the change of hydrophilic properties, which makes it possible to limit their mobility in soil and groundwater. Furthermore, long alkyl chain ILs guarantee significant surface activity, which in turn intensifies wettability of the plant surface and enables direct contact between used plant protection product and pathogens on the plant. This could eliminate the need to use additional compounds such as surfactants or adjuvants.

Herein, we present new, active dual functional ionic liquids based on currently used fungicidal agents or plant resistance inducers with modified properties of solubility in water, dissolution rate, reduced phytotoxicity, antifungal activity (tests against fungus that infects cereal crop and many types of fruits and vegetables such as: Alternaria alternata, Botrytis cinerea, Fusarium sp), antibacterial activity and antiviral activity on tobacco, tomatoes and potatoes.

These new ionic liquids can revolutionize agrochemical industry through reducing negative impact of pesticides on human health and environment.

This work was supported by the National Science Centre (Poland), project Preludium no UMO-2015/19/N/NZ9/02922. Moreover, Rafal Kukawka is Adam Mickiewicz University Foundation scholarship holder in the academic year 2017/2018.

Take Away Notes:

- However, methods of growing crops free of diseases and not requiring great amounts of are often little known and undervalued in nearly future would be a great improvement for agriculture. Thus it seems that the solution proposed by us to use plants resistance induction, as major line of plants defense against pathogen infections, is very interesting but not popular yet approach. Not only large area but also greenhouse farming could benefit from this solution. The profits that may come from the positive outcome of the project, and the commercial availability of the discovered SAR inducers, will be enormous and could reach almost every human and in the long term have great positive influence on populations health and condition of the environment thanks to the lowered use of harmful chemicals in agriculture. Thus it is very important to show new results and inform people in agriculture and biology society about new and safe methods of crop cultivars.
- Being aware of the dangers that overuse of crop protection products can bring to environment and human health, better and more effective methods of utilization of pesticides are seek. As a result (i) a need to increase the awareness of crop protection and the dangers that it brings in developed nations like the U.S. and EU, (ii) better and more effective utilization of pesticides, along with (iii) adoption of high end technologies become a key aspects of IPM (Integrated Pest Management) which is a new European policy implemented in all EU countries. This policy emphasizes the growth of a healthy crops with the least possible disruption of agro-ecosystems and encourages natural pest control mechanisms. Thus in 2009 European Union legislation set out the Directive 2009/128/EC of The European Parliament, which constitutes new directions in plant protection in European Union which will cause in near future successive withdrawal of non-ecological plant protection agents from the European market including some of the most popular pesticides. Moreover, this legislation forces chemical companies to concentrate their research toward non-toxic and eco-friendly analogues of currently used agrochemicals that in result will increase

competition on this market. Additionally, as a result of customers' expectations, sometimes more restrictive than governmental regulations, it is expected that further directives will be implemented by governments in order to substitute currently used pesticides.

- We envision that our the technology based on plant resistance inducers will become implemented to the market in which this solution may greatly contribute to increase in the quantity and quality of crops. The end result of this project is to deliver new products with broad-spectrum activity that will be available to a wide groups of customers.
- It also will be a great opportunity to interest other researchers and pesticides manufacturers to seek new, safe compounds as Plant Protection Agents.

Biography

Rafal Kukawka since 2014 is a PhD student at Faculty of Chemistry at Adam Mickiewicz University in Poznan, Poland. During his studies, he focuses on application of ionic liquids in plant protection. Moreover, he is Principal Investigator of a research project (project Preludium financed by Polish National Science Centre), performed at Poznan Science and Technology Park, concerning antifungal ionic liquids. Together with Prof. Smiglak group, he was awarded Gold and Silver Medal at the International Inventions and Innovation Fair INTARG 2017 at the International Warsaw Invention Show IWIS 2017 for work on plant resistance inducers as an innovative and safe direction in plant protection.

Mr Rafał Kukawka is Adam Mickiewicz University Foundation scholar in 2017/2018 academic year.

Invasion impact of the *Genista etnensis* (Raf.) DC. (Fabaceae) on Mt. Vesuvius

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Giovanni Battista Chirico[2], Ph.D., Department of Agriculture, University of Naples Federico II, via Università 100, 80055 Portici (Naples), Italy.
Guido Incerti[3], Ph.D., Department of Agri-Food, Animal and Environmental Sciences, University of Udine, via delle Scienze 206, 33100 Udine, Italy.
Giuliano Bonanomi[2], Ph.D., Department of Agriculture, University of Naples Federico II, via Università 100, 80055 Portici (Naples), Italy.

Vesuvius in southern Italy dominates the landscape of Napoli Gulf with its distinguishable grey bare slopes, exposed to continuous surface erosion processes and rock falls which have been hindering the development of the vegetation after the last volcanic eruptions (occurred in 1944). In the last 74 years the development of the vegetation became evident along some portions of the Grand Cone. This process is facilitated by the upslope expansion of the Genista etnensis (Raf.) DC. (Fabaceae), a vascular plant endemic of the Mt. Etna (Sicily) and of Eastern Sardinia, which has been imported to Mt. Vesuvius in 1906 as part of a reforestation program of the Vesuvius slopes.

In the present multidisciplinary study we investigated the impact of this exotic nitrogen-fixing shrub, on pioneer plant community of the Vesuvius, also in light of current and predicted climatic changes. Therefore, an intensive field investigation has been designed to explore the eco-hydrological conditions facilitating the expansion of the G. etnensis. Plant species and soils have been collected both underneath and outside the cover of G. etnensis canopies to gather relevant information about the interaction of the G. etnensis with the other species as well as to explore the small scale spatial gradients of soil fertility induced by the G. etnensis. Two permanent stations have been installed to monitor the differences in soil water content, soil temperature and air temperature between inside and outside the canopy cover.

We observed dramatic effects on plant diversity and distribution of the invaded ecosystem, mediated by the canopy of G. etnensis. However, the capability of this nitrogen-fixing plant to facilitate heterospecifics showed a clear ontogenetic shift, modulated by plant age and size. The collected data evidence that G. etnensis tends to create an island of fertility by increasing the organic matter content in the soil and improving the soil water retention properties. Moreover, the G. etnensis mitigates the daily soil temperature excursions, reducing the exposure of seeds to extremely high temperature values, particularly during the growing season, and the direct soil evaporation loss. These results suggest that the invasion of G. etnensis can promote alternative successional trajectories that may dramatically affects vegetation dynamics.

These data show that the translocations of native plants within the Italian territory can induce negative changes to the environment and to the communities. Therefore, the information obtained in this research are useful to identify specific management practices that can limit the spread and impact of this species.

Take Away Notes:

- Damage understanding on the biodiversity, soil and landscape related of exotic plants invasions in volcanic environments.
- This research provides fundamental information for management of nitrogen-fixing alien plants in volcanic environments.

Biography

I'm Postdoctoral Researcher on "Analysis of plant biodiversity and fuel in experimental areas of prescribed fire" at the University of Campania Luigi Vanvitelli (Caserta, Italy). Previously, I'm graduated in Agricultural Sciences and Ph.D. in Development and Management of Agricultural Resources and Forests at the University of Naples Federico II (Italy). I am a botanist and ecologist and my main areas of interest are floristics, plant taxonomy, vegetation science, community ecology, plant biology, biogeography, fire ecology, biodeteriogenic plants on monuments and archaeological sites, plant biodiversity assessment and conservation. I am also involved in several national and international research projects dealing with red lists, effects of climate change on alpine plant species, plant traits, ethnobotany, archaeobotanical reconstructions and plant eco-physiology.

Growth and physiology responses of *Phragmitesaustralis* to drought, flooding and their alternate in inland salt marshes, Northeast China

Xiaoyu Li, Ph.D.
Key Laboratory of Wetland Ecology and Environment, Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, China

The hydrological regime is the dominant factor associated with the degradation and restoration of inland salt marshes in Northeast China. As a special ecosystem in western Songnen Plain, Northeast China,Phragmitesaustralis saline-alkaline marsh degrade to saline meadow or even alkaline spots progressively, due to the interruption of the water supply. In order to understand the process of degradation and restoration of Phragmitesaustralis saline-alkaline marsh, four months of pot experiments were designed to examine changes in the growth and physiology of P. australis, and the response to different hydrological regimes (alternate flooding–drought treatments, flooding and drought duration). (1) Compared with four months flooding, the combined drought/flooding treatment that drought in one month and flooding in subsequent three months obtained the largest biomass and lower sodium ion absorption by plant shoots, although the later give rise to the highest population height. Subsequently, the accumulation of sodium ion in plant shoots increased significantly with the delay of flooding and increased drought periods, and the significant enhanced photosynthetic activity imply the evident physiological responses to drought stress. (2) With the increase of flooding duration, plant height reached to the highest value in full time flooding but the biomass reached to the largest in the treatment that only flooded 2 months. Although the Na+ and K+ did not show a regular change, they was the lowest in this treatment.(3) Plants in alternate flooding–drought conditions exhibited substantially more biomass accumulation and less Na+absorption compared with the single treatments of moisture, flooding, and drought. Photosynthesis physiology served as regulating and adaptive responses to different water regimes, with increased values after the short-term flooding, long-term drought, and flooding–drought cycles. Comparing all these changes in the growth, photosynthetic physiology and saline ions contents under different hydrological regimes,the growth of P. australis was promoted by flooding–drought cycles, which suggests that this may be an effective approach for restoration inland salt marshes.

Take Away Notes:

- Our studies exhibited that P. australishad adaptive growth and physiological strategies to drought and flooding. And we know what the wetland emergent plants will response when extreme hydrology happens, like drought and flooding.
- The flooding-drought cycles with a right frequency, will be a good restored method that not only save fresh water but also promoted the plants individual growth. This alternate cycles of drought and flooding could be used in other vegetation restoration in wetlands. This research was finished in 2012-2013, and the manuscripts were published between 2014 and 2017. Some plants, e.g. Scripustriqueter and Cares drum sacwere also restored successfully by this dry-wet alternation methods in freshwater marshes. These research was finished by my colleaguesin 2016 and 2017, which were after the research about P. australis in inland marshes.
- The further mechanisms were studied in my group since 2018. More complicated relationship among plants-hydrology-saline soil and the root exudation will be discussed.

Biography

Xiaoyu Li, Ph.D, an associate researcher in Northeast Institute of Geography and Agroecology, CAS. She graduated from Northeast Normal University and gained doctor degree of Ecology in 2010. The main field direction is plant eco-physiology, and research vegetation restoration in wetland after graduation of doctor. She was in charge of threeNational Natural Science Foundation of China, and one provincial scientific research projects.She visited USA Everglade Wetland Research Park between 2013 and 2015. There are more than 50 paper publication since 2010. She is also the reviewers of many national publications, such as Ecological Engineering, Crop and Pasture Science, Wetlands, Photosynthetica, etc.

The Brassinosteroids (BR) signaling regulation of plant seed number

Dr. Yan-Jie Zhang[1], Miss Yu Zhang[2], Miss. Hui-Ya Huang[2] and Prof. Wen-Hui Lin[1*]
[1]School of Life Sciences and Biotechnology,Shanghai Jiao Tong University, Shanghai, China
[2]Institute of Botany, Chinese Academy of Sciences, Beijing, China

Seed number is an important part of seed yield. Seed number regulation is a complex process and affected by different signals.Our research work focus on the organ (seed or seed precursor) initiation and the maximal possibility of seed number. In some dicot plants, like Arabidopsis, seed number depends on seed number per fruit (mainly on ovule number) and fruit number. Our previous work illustrated that Brassinosteroid (BR) positive regulated ovule/seed number through influencing the expression of downstream genes related to ovule early development by BR-induced transcription factor BZR1. bzr1-1D (P234L, gain-of-function mutant of BZR1) has enhanced BZR1 protein activity, placenta size and ovule/seed number per flower/silique. Soybean is an important dicot crop producing protein and edible oil. Phylogenetic analysis reveals BZR1-like genes are highly conserved in angiosperm and there are 4 orthologues in soybean (GmBZL1-4). The functional characterization of GmBZL2 illustrates that GmBZL2216L (P216L, conserved with P234L in Arabidopsis) enhances GmBZL2protein activityand increasesArabidopsis BR signaling and seed number, further demonstrating the conserved function and regulatory mechanism of GmBZL2. Overexpression of GmBZL2216Lin soybean enhances seed number, indicatingthepotential application of BR in seed yield of dicot crops. In monocot plants, like rice, seed (grain) number determines by grain number per panicle (mainly by panicle development and branch/spikelet number) and panicle number. Our results illustrates that BR regulates grain number through influencing BR-regulated transcription factors.For example,OsGATA7 modulated BR-mediated growth regulation and influencedrice architecture and grain shape/weight/number/yield. Although seed number regulation in Arabidopsis and rice has different mechanism, there are at least two common ways of BR regulation of seed number: non-specific increasing reproductive meristem size and specificinfluencing downstream related genes transcription.

Take Away Notes:

- This presentation summarizes the complicate processesand multipleregulatory factors influencingplant seed number in monocot and dicot plants, and introduces the Brassinosteroids regulation of seed number in Arabidopsis, soybean and rice.
- Seed number is an important part of seed yield, which has still not been systemically investigated, especially in dicot plants. Study the regulatory mechanism of seed number is not only for a scientific question for organ identity and initiation, but also has potential application in agriculture production.
- Our research work gives clues in BR (as well as other hormones) regulation of seed number and BR application in agriculture production.

Biography

Prof. Wen-Hui Lin is the principle investigatorof the research group of PlantHormones and Reproductive Development, which belongs to Department of Genetics and Developmental Science, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University. Prof. Lin graduated fromNational Key Laboratory of Plant Molecular Genetics, Institute of Plant Physiology& Ecology, Chinese Academy of Sciences and gained her Ph.D. degree. And she had postdoctoraltraining in University of California at Berkeley and Carnegie Institution for Science. She is interested in hormonal (brassinosteroids, auxin, cytokinin and hormones crosstalk) regulation of plant development and morphogenesis. Currently shefocuses on brassinosteroids-mediated seed development, seed number determination, and seed yield regulation.The detailed information of Prof. Lin and her group would be shown on the website of http://www.seedlin.sjtu.edu.cn.

TMK-mediated transcriptional auxin signaling in regulating plant development

Min Cao[a,b], Rong Chena, Pan Li[a,b],Tongda Xu[a,b,2*]

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[b]FAFU-UCR Joint Center and Fujian Provincial Key Laboratory of Haixia Applied Plant Systems Biology, Haixia Institute of Science and Technology. Fujian Agriculture and Forestry University, Fuzhou, Fujian, China

Auxin plays diverse and profound roles in plants, regulating essentially all aspects of plant growth and development, but how auxin achieves the functional diversity and specificity is largely unknown.Multiple auxin signaling integrated totriggerdistinctive auxin responses according to its concentration, which is essential for differential growth such as apical hook development. We showed that high auxin at concave side of apical hook stimulates the C-terminus cleavage and cytosolic translocation of Trans-Membrane Kinase (TMK), which phosphorylates non-canonical IAAs. Surprisingly, in contrast to previous report that auxin degraded AUX/IAA proteins through TIR1/AFB receptor to regulate gene expression, here we found that non-canonical IAAsproteins were stabilized by high auxin through TMKcleavage to negatively regulate gene expression and inhibit growth. This finding demonstrated a TIR independent transcriptional auxin signalingthat regulate growth inhibition in response to high auxin.

Biography

Tongda Xu got B.S degree in Peking University in 2003, Ph.D in University of California Riverside in 2010. In 2011, Xu become Young Investigator and setup the lab in TemasekLifescience Laboratory Ltdin Singapore; In 2014, Xu become Principal Investigator in Shanghai Center for Plant Stress Biology in China Academy of Sciences. Xu's lab is working on ABP/TMK based auxin sensing complex on plasma membrane, and aimed to investigate the molecular mechanism about how ABP/TMK regulate auxin dependent cell expansion, cell division and cell differentiation. In the meanwhile, his lab is also studying how auxin participates in other signaling pathways such as stress responses.

Molecular identification of *Macrophomina Phaseolina* associated with charcoal rot of melon in Jordan

Al-Abed, A*, Ph.D., Naser, Z, Department of Plant Protection, National Center for Agricultural Research and Extension, Baqa', Jordan.
Nida' M. Salem, Ph.D. and Wafaa Subh., Department of Plant protection, School of Agriculture, University of Jordan, Amman 11942, Jordan

This part of the research was carried out at the University of Jordan Laboratory's to confirm the identity of the fungal isolates from melon based on molecular analysis. Two isolates were identified molecularly utilizing the regions of fungal ribosomal DNA (rDNA) ITS that yielded a 584 bp fragment. The amplified DNA fragments were sequenced and BLAST analysis showed a 100% nucleotide sequence identity with Macrophomina phaseolina (GenBank Accession No. KF531825). So far, the molecular analyses confirmed that the isolated species corresponded to M. phaseolina, causal agent of charcoal rot in melon.

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 inorder 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 "Epeidemiological Studies on the Cereal Cyst Nemtode 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, Amman1992. I am working as a researches 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.

Wound signaling and cell fate transition in plant regeneration

Lin XU (Ph.D.)
Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, China

De novo organ regeneration, which gives rise to adventitious roots and shoots, is a type of plant regeneration for survival after injury. In Arabidopsis, two main cell fate transition steps are required to establish the root primordium during de novo root root regeneration from leaf explants. The first step from regeneration-competent cells to root founder cells involves activation of WOX11 and WOX12 expression by auxin. In the second step, WOX11 and 12 directly activate WOX5, WOX7 and LBD16 for initiation of root primordium. We also established a system to study de novo shoot regeneration from Arabidopsis hypocotyls without added hormones. Overall, wound signaling, auxin behavior and cell fate transition are successively involved in de novo organ regeneration.

Take Away Notes:

- De novo root and shoot regeneration systems without added hormones in Arabidopsis
- Wound signals and hormones control cell fate transition in regeneration
- WOX and LBD genes are involved in cell fate transition

Biography

Dr. Lin XU completed his PhD at the University of Strasbourg, France. In 2013 he became Professor and Principle Investigator at Shanghai Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. His current research focuses on mechanisms guiding plant regeneration. Lab homepage: http://bioinfo.sibs.ac.cn/xulin

Virus diseases of garlic in Indonesia and potential control measures

Sri Hendrastuti Hidayat[1]*, SitiShofya Nasution[1], Cindy Fitrasari[1], Diny Dinarti[2]
[1]Department of Plant Protection, Bogor Agricultural University, Bogor, Indonesia;
[2]Department of Agriculture and Horticulture, Bogor Agricultural University, Bogor, Indonesia

Garlic (Allium sativum L.) is one of the most important vegetable commodities in Indonesia. Bulbs retained from previous planting season, which have a high risk of virus infection, are used by farmers as sources of seed. Infection by key viruses were detected in garlic bulbs. The incidence of Onion yellow dwarf virus (OYDV), Garlic common latent virus (GCLV) was 100% on local garlic cultivars, 'LumbuHijau' and 'Sembalun'; whereas incidence of SLV was slightly lower (up to 75%). Heat vapour treatment of bulbs and thermotherapy in tissue culture were evaluated for their efficiencyin virus elimination. Combinations of temperature (25, 40, 45, 50 ^{o}C)and soaking time (5, 10,15 min) with heat vapour treatment were not been effective in suppressing GCLV or OYDV, but reduced SLV incidence in some extent.Thermotherapy at 33 oCin tissue culture was the best method to eliminate OYDV in garlic although the efficiency was not the same for all cultivars. The efficiency reached 60% for cv. Lumbu Hijau, but only 40% for cv. Sangga Sembalun. The effectiveness of tissue culture in producing virus-free garlic bulbs will be discussed in this presentation.

Biography:

Education Background

- 1997 PhD Entomology,University of Wisconsin-Madison, USA
- 1992 MSc Plant Pathology, University of Wisconsin-Madison, USA
- 1984 Sarjana Plant Protection, Bogor Agricultural University, Indonesia

Recent Position Faculty member at Department of Plant Protection, Bogor Agricultural University

Other Positions

- Member of Plant Quarantine Expert Committee, Ministry of Agriculture-Republic of Indonesia
- Member of Plant Protection Expert Committee, Ministry of Agriculture-Republic of Indonesia
- Member of Biosafety Task Force, Ministry of Environment – Republic of Indonesia

Research Experience (selected)

- Banana bunchy top virus (BBTV) Mitigation: Community management in Nigeria, and Screening Wild Banana Progenitors for Resistance (2015-2019) funded by Bill & Melinda Gates Foundation
- Integrated disease management of sugarcane streak mosaic in Indonesia (2014-2018) funded by ACIAR
- Improved agronomic practices to increase productivity of allium and solanaceous vegetable crops in Indonesia and sub-tropical Australia (2012-2018) funded by ACIAR
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Necrotic syndrome associated to a Plum pox virus chimera carrying a highly structured noncoding RNA

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A mutant of the potyvirusTobacco vein mottling virus (TVMV) with a 58-nt long "AU" rich element expected to fold as a stem-loop structure introduced at its 3´UTR (TVMV XBS8), has been reported to infect efficiently Nicotianatabacum causing only very mild symptoms (1). To assess the possibility that this RNA fragment may induce the symptom attenuation also in another potyvirus, a Plum pox virus chimeric virus(PPV-TVMV), including a 333-nt long fragment from TVMVpXBS8, was inserted between the NIb and CP coding sequences of PPV. The chimera was able to cause a systemic infection in Nicotianabenthamiana. Nevertheless, the systemically infected N. benthamiana leaves showed a severe necrosis response with the overexpression of PR2 protein and low viral CP accumulation level. To examine the virus progeny from systemically infected leaves, a high-throughput transcriptomic analysis by RNA-seq was performed. We found that the original infiltrated virus was still present, but the majority of the progeny was a virus variant in which the inserted sequence was deleted and created a C terminal mutant of NIb (NIbmut). Intriguingly, NIbmut was also selected in the systemically infected leaves of N. clevelandiiplants inoculated with PPV-TVMV and it was also associated with low viral CP accumulation, but not with the PR2-related necrosis response. Therefore, we propose that a highly structured noncoding RNA forced PPV-TVMV to escape from a non-identified deleterious effect during the process of virus-host interaction that caused: i) a reduced infection efficiency, explaining low virus accumulation in infected plants, and ii) exacerbation of necrotic responses of the N. benthamianaimmune system. We propose a speculative scenario based on classical arm race models in which plants have developed immune responses against the RNA sequence/structures of the chimera virus.

This work was supported by grants BIO2010-18541 and BIO2013-49053-R (Spanish Ministerio de Economía and Competitividad) and KBBE-204429 (EU).

Take Away Notes:

- The audience will know that the possible function of the noncoding RNA may involve in the development of the viral symptoms during infection.
- This work will to lean that the viral RNA genome may be spliced by host and create the viral mutant, which in turn affect viral infection. One should be awarded that several different viral species may co-existed in plant.
- The audience will learn how we identify the viral species from the infected plant.

Biography

Mingmin Zhao, PhD, Plant virologist. I am working as a professorin Inner Mongolia Agricultural University, China. I have been worked with plant viruses for many years since 2002. Especially in the research topic about RNA silencing and antiviral defense in plant. Currently, I am mainly interested in the epigenetical regulation of plant RNA viruses and the function of noncoding RNAs in plant viral infection.

SKIP, a splicing factor, links alternative splicing to SWR1 chromatin remodeling complex and controls flowering time in Arabidopsis

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Similar to other eukaryotes, splicing is emerging as an important process affecting development and stress tolerance in plants. Ski-interacting protein (SKIP), a splicing factor, is essential for circadian clock function and abiotic stress tolerance; however, the mechanisms whereby it regulates flowering time are unknown. In this study, we found that mutation of SKIP, skip-1, confers early flowering phenotype under long day (LD) and shot day (SD) conditions. SKIP is required for the splicing of serrated leaves and early flowering (SEF) pre-mRNA through directly binding, which encodes a component of the ATP-dependent SWR1 chromatin remodeling complex (SWR1-C). It has been reported that the SWR1-C exchanges histone H2A for H2A.Z, producing variant nucleosomes. The SWR1-C is required for H2A.Z deposition at flowering locus c (FLC), MADS affecting flowering (MAF) 4, and MAF5 chromatin (which encode central flowering-time suppressors), and promotes transcription at these loci. The skip-1 mutation caused the elevated accumulation of alternatively spliced SEF isoforms, including those showing intron retention. However, the level of mature SEF mRNA encoding functional SEF protein was reduced by skip-1. Defects in the splicing of SEF pre-mRNA reduced H2A.Z enrichment at the chromatin of FLC, MAF4, and MAF5, suppressed the expression of these genes; activated the expression of suppressor of constans 1 (SOC1), flowering locus T (FT), and twin sister of FT (TSF) (which encode flowering-time integrators); produced an early flowering phenotype in skip-1 plants. Our findings indicate that SKIP regulates SWR1-C function via alternative splicing to control the floral transition in Arabidopsis thaliana.

Take Away Notes:

- Splicing and chromatin remodeling are the key regulatory mechanisms of plant development. The talk will present the cross talk between alternative splicing and chromatin remodeling in regulating gene expression and controlling flowering time.
- The research work involved in the roles of alternative splicing, epigenetic modification in plant development such as flowering time control. The results are obtained by combined DNA recombination technology, transgenic techniques, RIP, ChIP, and qRT-PCR. The talk will help the audiences get more ideas to perform their research work.
- The talk will give a brief introduction on the molecular mechanisms of alternative splicing, chromatin remodeling and flowering time control in plants, which will extensively expand the audience's research and teaching in the future.

Biography

Xiaoxue Wang is a professor in Rice Research Institute at Shenyang Agricultural University. She obtained her Ph.D. in 1994. She used to be a visiting scientist and postdoctoral associate at Peking University, Yale University and University of California at Berkeley in the U.S.A.. In 2005, she worked at National Institute of Biological Sciences, Beijing. She is currently a professor in Agronomy College at Shenyang Agricultural University, China. She has published over 30 papers in the journal of The Plant Cell, BMC Biology, The Plant Journal, Plant Biotechnology Journal, Critical Reviews in Plant Sciences. Her researches focus on molecular mechanisms of plant development and responses to abiotic stresses by using Arabidopsis and rice as model organisms.

COP9 SIGNALOSOME 5A protein interacts with FLOWERING LOCUS T (FT) and mediates cell cycle and flowering

Soo-Jin Kim*, Ph. D., Sun Young Kim, Ph. D., SnježanaJurić, Ph. D., JiHoonAhn, Ph. D.
Korea University, Republic of Korea

CSN5A is a subunit of the COP9 signalosome and is well known for its proteolytic mechanism by ubiquitination as a photomorphogenesis inhibitor. However, it is not well known that the CSN complex is involved in the cell cycle. The csn5a-1 mutants, completely devoid of CSN5A expression, were identified as a cell cycle arrest in the G2 phase. Since csn5a-1 exhibits post-embryonic growth arrest, this phenotype seems to be associated with the cell cycle. As CSN5A interacts with FLOWERING LOCUS T (FT) in our previous results, we analyzed the flowering phenotype of csn5a mutants in order to investigate the role of CSN5A in ambient temperature responsive flowering. The csn5a-1 flowered early at 16°C under long-day conditions, but they showed a normal flowering time phenotype at 23°C under the same conditions. In this study we will show the relationship between temperature-dependent flowering insensitive phenotype and cell cycle.

Biography

I am a research professor in the Korea University and my major study is the ambient temperature-responsive flowering mechanism in Arabidopsis.

Identification and characterization of nitrate regulatory genes in plants

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Nitrate is not only an important nutrient but also a signaling molecule for plant normal growth and development. However, the nitrate regulatory genes and underlying mechanismsare limited and remain tobe identified and characterized.Here, we isolated the Cleavage and Polyadenylation Specificity Factor 30 gene (CPSF30-L) as nitrate regulatory gene by using forward genetics. In cpsf30 mutant, the induction of nitrate-responsive genes was inhibited independent of the ammonium conditions. The nitrate content was lower in cpsf30 mutant than in wild type, which may be caused by the reduced expressionof the nitrate transporter/sensor gene NRT1.1 and increased expression of several nitrate assimilatorygenes.Molecular and genetic evidence suggests that CPSF30-Lworks upstream of NRT1.1and independentlyof NLP7 in nitrate signaling. Further investigationrevealed that CPSF30-Laffected the pattern of polyadenylation sites of 3'-UTRof NRT1.1. Transcriptome analysisdisplayed that four nitrogen-related clusters were enriched in the differentially expressed genes of the cpsf30 mutant.These findings indicate that CPSF30-Lplays a key role in nitrate regulation in part through modulating NRT1.1expression, thus adding an important component to thenitrate signaling network.Although nitrate regulatory genes have been identified, our understanding of thenitrate regulatory genenetwork is still incomplete. It has been reported that the genesNIN-like protein 7 (NLP7) and NRT1.1 are two key nitrate regulators and ChIP-chip assay showed that NLP7 might bind to NRT1.1.However, their relationship and underlying mechanismremain unclear.Our results showed that NLP7 modulatedthe expression of NRT1.1 in the presence of ammonium.ChIP-qPCR and EMSA assays indicate that NLP7can bind to specific regionsof the NRT1.1 promoter. Molecular and genetic analyses suggest that NLP7 works upstream of NRT1.1in nitrate regulation when ammonium is present and NLP7 may function in another pathway independent of NRT1.1to regulatenitrate signaling. In addition, transcriptome analysis showedthat four nitrogen-related clusters were regulated by both NRT1.1 and NLP7.Thus, NLP7 acts as an important factor in nitrate signaling via regulating NRT1.1under ammonium conditions.The above findings about the characterization of CPSF30-Land the study for the relationship between NLP7 and NRT1.1provide more insights into the mechanism of nitrate regulation and the network of the nitrate regulatory genes.

Take Away Notes:

- We used an effective forward geneticsapproach for discovering new genes involved in nitrate signaling.
- Our study demonstrates the new role of CPSF30-L in nitrate regulation, expanding our understanding of the function and underlying mechanisms of CPSF30-L.
- The study on the relationship between nitrate regulatory genes laysthe fundamental base for deciphering the mechanism and network of nitrate regulation.
- Nitrogen regulatory genes play essential roles in nitrogen use efficiency ofplants. Identification and characterization of nitrate regulatory genes will provide theoretical basis andsupport for breeding new crop varieties with high nitrogen use efficiency and improving crop nitrogen utilization.

Biography

Yong Wang obtained his Ph.D degree from University of Lausanne in Switzerland in 2006 and did postdoctoral studies from the University of California, San Diego in USA during 2006.1-2010.11. Since Dec. 2010, he has been working as a professor at ShandongAgricultural University in China.He has published many papers in reputed journals including "the Plant Cell", "Plant Physiology", "New Phytologist"etc.

Removal of airborne dust and associated metals by plant leaves

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As the capital of China, Beijing is continuously exposed to high amount of airborne dust, thus it is necessary to find improvement methods. As an ecological and friendly way in improving air quality, phytoremediation were investigated in three aspects: (1) 32 urban plant species leaves were investigated in removing airborne dust and its associated metals on Beijing roadside sites in autumn, with Metal Accumulation Index (MAI) values calculated. Results showed that leaves could remove dust from 0.510 to 23.0 g m−2 with an overall mean of 7.50 g m−2. Plant species with dust accumulation rate above the mean including Koelreuteria paniculata, Ulmus pumila, Syringa oblata, Malus micromalu, Weigela florida cv. Red Prince, Ailanthus altissima, Salix babylonica, Robinia pseudoacacia, Ligustrum × vicaryi, Euonymus japonicus, Prunus cerasifera f. atropurpurea, Magnolia denudata, and species with higher MAI values including Amygdalus persica, Magnolia denudata, Syringa oblata are suggested to be considered in future green belt planning in Beijing. (2) To provide more insight into the removal ability of urban air dust and associated metals by plant leaves, above 15 plant species leaves were analysed for size fractions of leaf surface dust (SD) and inner wax dust (WD). Seven associated metals Cd, Cr, Cu, Fe, Mn, Pb and Zn were also measured and MAI was calculated for different species leaves at various dust sizes and soluble forms respectively. In result, most species leaves collected larger ratios of SD than WD. Whilst SD was presented at all particle size fractions for all plants, nearly all species leaves collected higher proportions of WD>10 μm. Metals were observed in all sizes of SD/WD. (3) To search a new way of evaluating the long-term pollution situation of airborne particles, concentrations of leaf surface dust and associated metals (Cd,Cr, Cu, Mn, Ni, Pb, Zn) of five common plant species were investigated at seven sampling sites in Beijing. MAI of leaf surface dust was also calculated, and comparison was made between our leaf surface data and the particulate observation data from adjacent air monitoring stations through statistical analyses. As a result, leaf SD concentration of Ulmus pumila can quantitatively evaluate monthly mean PM10 mass with relative error of 1.2-10.6%, whilst leaf dust data of Ailanthus altissima can assess monthly mean PM2.5 mass with relative errors as 0.18-3.7%. The MAI value can be used as an indicator for overall airborne dust metal pollution. (4) To understand micro morphological mechanism of leaf dust and associated metals removal, leaves of 9 landscaping tree species were collected from roadside of Beijing and studied for their micro-morphological (stoma, epidermal hair, etc.,) features with Environmental Scanning Electron Microscope (ESEM) as well as associated particulate matters (PMs) using Energy Spectrometer (EDS). The result shows that leaves of plants were one of the main means/ways/channels to retain airborne PMs and the retention abilities were various due to differences of their epidermal micro structures.

Take Away Notes:

- Urban planting designers could apply the plant species well remove dust and associated metals by their leaves in this presentation when air dust and associated metals pollution exists.
- Environment quality monitoring technicians could assess PM_{10} and $PM_{2.5}$ concentration by taking advantage of the calculation method of this presentation.
- The presentation provides a new sight of plant mechanism in removing air dust and metals. It will inspire researchers to investigate more interested points.
- The presentation provides attractive science materials for educators on Environment, Ecology and related fields.
- The presentation will provide audience with more science about trees and will arouse their love and protection consciousness to our ecological environment.

Biography

Yanju Liu is an environmental biology professor and vice manager in Beijing Milu Ecological Research Center, Beijing, P.R. China. She has gained her Ph. degrees in Botany from Institute of Botany, Chinese Academy of Sciences. She ever worded as a post doctor in University of California at Berkeley, USA and Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences in China, and as an honorary research fellow in University of Birmingham, UK. Her research focuses on environmental science and pollution remediation. She has contributed various articles and monographs mainly on phytoremediation of indoor air pollution and soil pollution; airborne particulate matter pollution; response of plant to air pollution; air dust storm, etc.

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DAY 2

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Will Die Slowly family in *Arabidopsis* development and their ERK docking sites for the interaction with MAP kinase pathways

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Will Die Slowly (WDS) gene family was identified and was suggested to have anti-cell death and anti-senescence functions by phenotypic analysis of single or double mutants. wds1 plants started to show signs of leaf senescence sooner than wild type. The lack of remarkable differences between the phenotypes of WT, wds1, wds2 and wds1/wds2 plants indicates that WDS1 and WDS2 do not mediate cell death pathways that are responsible for shaping the architecture of the Arabidopsis plant. The expression level modulated at different developmental stages, reaching a peak when 50% flowers have opened. WDS1 is predicted to be located in the cytoplasm, to contain three possible ERK docking sites, to interact with a protein that appears to function in the repression of genes that may induce apoptosis via a mitochondria mediated pathway and also a protein that seems to be part of an ubiquitin ligase complex. Overexpression of WDS1 in Arabidopsis enhanced the tolerance to osmotic stress.

Biography

Tim Xing has completed his Ph.D from Leicester Polytechnic in England and postdoctoral studies from University of Toronto. He is an associate professor in Carleton University, Ottawa, Canada. He has published over 70 papers in reputed journals and serving as an associate editor of several international journals.

Characterization of a new isoform of starch synthase in *Solanum tuberosum*

François Sevestre, Ph.D fellow
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Potato (Solanum tuberosum) is a staple crop that is cultivated for its starch rich tubers. Potato starch has many industrial uses, for example as thickener in food industry or as adhesives in cardboard production. Starch is one of the major storage polysaccharides in plants. It accumulates in plastids as insoluble semi-crystalline granules. It is composed of two polymers: amylose and amylopectin. Amylopectin represents 75% of starch dry weight. Both amylose and amylopectin are glucose polymers linked by □-1,4 O-glycosidic linkages and branched by □-1,6 bounds. Amylopectin displays complex and very organized secondary and ternary structures. The latter are tightly regulated and essential for granule formation.

Starch biosynthesis requires the concerted activities of distinct enzyme families including Starch Synthases (SSs), Branching Enzymes (BEs) and DeBranching Enzymes (DBEs). Moreover, each family of enzymes comprises several isoenzymes regulating amylopectin chain length distribution. Starch synthases catalyze the formation of □-1,4 bounds using ADP-glucose as a donor substrate and transferring the glycosyl moiety onto an elongating glucan chain. Five starch synthases are already well characterized. Among them, starch synthases 1, 2 and 3 are respectively involved in elongation of short, medium and long chains of amylopectin whereas Starch synthase 4 is involved in the initiation process. GBSS (Granule bound starch synthase), which is present within the granule matrix, is responsible for the synthesis of amylose.

In the lab, with identified 2 other SS isoforms, SS5 and SS6, by proteomics of potato starch. Phylogenetic analysis of SSs sequences including SS6 have shown that the latter is most closely related to SS4. Furthermore, sequence alignment highlighted the presence of two highly conserved motifs responsible for SS catalytic activity in SS6, suggesting that this isoform plays a yet uncharacterized function in starch metabolism. My thesis work is to decipher SS6 activities and also understand its function in planta. For this purpose, Solanum tuberosum is a good subject of study, due to the relative ease of production of genetically transformed plants, the existence of genome sequence but also because of the economic importance of the potato starch production.

This presentation will report the advances in characterization of this new isoform of starch synthase in Solanum tuberosum.

Take Away Notes:

- My presentation will provide an overview of the current knowledge on the starch synthesis by starch synthases. It will also show both in vivo and in vitro techniques applied to resolve the role starch related enzymes in potato. It's a good example of use of genetic transformation and CRISPR/Cas9 system in plant research.

Biography

I received B.S and M.S in plant science from French university of Rennes1 and I am currently in first year of Ph.D. degree. I previously work on potato transformation via Agrobacterium tumefaciens and protoplasts transfection using CRISPR/Cas9 the system.

Mechanisms of isolation of excess salt in leaf tissue of halophytes

Elena V. Voznesenskaya PhD[1*], Nuria K. Koteyeva PhD[1], and Gerald E. Edwards PhD[2]
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Halophytes have in common means of preventing excess accumulation of salts in the cytoplasm of leaves by storage in vacuoles and by excretion. Two different means of salt excretion are recognized between salt excreting halophytes: one by salt accumulating in trichomes over a limited period of time, the other by specialized salt excreting glands which function during the entire leaf life.

Salt ion isolation is a characteristic of succulent halophytes which developed increased volume of water storage tissue as an adaptation to salt stress. Analysis of gas exchange parameters of succulent Salsola species (family Chenopodiaceae) with C3, C4 and C3-C4 intermediate photosynthesis showed high salt tolerance of all three photosynthetic types. Application of fluorescent marker on the intracellular localization Na+ by CoroNa Green, as well as elemental analysis of its level by scanning electron microscopy (SEM EDAX) showed a significant increase in salt accumulation in vacuoles of water storage tissue, together with increased osmolality of leaf tissue, demonstrating the importance of leaf succulence. In this family salt accumulating trichomes were characterized (e.g. in Atriplex, Chenopodium, Bienertia). They are comprised of a single celled head which accumulates salt, and one-to-two cellular stalk. Usually such trichomes are numerous and very active in young leaves and then they exfoliate during leaf maturation with excretion of salt crystals on the leaf surface. Application of CoroNa Green showed significant accumulation of Na+ in the vacuoles of the head cells beginning from the earliest stages of leaf development which decreased as the head matured.

Minimizing salt accumulation in leaves by excreting excess salt via salt glands is characteristic of monocot as well as dicot halophytes. These glands are usually multicellular in dicots and bicellular in grasses. The comparative study of plants from different phylogenetic lineages is one means of understanding the convergent evolution of secretory systems in different lineages of dicot and monocot plants. Mechanisms of salt tolerance were analyzed for three halophytic grass species, Oryza coarctata, Spartina anglica and Urochondra setulosa which belong to different lineages. In S. anglica and U. setulosa, the glands have a classical bicellular structure. However, O. coarctata is unique in having unicellular glands. There were also significant differences in the ultrastructural features of salt glands which suggests diversity in evolution of the steps involved in salt excretion. Further studies are needed between species on the steps involved in import of salts into salt glands, their facilitated movement across membranes and energy dependent excretion.

In summary, studies among halophytic species from different phylogenetic lineages indicate some fundamental mechanisms which confer salt tolerance and support of plant life functions at the leaf level, including increased levels of compatible solutes, salt isolation (e.g. in vacuoles), storage in trichomes, and excretion from salt glands. The ways these are expressed between species vary significantly, but there are similarities in some structural and physiological solutions between different systematic groups.

Supported by the Russian Science Foundation (16-16-00089).

Biography

Elena Voznesenskaya is a senior researcher in laboratory of Anatomy and Morphology, Komarov Botanical Institute, Russian Academy of Sciences. Voznesenskaya was graduated from St. Petersburg State University, Russia, where she was awarded a Master of Science degree in Plant Biology. Her PhD in plant sciences was carried out at Komarov Botanical Institute where she was awarded in 1977 for the investigation of the structure of assimilating organs in representatives of family Chenopodiaceae in relation to the peculiarities of photosynthetic metabolism. Voznesenskaya's recent research interests are in two main areas: 1. The evolution, development and functioning of Kranz anatomy in C4 plants and 2. The stress tolerance mechanisms.

The Egy3 – strongly conserved protein of unknown function

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Site-2-proteases (S2P) are intramembrane zinc metalloproteases occurring widely in all living organisms, from bacteria to humans. S2P proteases comprise of at least four hydrophobic regions and their characteristic feature is the presence, in their first transmembrane domain, of the HExxH motif, responsible for zinc ion binding. Two other motifs were also shown to be highly conserved in S2P: GpxxN/S/G located within the second TM and the NxxPxxxxDG located in the third TM. The aspartic acid present in the last motif was shown to be crucial for proteolytic activity of these proteases due to its engagement in zinc ion coordination. In Arabidopsis thaliana there are six genes encoding the S2P homologs. The proteolytic activity of four of these proteins was experimentally confirmed. One of these homologs, named Egy3, was, however, described as proteolytically inactive, since it lacks the HExxH motif and substitution of the aspartic acid in NxxPxxxxDG motif with glutamic acid. Our results indicate, however, that the protein is strongly conserved in other higher plant species. We made an attempt to predict in silico 3D structure of EGY3. We also investigate effects of Egy3 absence on photosystem II proteins accumulation level in Arabidopsis thaliana chloroplasts. The abundance of apoproteins forming peripheral antennae (Lhcb1-Lhcb6) remain unchanged, similarly the abundance of PsbC- one of apoprotein forming inner antennae remain unchanged as well as abundance of psbD- one of the proteins forming photosystem II reaction center. We observed, however, a decreased abundance of PsbA, which also form photosystem II reaction center. The results of qPCR analysis indicate that changes in the PsbA accumulation level correlates with changes at the gene transcription level.

Take Away Notes:

Why a probably inactive homolog of site-2- proteases seems important for plant physiology?

How 3D structure of Egy3 probably looks like? What is possible function of Egy3?

- The Egy3 is probably inactive homolog of site-2-proteases - relatively recently discovered class of proteases, which are thought to release the transcription-factors and anty-σ from the membrane and thus, participating in regulation of genes expression. The Egy3 seems to be conserved evolutionary, however its function remains unknown. This makes the Egy3 an interesting subject of research.
- The intramembrane proteases are, relatively new field of research. Even less is known about their inactive homologs, like Egy3. Some of them were proven to be crucial for growth and physiology. The aim of the presentation is to drew attention to uninvestigated but strongly conserved evolutionary group of proteins.

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.

Screening of triticale winter breeding lines for resistance to Fusarium head blight

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Fusarium head blight (FHB) 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. We determined resistance to Fusarium head blight of 71 winter triticale lines/cultivars (including 52 lines showing increased resistance in the previous year, 3 check cultivars and 14 newly obtained lines). Triticale was sown in field experiments in two locations in Poland. At flowering, triticale heads were inoculated with three F. culmorum isolates. FHB index was scored and after the harvest, percentage of Fusarium damaged kernels was assessed.

The average FHB indexes were similar in both locations: 17.9% (10.5-30.0%) in Cerekwica-Poznań and 6.9% (6.0-32.0%) in Radzików. After the harvest and grain threshing, percentage of kernels damaged by Fusarium (FDK) was determined. The percentage of kernels with symptoms of FHB (FDK m) ranged from 13.7 to 53.6% (an average 33.3%), and the number of infected grain (FDK L) ranged from 16.2% to 55.6% (an average 36.6%). The lowest mass of infected grain (FDK m) was determined in the MAH 33544-3 line, and the lowest number of infected grain (FDK L) in the BOHD 1025-2 line. These lines showed low grain infection also in the previous year. The DS.9 line showed low weight and number of infected grains and low head infection rate (IFK 5.7%) in 2017 as well as in previous years of research. For all tested lines, a decrease in yield components was observed: grain weight per head and weight of a thousand kernels, in comparison to lines without inoculation (control). The reduction of grain weight per head ranged from 11.8% in MAH 34964-2 line to 53.8% in DANKO 13/16 line (an average 33.4%). The reduction of the number of grains per head ranged from 7.0% in MAH 34964-2 line to 45.5% in DANKO6 line (an average 24.4%).

Out of the yield components, the reduction in thousand kernels weight was the lowest and was on average 15.5%. The lowest reduction in all examined components was estimated for the MAH 34964-2 line. There was a high correlation between the mass and the number of infected grains r = 0.988. The index of FHB correlated significantly with the damage of the kernels and the reduction of the grain mass from head, however the coefficients were low. In addition, the reduction of thousand kernels weight correlated with mass (FDK m) r = 0.588 and with the number of damaged kernels (FDK L) r = 0.760.

Acknowledgements: This work was supported by Ministry of Agriculture and Rural Development - grant number HOR. hn.802.14.2017

Take Away Notes:

- Triticale genotypes were much more infected by Fusarium in recent years, on the similar level to wheat

Biography

1974	Master of Sciences degree in the field of Botany, at the University of Adam Mickiewicz in Poznań.
1985	Doctor of Philosophy degree in the field of Agricultural Sciences, at the Institute of Plant Genetics, Polish Academy of Sciences in Poznań
2007	Doctor of Science degree in the field of Agronomy, at the University of Life Sciences in Poznań
2008-till now	The leader of Cereal Genomics Team at the Institute of Plant Genetics, Polish Academy of Sciences in Poznań
2014	Professor degree in the field of Agricultural Sciences, at the Institute of Plant Genetics, Polish Academy of Sciences in Poznań

Chemical composition and antifungal activity of the essential oils of *Satureja montana* and *Mentha longifolia*

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In the interest of sustainable agriculture and to seek efficient alternatives, growing interest is being shown in developing natural phytosanitary products as an alternative to the tradition use of synthetic chemical products. Here we include essential oils from aromatic plants. Their antioxidant, antifungal, antimicrobial, germination inhibiting properties, etc., have been well-studied, often with very promising results. Those belonging to the genus Satureja stand out with its different types of biological activity, which have been well-described in the bibliography, and data are available that back its potential for antimicrobial, antioxidant and antifungal activity.

The objectives pursued in this work were to characterise the chemical composition of S. montana and M. longifolia and study its antifungal activity against fungi, which damage harvests and farming products.

Essential oils were identified by gas chromatography with a mass spectroscopy (GC/MS) detector, supplemented with the calculation of Kovats retention indices and some of the main compounds by pure pattern coinjections. Quantification was done with similar GC equipment, but equipped with a flame ionisation detector (FID). The majority compounds were p-cymene (11.6%), □-terpinene (14.1%) and carvacrol (47.4 %) in summer savory, and piperitone oxide (23.1%) and piperitenone oxide (50.6 %) in M. longifolia.

The "in vitro" antifungal activity of essential oils was evaluated following the modified methodology by Singh et al., (2008). Bioassays were run with 100, 200 and 300 μg/mL doses. The antifungal capacity of essential oils was evaluated on phytopathogenic and post-harvest fungi on Alternaria alternata, Botryotinia fuckeliana, Curvularia hawaiiensis, Fusarium equiseti, Fusarium oxysporum lycopersici, Rhizoctonia solani and Verticillium dahliae to obtain a botanical enviro-friendly and low-risk biofungicide.

S. montana oil gave excellent results because the 300 μg/mL dose inhibited the growth of all fungi under study, with 100% mycelial growth inhibition (MGI) values for all the fungal species, except for B. fuckeliana, whose MGI value was 92%. The 200 μg/mL dose completely inhibited the growth of four of the seven studied fungal species, while the 100 μg/mL dose maintained antifungal capacity with MGI values ranging from 50-80% on the assayed fungi.

The mint essential oil (M. longifolia) also gave satisfactory results for the 300 μg/mL dose, with MGI values between 45% and 60%, 77% on Fusarium oxysporum lycopersici, and a 100% MGI value on Verticillium dahliae.

This study evidences the very high potential of the Satureja montana essential oil to control fungi and is a good alternative to agrochemicals.

Take Away Notes:

- Essential oils as an alternative to agrochemicals.
- Evaluation of the antifungal activity of essential oils.
- Cooperation with other research groups.

Biography

She graduated in Biology Sciences by the Universitat de València (UV). She did her PhD at the UV in the Dept. of Biotechnology of the Universitat Politècnica de València (UPV). She is a University Professor in the area of botanical Knowledge. She is a teacher at the School of Agricultural Engineering and Environment, in the Department of Agroforest Ecosystems at the UPV. She has occupied different job posts at the UPV, including Vice-Rector and Head of Department. She received Universitat Ramon LLul Research Award – IQS – the Generalitat de Catalunya, and the Teaching Excellence Award by the UPV – Generalitat Valenciana.

Identification and characterization of poliploid plant of PLANT *Heliconia chartacea* var. Sexy Pink

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One of the sectors that have the highest growth rate in the national and international market is floriculture. Ornamental plants are distinguished by their beauty. They enchant both through their exotic forms and by the variation of colors, among which stands out are the Heliconia chartacea var. Sexy Pink. The consumer demand for news has forced producers to launch quicker, new varieties to remain competitive in this product segment. In this sense, biotechnological research was carried out to induce polyploidy in vitro by somatic doubling using colchicine in three concentrations (0.01%, 0.05% and 0.1%) in order to obtain a higher rate of genetic variability causing larger and better plants, and as a bridge for gene transfer between different levels of ploidy. In this context, the objective of this work was to evaluate the plants established in the field, from in vitro polyploidy induction assays to determine the morphological, physiological, molecular and productive characteristics of 42 clones of H. chartacea var. Sexy Pink. The characterizations were performed by utilizing 49 morphological and agronomic descriptors to determine the number of polymorphic loci through AFLP analysis. Furthermore, characterization of leaf blade structures and stomatal density evaluations by means of microscopy, along with identification of ploidy levels using flow cytometry were also determined. As the genotypes 13, 20, 36, 37 and 40 did not present inflorescences during the two years of evaluation and did not present any other characteristic of commercial interest, they were considered unfit for selection for future selection and breeding work. The genotype 35 showed the highest morphological variations with changes in the position, color of the inflorescence, along with exhibiting the edges of the whole leaf blade. Clone 18 showed plant height and inflorescence size reduced. Clone 26 presented total defoliation during flowering, which makes this genotype more interesting for landscaping. Combinations of the primers used for AFLP analysis revealed a total of 519 bands, ranging from 100 to 800 base pairs. The total number of loci per primer varied from 157 to 188, while the amount of genetic variation obtained by the analysis of molecular variance showed that 99.67% of the genetic variability is within the treatments with colchicine analyzed, and only 0.33 % Among treatments of H. chartacea clones. The stomata of all clones showed tetracytic morphology and guard cells without significant alterations. The highest stomatal density were observed in clones 1 and 14 for the adaxial part of the leaves. Whereas for the abaxial part, clones 10, 12 and 14 were the ones with the highest values. The lowest values were verified in clones 7 and 35 for the adaxial part and 7 and 13 for the abaxial part of the leaves. The work allowed the identification of 4 tetraploid and 11 mixoploid genotypes using the flow cytometry technique. Helping in the identification of potential genotypes for genetic improvement program and future in obtaining new varieties.

Take Away Notes:

- The audience can get a great knowledge from the presentation. The study presents in an objective way moderns and efficient technique to reach its goals. Taking under consideration the congress theme, a lot of the participants will have similarly objectives in their respective studies. Probably they will be capable of identify tools that they are familiarized with. Or will they have the opportunity to get to know new ones. With this background they will be capable to apply this information in a practical way. The discussion about the methods and design will be clear and understandable, being easy to the audience to access the information. This work's approach to design's problem it is made in a direct way, evidencing its particularities and surely will help to improve the quality of future design. The conclusion of the study points directly to the hits and flaws of the design. Our research will help in the identification of potential genotypes for genetic improvement program and future in obtaining new varieties.

Biography

Agronomist by the Universidade Federal de Viçosa from Viçosa, Brazil (1998). PhD in Genetics and Plant Breeding by Universidade de São Paulo, Piracicaba, Brazil (2003) and post-doctorate in forestry genomics at the University of Florida, Gainesville, USA (2016). Associate Professor at Universidade Federal do Amazonas since 2002. Her area of expertise is focused on conservation, breeding and genomics with emphasis on amazon species. It is a consultant for scientific funding agencies in Brazil.

Comparative analysis between the reproductive strategies of the cultivated *Moringa oleifera* and its wild and endangered relative *Moringa peregrina*

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The Moringaceae is a family of 13 species portraying a range of adaptations to mostly dry or wet tropical habitats.

This study is focused on comparative analysis of two closely related species; Moringa peregrine; a wild plant, native to Israel, in the dry tropical regions, and Moringa oleifera; a native to the wet tropics of India and is now prevalent throughout warm tropical or Mediterranean regions. Both species are utilized for food, medicine, energy and cosmetics.

Despite the increasing interest in these plants, very little is known about their sexual reproduction and its significance for the production of seed-oil yields. In order to characterize the reproductive strategies of both species we conducted a study on mature trees under Mediterranean conditions. We recorded bloom phenology and compared the foraging behavior of the two most frequent flower visitors; the honey bee (Apis mellifera) and the carpenter bee (Xylocopa pubescence). We found that M. peregrina bloom was bimodal while that of M. oleifera peaked only once. Visitation rate and number of visited flowers of the honey bee were significantly higher than those of the carpenter bee.

The pollen grains of both species were found to be uniquely immersed in copious amounts of a cream-like substance (pollenkit). Removal of this pollenkit resulted in reduced viability under hot temperatures (40°C) and reduced invitro germinability, which was restored when it was pre-hydrated.

Close inspection of the pistil revealed that the style was a hollow tube with the receptive tissue present > 1mm inside the tube. Attempts to force pollen inside the stylar tube resulted in a significantly larger number of grains reaching the receptive region when the pollenkit was present, further stressing the significance of this unique media to the reproductive success. The stylar tube was also found to preserve pollen viability under extreme temperatures.

Is autophagy involved in nitrogen remobilization during plant organs senescence in Populus trichocarpa?

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Senescence of plant organs, despite its destructive character, belongs to processes which are well-regulated. This regulation is necessary to achieve the main goal of senescence – remobilization, which allows to transport valuable nutrients from senescent organs to another parts of plants. Recent studies have shown that one of the main mechanisms that is needed to properly course the remobilization in leaves is autophagy. However, little is known about root senescence. These organs, especially fine ones, are responsible for water and nutrients absorption and at the end of growing season when demand for water decreases most of them undergoes senescence and die. Given that the biomass of fine roots in forest ecosystems is often equal or greater than leaf biomass, remobilization process is important also in the case of nutrients cycling in nature.

The aim of our research was to check whether processes related to nitrogen remobilization are switched on and are crucial during senescence of fine roots. We compared fine roots and leaves in order to check if common mechanisms can be identified during senescence of such diverse organs, which play different function and are characterized by dissimilar structure. GCMS analyses were performed to analyze nitrogen content and qRT-PCR were conducted for analyses of the expression of genes encoding enzymes related to possible nitrogen translocation. Additionally, to confirm that in studied organs autophagy process are also active several studies (qRT-PCR, Western blot, Immunolocalization and TEM) were carried out.

Our results suggest that as well in leaves as in fine roots autophagy plays a critical role during senescence. In both organs, we observed increased expression of autophagy-related genes (atg) and amount of ATG8 protein. Moreover, in senescent cells, we observed plenty of autophagic structures such as autophagic bodies or autophagosomes. These alterations are correlated with a decrease of nitrogen amount and changing the expression of mRNA encoding proteins, necessary for nitrogen translocation e.g. glutamine synthetase (GS1) and glutamate dehydrogenase (GDH). It has been shown that different ephemeral organs undergone senescence in a similar way and involved the same mechanisms. One of them is a dual role of autophagy, which apart from degradation and executive role during senescence, is important also for remobilization of nitrogen.

This work was supported by grants no. 2012/07/E/NZ9/00194 and 2016/23/N/NZ3/00073 from the National Science Centre.

Take Away Notes:

- Mechanisms of senescence of fine roots and leaves are universal and undergo in a similar manner.
- Autophagy is involved in senescence and takes part in remobilization of nitrogen.
- Root senescence can be treated as developmental example of programmed cell death in plants.

Biography

Natalia Wojciechowska graduated from Nicolaus Copernicus University in Toruń (Poland), Faculty of Biology and Environmental Protection. During her master thesis, she focused on biogenesis snRNP in microsporocytes of Larix decidua Mill. Since 2014, Natalia is a Ph.D. student at the Faculty of Biology, Adam Mickiewicz University in Poznań (Poland). Her Ph.D. thesis is related to issues associated with programmed cell death process occurring during the senescence of ephemeral organs of Populus trichocarpa. She is familiarized with different field (using rhizotron system) and laboratory (microscopy, plant physiology, molecular biology) techniques. During Ph.D. studies she used various morphological, cytological, physiological and molecular markers to confirm and describe senescence process.

Potential antagonist of endophytic microorganisms isolated from *Butia purpurascens* and *Butia archeri*

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Butia purpurascens and Butia archeri are species of the family Arecaceae endemic to the Cerrado, being the distribution of Butia purpurascens restricted to the state of Goiás. Due to the lack of data about the endophytic microorganisms associated with these plants, and knowing that many microorganisms synthesize biomolecules that may aid in the biological control of pests, this work aimed to isolate and evaluate the potential of these symbiotics to inhibit the phytopathogens Fusarium sp. and Rhizoctonia solani. A total of 14 fungus morphotypes were isolated, being the isolates Fusarium oxysporum, Penicillium purpurogenum, Hamigera insecticol and Codinaeopsis sp. selected for antibiosis testing, because they present potential growth in the presence of the tested phytopathogens. Regarding bacteria, a total of 88 lines were obtained, but only 12, screened for the final inhibition tests. Fungal isolates exerted inhibition characterized as low, being the highest inhibition rates of Fusarium sp., considering 10 days of evaluation, observed in the presence of Fusarium oxysporum (Im% of 22.37). The highest inhibition of Rhizoctonia solani occurred in the presence of Codinaeopsis sp. (Im% 26.34). Bacteria, however, showed satisfactory inhibition rates against the two phytopathogens tested. Against Fusarium sp. a peak inhibition was observed after 96 hours of colony growth (75.55%), but the highest overall mean of inhibition was detected using Bacillus sp. (Im% of 36.82). Against Rhizoctonia solani the inhibitory activity of the bacteria increased with the time of exposure of the phytopathogen to the endophytic isolate, with an activity peak occurring at 10 days of culture in paired culture. In this period, the bacterium Enterobacter cloacae inhibited this phytopathogen at a rate of 79.9748% and presented general inhibition index of Im% 43.89. The sensitivity of Rhizoctonia solani to Enterobacter cloacae, increased with contact time, opens up possibilities for deeper assessments of the potential of this endophytic to be used in the biological control of this pest. Tests in greenhouse and field may contribute to better elucidate these aspects.

Take Away Notes:

- Knowing the endophytic community associated with native and poorly explored plants of the Cerrado biome contributes to the knowledge of the symbiotic microbial diversity that tropical plants shelter. The little knowledge about this microbiota is currently considered an obstacle to a better description of the general biodiversity that the planet harbors.
- Exploring microbial diversity can allow access to yet unknown biotechnological products and services. Microorganisms with high potential for biological control or plant growth promotion can be discovered in in vitro tests.
- Given the need to develop biological control practices that reduce the use of pesticides, this work opens up prospects for greenhouse and field trials. It also opens perspectives for these endophytes to be tested against other plant pathogens.

Biography

I have extensive experience in the area of Applied Microbiology. I have worked with endophytic microorganisms during the master's and doctoral studies and currently I develop tests with plant growth promoters (phosphate solubilizers and phytohormones producers) and research the microbial diversity associated with Cerrado plants. Oriented in a postgraduate program with research line in Applied Microbiology and Biodiversity. I have published several articles within this line, focusing on promoting plant growth, plant-microorganism relationship and access to microbial diversity.

Chlorophyl a fluorescence in evaluation of LED light influence on crops of the *Poaceae* family

Krystyna Rybka[1]*, Ph.D.; Patrycja Siedlarz[1], MSc; Piotr Stefański[2], MSc Eng.; Przemysław Matysik[2], PhD, Zygmunt Nita[2], PhD
[1]Plant Breeding and Acclimatization Institute - National Breeding Institute, IHAR-PIB;
[2]Plant Breeding Strzelce Ltd. Co., Strzelce, Poland

Shortening of crop breeding cycles is essential for competitiveness of breeding companies. This implies reduction of variety costs production thus enhancement of the seed companies competitiveness. The proposed solution involves the use of diodes (LED) emitting light exactly in the chlorophyll absorption range for SSD (Single Seed Descent) cereal crops breeding process. Seven LED illuminators differing in the ratio of blue to red and the amount of deep red light, enriched by yellow and green wavelengths were tested. Research was carried out in the experimental greenhouse of Hodowla Roślin Strzelce Sp. z o.o., Poland. Plant material consisted of genetically stabilized varieties of spring wheat, spring barley and oats. The seeds were sown in cell multiplexes, in 7 replicates x 10 plants of each species. Multiplexes were placed in a greenhouse chamber, in which 7 different illuminators were installed. Under each of them, on the basis of the same scheme, multi-pots with wheat, barley and oats were placed. Plants grew at an average temperature of 22˚C and humidity of 80%. On bases of morphological characteristics and interpretation of Chl a fluorescence transient as well as OJIP test the influence of light spectra on the plant development were evaluated. It was concluded that: There is no single illuminator suitable for all kinds of cereals, each species has individual lighting requirements; the sum of the spring wheat growth most similar to the control was under the SpectroLight-1 illuminator; the sum of the spring barley growth closest to the control was under the illuminator with a xenon bulb; the sum of the oat growth most closely related to the control was under the SpectroLight-2 illuminator.

Acknowledgements: This research is supported by the National Centre for Research and Development, Poland as PBS3/B8/19/2015 grant.

Take Away Notes:

- The audience will be able to get the knowledge about LED light spectrum influence on cereal plants growth.
- The results can be used as a concept for lightens modernization in greenhouses dedicated for cereal breeding purposes.

Biography

Krystyna Rybka, PhD in agronomy/biochemistry Plant Breeding and Acclimatization Institute - National Breeding Institute, IHAR-PIB, Radzików, Poland; MSc in chemistry, Warsaw University, Warsaw, Poland Employee of Plant Breeding and Acclimatization Institute - National Breeding Institute, IHAR-PIB. Leader of the project "Development and implementation of methods for shortening of cereal breeding cycles by lighting conditions optimization" financially supported by the National Centre for Research and Development, Poland as PBS3/B8/19/2015 grant. Author of 59 scientific papers from which 28 are placed on ResearchGate profile.

Application of exogenous synthetic strigolactone GR24 on in vitro *Medicago truncatula* plants with modified auxin transport in conditions of phosphate deficiency and excess

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AgroBioInstitute, Bulgaria

One of the most important nutrients required for normal development of plants is phosphorus. Both phytohormones auxin and strigolactones participate in the plant response associated with the phosphate signaling. In terms of phosphorus starvation, plants have developed mechanisms for overcoming stress, expressed in the formation of shortened and thickened cluster roots. Medicago truncatula plants with overexpression and downregulation of MtLAX3 gene (involved in polar auxin transport), transcriptional reporters of MtLAX3 (expressing reporter genes GUS and GFP under control of LAX promoter) and wild type plants were in vitro cultivated in extreme conditions of phosphate deficiency and excess. Phenotypic characterization and morphometric measurements were performed for the root system before and after treatment with synthetic strigolactone GR24. The relative transcript level of MtLAX3 and MtMAX2 (involved in the strigolactone signaling) was measured. The expression of GUS reporter gene fused to MtLAX3 promoter was traced in different organs and tissues by histochemical GUS assay.

Take Away Notes:

- New information about the interaction between two phytohormones auxin and strigolactones.
- Exogenous application of GR24 influenced on the root phenotype of plants with modified expression.
- The results obtained on the model legume plant M. truncatula turn light on the interaction between the two hormones in conditions of phosphate starvation or excess and could be translated to the important forage plant Medicago sativa (alfalfa).

Biography

I have done my PhD on Genetics in 2015 in AgroBioInstitute (ABI), Sofia, Bulgaria. I work in ABi since 2009, currently as an Assistant Professor in Functional Genetics group. I am interested in functional genomic studies on model plants Arabidopsis thaliana, Medicago truncatula, Lotus japonicus, plant development, nodulation, hormonal interaction. I have expertise in gene cloning, genetic transformation and analyses in the area of plant system biology and functional genetics, genomics and transcriptomics. Since 2016 I am team leader of a project focusing on the hormonal crosstalk between auxin and strigolactones in M. truncatula plants with modified auxin transport in the conditions of phosphate deprivation or access. In 2017 I won a project related to functional and bioinformatics analyses of GRAS TF in M. truncatula and M. sativa. https://www.researchgate.net/profile/Miglena_Revalska2/contributions

Stability of resistance to Fusarium head blight and *Fusarium* toxin accumulation in winter wheat lines evaluated in the years 2015-2017 in two environments

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Piotr Ochodzki, Ph.D., Department of Plant Pathology, Plant Breeding and Acclimatization Institute - NRI, Radzików, Poland
Dorota Walentyn-Góral, M.Sc., Department of Plant Pathology, Plant Breeding and Acclimatization Institute - NRI, Radzików, Poland
Maciej Majka, M.Sc., graduate student, Department of Genomics, Cereal Genomics Team, Institute of Plant Genetics Polish Academy of Sciences, Poznań, Poland

Fusarium head blight (FHB) resistance of advanced winter wheat breeding lines was evaluated for three years (2015-2017) 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.

Take Away Notes:

- 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 what phenotypic markers (head infection, kernel damage) were good predictors of mycotoxin (trichothecenes) concentration in grain, which does no 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 Radzików. 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.

Stimuli from prey induce expression of digestive enzymes in the carnivorous plant of the genus *Nepenthes*

Assoc. prof. Andrej Pavlovič*, PhD.; MSc. Michaela Saganová; Dr. Boris Bokor; MSc. Tibor Stolárik
Palacky University, Czech Republic

Carnivorous plants of the genus Nepenthes have evolved passive pitcher traps for prey capture. In this study we investigated the ability of chemical signals from prey (chitin, protein, ammonium) to induce transcription and synthesis of digestive enzymes in carnivorous plant Nepenthes x Mixta. We used real-time PCR and specific antibodies generated against aspartic proteases nepenthesins, type III and type IV chitinases to investigate the induction of digestive enzyme synthesis in response to different chemical stimuli from prey. Transcription of nepenthesins was strongly induced by ammonium, protein and live prey; chitin induced transcription only very slightly. This is in accordance with amount of released enzyme and proteolytic activity in digestive fluid. Although, transcription of type III chitinase was induced by all investigated stimuli, significant accumulation of enzyme in digestive fluid was found mainly after protein and live prey addition. Protein and live prey were also the best inducers for accumulation of type IV chitinase in digestive fluid. Although ammonium strongly induced transcription of all investigated genes probably through membrane depolarization, strong acidification of digestive fluid affected stability and abundance of both chitinases in digestive fluid. The study showed that the proteins are universal inductors of enzyme activities in carnivorous pitcher plant best mimicking the presence of insect prey. This is not surprising, because proteins are much valuable source of nitrogen than chitin. Extensive vesicular activity was observed in prey-activated glands using transmission electron microscopy.

Take Away Notes:

- Basic research. Help to understand how is the enzyme synthesis in carnivorous plants regulated by different stimuli from prey. This can be important because some enzymes in carnivorous plants are interesting target for plant biotechnology (neprosin, nepenthesin).

Biography

Andrej Pavlovič is an associated professor in the Department of Biophysics at the Palacký University in Olomouc, Czech Republic. He received his Ph.D. in plant physiology from the Faculty of Natural Sciences of Comenius University in Bratislava, Slovakia. In 2015, he defended his habilitation thesis entitled: Cost/benefit model for the evolution of botanical carnivory: from molecules to ecology. His research has focused on photosynthesis, digestive enzymes and nutrient uptake in carnivorus plants. Currently, his main area of interest is regulation of digestive enzyme secretion in the carnivorous plants. He is the author of ≈ 30 peer-reviewed papers, associate editor of journal Photosynthetica, and a national representative to The Federation of European Societies for Plant Biology (FESPB).

Feedstock production from nickel contaminated land for bioenergy purposes

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Global human population continuously increases along with an increasing concern of energy security, global warming and associated climate change effects. Biomass based renewable energy has attracted the interest worldwide due to its potential use as a carbon-neutral, clean and eco-friendly source. At the same time, the scarcity of soil resources will inevitably lead farmers to the exploitation of marginal and contaminated lands. Heavy metals, along with mineral oils, are the most frequent contaminant in European soils. Nickel (Ni) has become a serious concern as its concentration has reached especially high values in polluted soils and surface waters. This element, in elevated concentrations can be phytotoxic, and can be transferred to edible plant parts at rates sufficient to cause a threat to human health. Therefore, there is no other alternative besides developing new agricultural scenarios suitable to allow safe and economically valuable agriculture on areas that are currently considered inappropriate and toxic. The new strategies to be developed should combine biomass production and nickel management in order to minimize the risks for crops and human beings, and provide regular revenue to the farmers.

Physic nut (Jatropha curcas L.) and giant reed (Arundo donax L.) are two multipurpose energy crops that could be used for Ni phytoremediation purposes, and at the same time for the production of bio-oil (from physic nut) and solid biomass (from giant reed). Results from our previous experimental works show that physic nut, when cultivated in soil with a Ni concentration up to 200 mg kg-1 did not appear any toxicity symptoms, and the concentration of Ni to the aerial biomass was up to 1.3 mg kg-1. Giant reed was extremely tolerant to high Ni soil concentration. In a content of 2540 mg Ni kg-1 soil, all plants were growing very well and the metal concentration in the aerial biomass was up to 16 mg kg-1. In conclusion, by cultivating physic nut and giant reed in Ni contaminated sites will contribute to their remediation and restoration. Furthermore, by exploiting the produced biomass for bioenergy uses represent an opportunity to boost local economies and respond to the expected increase in demand for energy. This solution could be very important in stimulating rural development and in creating new job opportunities at both regional and national levels.

Take Away Notes:

- Knowledge and insights for practitioners about the non-invasive and publicly acceptable technology of soil phytoremediation and bioenergy production simultaneously.
- Create a better understanding on the safe and sustainable exploitation of Ni contaminated land with economic revenue.
- Information of farmers, cooperatives, industrial actors and businesses for new market opportunities.
- The prospects of job creation for women, men and young people, both within their family farms and along the supply chain of the produced biomass.

Biography

Panayiotis Trigas has a great interest in the origin, evolution and diversity of vascular plants, and in particular, how different factors may influence patterns of diversification. More specifically, he has been working with the vascular plant diversity of the Mediterranean region, focusing on the evolution, diversity and conservation of range restricted species. He is also pursuing research focusing on understanding biogeographic patterns and historical processes that have shaped distributions of vascular plants, especially on islands and mountainous areas. In addition, he is interested in the diversity of aromatic and medicinal plants and crop wild relatives in the Greek flora, focusing on the development and conservation of plant genetic resources.

The FLN1, pTAC10 and pTAC16 proteins as potential targets for EGY2 protease

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Egy2 belong to site-2 proteases. Proteases of these type are integral membrane proteins able to perform the proteolytic cleavage within the cell membrane and are thought to participate in signal transduction pathways by releasing of membrane-anchored transcription factors in a process called regulated intramembrane proteolysis (RIP). The Egy2 protein is known to be proteolytically active and located in thylakoid membranes. Its physiological function remain, however, elusive and its substrates remains unknown. Using the reverse genetic approach, we have investigated the consequences of absence of Egy2 proteases for Arabidopsis thaliana chloroplasts. The analysis were performed on two separate Arabidopsis thaliana mutant lines with T-DNA insertion in Egy2 encoding gene. Both Arabidopsis thaliana egy2 mutant lines display changes in expression level of chloroplast genes located on two operons PSBA and PSBC/PSBD. We observed a significant increase in abundance of PsbA transcript and reduced accumulation level of PsbD and PsbC transcripts. The observed changes in gene expression correlated with changes in abundance of proteins encoded by these genes. In both Arabidopsis thaliana egy2 mutant lines accumulation of PsbA protein was observed as well as decreased accumulation level of PsbC and PsbD genes. The analysis of thylakoid membranes proteome revealed that the absence of Egy2 protease leads to accumulation pTAC10, pTAC16 and FLN1 proteins. These proteins are known as associating with core complex of plastid encoded RNA polymerase and influencing its transcriptional activity. The RNA polymerase in turn is responsible for transcription PSBA and PSBC/PSBD operons. Thus, results support the hypothesis that FLN1, pTAC10 and pTAC16 are substrates for Egy2 protease and participate in regulation of expression PSBA and PSBC/PSBD operons.

Take Away Notes:

What are site -2 – proteases? Why they are important for plant physiology? What is regulated intramembrane proteolysis?

- The Egy2 protease belongs to site-2-proteases, which are relatively recently discovered class of proteases. Their functions are unique since the proteases are thought to release the transcription-factors and anty-σ from the membrane and thus, participating in regulation of genes expression. A little is known about functions and substrates for these type of proteases, however some of them seems to perform important role in chloroplast biogenesis. This makes the plant intramembrane proteases an extremely interesting field of research.
- The discussed subject concerns basic research. The intramembrane proteases are , relatively new field of research. They perform the proteolytic cleavage within a biological membrane, what makes them very unique since the proteolysis is considered to be process a closely related with hydrophilic environment. Also function of these type of protease seems unusual, since they seem to be specialized in cleavage of transcription factors and anti-σ factors The knowledge concerning their functions and substrates remain, however, elusive and limited mainly to a model plant – Arabidopsis thaliana.

Biography

Małgorzata Adamiec Ph.D - currently an associate professor in Plant Physiology Department at Faculty of Biology, Adam Mickiewicz University. 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.

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”

Absorption of macronutrients influenced by nitrogen fertilization in *Anacardium othonianum* seedlings

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The levels of nitrogen available to plants can affect plant structure and physiology, as well as alter the absorption of other essential nutrients. Among the essential nutrients for plant growth, nitrogen is one of the most required. Knowing the requirement of N by the plant is fundamental to the practices of mineral nutrition, allowing gains in plant development, because this nutrient contributes to the synthesis of various organic compounds, such as amino acids, proteins, enzymes and nucleic acids. In order to know the nutritional uptake in Anacardium othonianum Rizz. seedlings kept under different concentrations of N, a greenhouse experiment was installed in a hydroponic system. The treatments were seven doses of nitrogen (0.0, 2.5, 5.0, 7.5, 10.0, 12.5 and 15.0 mmoL L-1) in the nutrient solution of Hoagland and Arnon during 120 days after transplanting the seedlings. The nutritional contents of N, P, K, Ca, Mg and S in leaves, stem and root were determined.

The N and P contents in the stem were not influenced by the N doses of the solution, reaching a mean value of 3.64 g kg-1 and 1.47 g kg-1 respectively. The maximum N values in the leaves were 3.16 g kg-1 and in the roots 5.29 g kg-1, at the estimated doses of 9.7 and 14.4 mmoL L-1 of N. The maximum content of nitrogen was found in the roots. This is due to the fact that this is the plant organ required directly for the absorption of the N present in the solution, the higher N uptake by the roots was observed in the plants submitted to the dose of 14.4 mmoL L-1. At doses higher than that, the decrease in N uptake by the roots was verified.

Under the absence of N in the solution (0 mmoL L-1), the highest values were obtained for the contents of K, 2.54, 1.75 and 1.90 g kg-1 in leaves, stems and roots, respectively. The increase of N doses in the nutrient solution decreased the contents of K until the doses of 11.9, 9.1 and 13.0 mmoL L-1 of N for leaves, stems and roots, this was also verified with the Ca content in the leaves, since the highest accumulation of this nutrient was 0.75 g kg-1 in dose of 0 mmoL L-1 of N. The highest leaf Mg content was also observed in the treatment with absence of N of the solution, the estimated value being 0.391 g kg-1. According to the increase in N availability, there was a decrease in the Ca and Mg leaf contents.

It was concluded that the dose of 9.7 mmoL L-1 of N was the one that best stimulated the nitrogen content in the leaves, while the total absence of N stimulated the foliar availability of K, Ca and Mg in plants of A. othonianum, demonstrated the use of such ions in plant metabolism, in an attempt to supply the absence of nitrogen.

Take Away Notes:

- Knowing the effects of different doses of N in a native plant with great commercial potential such as Anacardium othonianum Rizz. is essential to predict a correct fertilization, mainly about the amount of nitrogen, since this is generally the most required nutrient by the plants, especially in the initial stage of development.
- A recurrent problem in conventional agriculture is knows the ideal amount of nitrogen to be applied to maximize yield, without impairing the effects of other nutrients through ionic competition at the active sites of absorption, as well as avoiding unnecessary financial costs with fertilizers that contaminate of the environment.
- The present work contributes to improve the efficiency of the use of nitrogen and to understand the absorption of the macronutrients in function of several nitrogen fertilizations, in order to know the ideal dose for the production of healthy seedlings of A. othonianum that can be established in the field.

Biography

I have extensive experience in the area of plant nutrition, I worked with nutrient solutions in hydroponic crops in my master's and doctoral research. I advise in this line in a postgraduate program in Agronomy and published several articles with this theme in the last five years focusing on the effects of nutrition on the physiology / metabolism and plant growth of the Cerrado biome.

I hope that the present work can contribute to the nutritional requirement knowledge of A. othonianum, which is a plant of extreme importance for the Cerrado biome, but still little studied.

Impact of silicon (Si) nutrition on barley plants under potassium (K) deficiency: Insight into transcriptional, hormonal and metabolic regulation

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Silicon (Si) is the most abundant mineral element in the Earth's crust. During the last decade, several studies have addressed the mechanism(s), by which Si promotes plant growth and development. Thereby, it turned out that silicon mainly protects plants from biotic and abiotic stresses. In particular, Si has been shown to enhance plant tolerance to drought stress. In addition, Si has been shown to mitigate nutrient deficiencies in several crop species. For instance, in sorghum plants, Si alleviated K deficiency symptoms by enhancing hydraulic conductivity and improving the plant water status under K-deficient growth conditions (Chen et al., 2016a). Moreover, in soybean plants exposed to K deficiency, Si application could reduce K-deficiency symptoms by increasing the level of free polyamines and by decreasing H2O2 production (Chen et al., 2016b). However, studies considering the relevance of Si nutrition on metabolites and phytohormones or molecular mechanism(s), by which Si nutrition enhances K deficiency responses, have remained unclear. To address these questions, we performed hydroponic experiments with barley subjected to K deficiency in the presence or absence of silicon. Our results showed higher uptake and translocation of K under K deprivation when Si was supplied into the medium. Moreover, Si resulted in higher chlorophyll and photosynthesis activity in K-deficient plants, which was associated with higher biomass under K deficiency. Current analyses on the role of phytohormones involved in Si-dependent processes will be presented and discussed.

The present study provides a few major benefits of silicon in agriculture: 1) silicon plays vital role to mitigate individual nutrition deficiencies 2) silicon enhances mineral uptake efficiencies and 3) Si-treated plants are able to cope better under potassium deprivation.

Biography

I received my bachelor's degree in Agriculture and Plant Breeding, in Azad University of Karaj and my master's degree in Agricultural Biotechnology, at the University of Tehran, Iran. To further develop my scientific career, I completed two biotechnology internship programs at the Department of Genomics and Department of Microbial Biotechnology and Biosafety at the Agricultural Biotechnology Research Institute of Iran (ABRII). Currently, I am a PhD student at the Department of Physiology and Cell Biology at the IPK, Germany, and the main focus of my project is on the physiological and molecular mechanisms underlying the beneficial effect of silicon on barley plants under drought stress or potassium (K) deficiency.

The influence of single color lighting during barley androgenesis on regeneration efficiency

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Constantly increasing competition on the cereal seed markets puts an requirement of the rapid production of new varieties in front of breeders. Breeding based on doubled haploids (DH) is gaining a growing importance. Androgenesis is one of the most important method that have been extensively used in plant breeding programs to produce double haploids. The method is effective, however, the problem of albinism among regenerates still exists. Modifications of both: nutrient media and conditions in which anthers are induced are of key importance for effective regeneration. The aim of the research was to check the influence of six individual bands of light: royal blue, blue, green, amber, red and deep red on the androgenesis process of barley (Hordeum vulgare L.) and formation of total number of regenerates and the green/albino ratio. The research was carried out on spring barley using standard nutrient solutions and mannitol as a stress factor. LED (light emitting diodes) illuminators were used, due to possibility of arbitrarily designing of light spectrum and no heat release below the lamp which in other systems always threatens to overheat the petri dishes. In order to avoid the impact of the donor plant and thus the influence of the quality and developmental stage of anthers obtained from various plants and spikes, the anthers from each ear were divided into tested and control groups within collection along the ear. Androgenesis in one part of anthers was induced under the LED illuminators whereas in the other, control one, was induced in the dark. The obtained results allowed to indicate illuminators that have a positive effect on the amount of the regenerates obtained using androgenesis and illuminators that increased the ratio of green to albinotic regenerates in comparison to the control. Among the six examined illuminators, two negatively influenced the androgenesis process.

Acknowledgements: This research is supported by the National Centre for Research and Development, Poland as PBS3/B8/19/2015 grant.

Take Away Notes:

- The audience will be able to get the knowledge how to improve androgenesis research using single color light spectrum illuminators. How to improve the yield of the process and increase the amount of green regenerates.
- The results can be used by subjects having a small regenerative ability of in vitro cultures.

Biography

Patrycja Siedlarz, MSc in Molecular Biotechnology, University of Rzeszow, Poland.

2015- to the present employment in Plant Breeding and Acclimatization Institute - National Breeding Institute, IHAR-PIB and working on the project “Development and implementation of methods for shortening of cereal breeding cycles by lighting conditions optimization” financially supported by the National Centre for Research and Development, Poland as PBS3/B8/19/2015 grant. Up to date 1 publications and 3 poster based on the project results.

2013-2015 - Member of the research group at the Department of Biotechnology, Institute of Applied Biotechnology and Basic Sciences, University of Rzeszow.

Participation in research on yeast in vitro cultures. Project finished with 1 publication, 3 posters and one patent registration in the Polish Patent Office, no. 410904, title: “Method for producing biotechnological products”.

Assessment method of ensuring the microbial salad safety

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Food products, like vegetables, salads and fruits are consumed directly and could be contaminated with various dangerous micro-organisms witch can endanger the health of consumers. Therefore, ultrasound treatment has been selected as a possible treatment for their elimination. The antimicrobial activity of ultrasound was tested against microorganisms Salmonella typhimurium ATCC 14028. The bacteria used in this study were stored at Micro-Bank at -72 ± 3 ^{o}C before the start of the experiments. Bacteria have been revitalized in the brain heart infusion broth for 24 hours at optimal temperature and were grown on TSA agar slants for 24 hours at 37 °C temperature. After cultivation colonies were rinsed and diluted with saline solution. The suspension of bacteria cells was added into the sterile bottle with 900 ml sterile water. After this the sterile water and suspension of bacteria were poured out into sterile bottles of 70 ml. 10 g of lettuce samples were placed into each bottle with samples. There was used high-intensity ultrasonic system with submergible horn (Hangzhou Create Ultrasonic Technology Co.,Ltd) operating at a frequency of 28 kHz. 300 and 600 W UV power frequencies were selected for bacterial inactivation. Titanium sonotrode with diameter of 10 mm was submerged directly into the microorganism suspension (70 ml) and treated for 10, 20 and 30 min. At least three replicates of each treatment were performed. The Salmonella typhimurium is a gram-negative bacterium, which can be found on plants as a result of poor sanitary conditions. This bacterium has smaller cells, which is a sign of increased resistance to ultrasound. This study showed, that ultrasound treatment wasn't as effected as predicted. The usage of 300 and 600 W UV power failed to destroy the pathogen cells, the effect of 300 W UV was not effective, as well as 600 W UV 10 minutes treatment. 600 W UV frequencies after 20 or 30 minutes had effected bacterium and decreased their amount to 100 times, but still remained (7.6 ± 1.5) 102 CFU/ml. These results showed, that ultrasound treatment should be used with additional measures in order to eliminate pathogens.

Acknowledgement: This research was supported by the Research, Development and Innovation Fund of Kaunas University of Technology (grant No. MTEPI-P-17018). "Multiplex technology impact for sterilisation of vegetables and fruits".

Take Away Notes:

- The efficiency of Ultrasound treatments on plants
- Possible Ultrasound treatments to reduce microorganisms
- Witch Ultrasound regiments could be used in addition to other treatments

Biography

Dr. Antanas Šarkinas has studied Biology in Faculty of Natural Science at Vilnius University. He is working at Food Institute of Kaunas University of Technology in Microbiology department since 1980. His research programs focuses on antimicrobial activity of plant and berry extracts of newly bred hybrids on different microorganisms, and antimicrobial activity of ultrasound and its decontamination properties for vegetables and fruits. He has published more than 15 articles in international peer-reviewed journals.

Classification of medicinal plants according to their antioxidant capacity using chromatographic profiles and chemometrics

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High-performance liquid chromatography (HPLC) combined with chemometric methods were successfully applied to classify 42 medicinal plant extracts (commercially available) according to their antioxidant capacity determined using DPPH* radical scavenging method: high (group 1), medium (group 2), low (group 3). The chromatographic separations were run on a Zorbax SB-C18 column (250 mm x 4.6 mm, 5 µm particle size) from Agilent and conducted using six different detection wavelengths: 242, 260, 280, 320, 340 and 380 nm, respectively. The optimum method (maximum number of compounds separated and maximum resolution) consisted of a multistep isocratic and gradient elution system using solvent A, 10 mM ammonium acetate pH 5 and as solvent B acetonitrile. The evaluation of the numerical data corresponding to the six wavelengths was performed by employing appropriate multivariate methods: principal component analysis (PCA), fuzzy principal component analysis (FPCA) and linear discriminant analysis (LDA) applied to the first relevant principal components (100% cumulative proportion). A good classification of the samples into high and medium/low antioxidant activity was obtained from PCA analysis at 242 nm. The results obtained by applying LDA to the scores corresponding to the first relevant PCs indicate a highly accurate separation of the medicinal plant hydro-alcoholic extracts within the three groups, in good agreement with their antioxidant capacity estimated by the above mentioned method (96.7 % for PCA at 260 nm and 73.8, respectively for FPCA at 242 nm). In conclusion, the HPLC method combined with chemometrics can be viewed as a useful holistic tool to classify the medicinal plant extracts according to their antioxidant capacity and predict them with high accuracy and precision.

Genome-wide characterization and analysis of RabGAP gene family related to salt stress tolerant in wild and cultivated tomato species.

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RabGAP (RabGTPase-activating protein) is an important class of proteins responsible for directing deactivation of RabGTPases protein by hydrolyzing GTP. The RabGTPases are known to be implicated in the regulation of the trafficking vesicular and salt stress tolerance. The cultivated tomato (Solanum lycopersicum) is one of the most important crops of the world, however, the abiotic stress, among them saline stress, is the main limitation for the increase its yield, development and agronomic properties. On the other hand, wild tomato species such as Solanum pimpinellifolium, Solanum habrochaites, Solanum pennellii or Solanum chilense, among others, are tolerant to abiotic stress, and thrive in salinity and drought extreme environments due to a diverse set of genes and mechanisms that allow them to adapt to these different habitats. The recent sequencing of the S. pennellii genome, in addition to S. lycopersicum and S. pimpinellifolium genomes, provides an excellent opportunity for genome-wide profiling of RabGAP genes and identify their function in response to salt stress in different and related tomato species. In this sense, with HMM and domain scanning we have identified 24 RabGAP genes with TBC and Rab3-GTPase domain in each one of the three-tomato species. Gene and amino-acid structure, phylogenetic and synteny analyzes, prediction protein-protein interactions, and temporal expression analysis in different organs provided insight about the role of RabGAP proteins in tomato. Analysis of gene expression using microarray database and qRT-PCR of RabGAP genes family in wild and cultivated tomato species in response to salt stress are conducted in search of candidate genes that could be used in programs of genetic improvement for the development of tolerance to salinity in crop plants.

Take Away Notes:

- In-silico predictions of protein-protein interaction together with differential expression analysis in organs and stages of development suggest the role of RabGAP proteins in tomato development.
- One third of the RabGAP genes in tomato, to evolutionary level, are the product of segmental duplications and positive selection.
- The genes of the RabGAP family in tomato are differentially regulated under conditions of salt stress, suggesting that could be associated with tolerance to this stress and be candidates for programs of genetic improvement.

Biography

Jose Antonio Madrid Espinoza is an Engineer in Bioinformatics, Ph.D student in Genetic Engineering of Plants in the Institute of Biological Sciences of the University of Talca (UTALCA) and Master student in Education in the Andrés Bello University (UNAB), Chile. Focus on the functional and bioinformatic characterization of proteins that regulate the content of flavonoids in fruits of vitis vinifera, the identification and study of tomato genes associated with the regulation of endocytosis and vesicular trafficking, and the design of molecular strategies to improve tolerance to abiotic stress (mainly salt and drought) of food-importing crops.

Variation in plant biochemistry affects acceptance of lupins by the pea aphid

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The pea aphid Acyrthosiphon pisum (Harris) (Hemiptera: Aphididae) is globally distributed throughout all temperate regions of the world but it has become an important pest on legumes also in tropical regions of Africa. One of the alternative methods to the use of neurotoxic insecticides is the exploitation of the natural or bred traits that enable plants to defend themselves against herbivores. Plant acceptance by pea aphids depends on the presence of allelochemicals, which are either the chemical markers of its host plant or toxicants in the non-hosts. The aim of the present work was to establish the level of acceptability of all species of lupines that occur in Poland (the wild species Lupinus polyphyllus Lindl. and cultivated lupines of three species: L. albus L., L. luteus L., and L. angustifolius L.) to the pea aphid infestation and determine the effect of cyclitols and alkaloids on aphid behaviour during probing.

Basing on EPG (Electrical Penetration Graph) monitoring of the pea aphid behaviour during penetration in plant tissues, we found that aphids did not ingest phloem sap while probing on L. angustifolius and the probes were very short. All varieties of L. angustifolius were rejected by aphids during an early stage of probing in peripheral tissues, i.e., epidermis or mesophyll. On L. polyphyllus and on both studied varieties of L. albus, the probes were short and none of the aphids on these plants reached phloem vessels. It is likely that the rejection of these lupins was caused by chemical factors detected by aphids at the epidermis and mesophyll level. On L. luteus the total and mean duration of probing, time to reach phloem phase, and the duration of the first phloem phase were comparable to those in aphids on control plant Pisum sativum. Eighteen alkaloids were identified: one piperidine alkaloid (ammodendrine), one indole (gramine), ten quinolizidine alkaloids (one tricyclic and nine tetracyclic compounds), and six esters. All lupine varieties that contained lupanine, its derivatives and especially their esters appeared to be unacceptable to the pea aphid, independent of the total concentration of any specific lupanine alkaloid. In contrast, sparteine and its derivatives did not seem to affect aphid probing significantly. The following cyclitols were found in lupine species: myo-inositol, D-ononitol, and D-pinitol. L. angustifolius also contained D-chiro-inositol. Cyclitols had no significant effect on aphid probing and feeding and lupin susceptibility to the pea aphid infestation.

Take Away Notes:

- The quantitative and qualitative differences in alkaloid profiles of lupins are responsible for the variation in the susceptibility to the pea aphid infestation.
- The differences in content and composition of cyclitols in plants are not the source of differences in suitability of lupins for the pea aphid.
- The exploitation of natural plant resistance mechanisms to aphid infestation in directed plant breeding may contribute to the limitation of the use of insecticides.
- The application of electronic monitoring of aphid probing (EPG = Electrical Penetration Graph) is a useful tool in the search for natural plant defence mechanisms against aphids.

Biography

I am a full professor at the Faculty of Environmental Management and Agriculture, University of Warmia and Mazury in Olsztyn, Poland. My scientific activity embraces the following areas: economic importance and limiting factors of insect pest populations of selected crop plants, factors determining the susceptibility of stored products to insect pests, environmentally friendly methods of insect control in arable crops, and biochemical and behavioural aspects of aphid-plant interactions. I teach applied entomology to students of agriculture, forestry, and environmental protection.

Effect of light deficit on plant-aphid interactions

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The intensity of light is one of the crucial environmental factors that determine the life of autotrophic plants, including basic life processes such as the level of photosynthesis and photoperiodic reactions. Light also plays signaling and regulatory roles in developmental processes and defence responses of plants. The indirect effects of inadequate irradiation on plant secondary metabolism appear important in the ecological context, especially when considering plant relationships with other organisms. The level of carbohydrates as the end product of photosynthesis is extremely important in the mobilization of defense mechanisms of plants against biotic stressors. The pea aphid Acyrthosiphon pisum Harris (Hemiptera: Aphididae) is a worldwide oligophagous species that infests leguminous plants and transmits over 30 virus diseases. The present study reports on aphid performance, settling preferences, probing behaviour and feeding activity as well as plant responses to aphid feeding in complete darkness (NL), with light at minimum level required for photoperiodic reaction (LL), and under full light (FL) conditions. We provide information on how the extended periods of low irradiation or light deprivation affect plant suitability to aphids and how the pea aphid infestation affects the plant defense system, especially the accumulation of phenolic compounds, under the low light stress.

The lack of or insufficiency in light supply and aphid infestation had a profound effect on plant metabolic status. However, the potency of metabolic responses to these factors depended on the variation in light intensity level-aphid infestation combination, with light intensity level having a priority in this interaction. The intrinsic rate of increase and net reproduction of aphids were more than four and 16 times lower, respectively, on LL and NL than on FL plants. In contrast to aphids on FL plants, the majority of A. pisum rejected LL and NL plants during settling and failed to locate phloem on these plants. In contrast to aphids on FL plants, the majority of A. pisum rejected LL and NL plants during settling. Aphid probing activities were not impeded on LL and NL plants but the probes were significantly shorter than on FL plants and consisted mainly of non-phloem activities. The contents of chlorophyll a, chlorophyll b, carotenoids, saccharides, and phenolics and the activity of β-D-glucosidase were notably lower in LL and NL plants than in FL plants. In aphid-infested plants under FL conditions, a significant decrease in cholorphyll a, chlorophyll b, carotenoids, and phenolics content and β-glucosidase activity occurred. The increase in light intensity from complete darkness to the minimum level required for photoperiodic reaction did not stimulate evident changes in the measured plant biochemical parameters.The low β-D-glucosidase activity and low content of phenolics in the light-deprived plants that have reduced ability to photosynthesize shows that under the biotic stress of aphid infestation plants invest in supporting basic metabolism rather than in defense against herbivores.

Take Away Notes:

- This research is a basic reseach and a contribution to understand the interaction between plants and herbivores under environmental stress. The main message is that the minimum light offered to plants may be sufficient for plant survival but not sufficient for the nutrient production for aphids. Under the biotic stress of aphid infestation, the light-deprived plants with low phlotosynthetic pigments content invest in supporting basic metabolism, which is manifested in low β-glucosidase activity and low content of secondary plant compounds.
- The results of the research may be used for the interpretation of data on plant-herbivore relationships in plant physiology and insect physiology.
- The results of the research may be used also in the context of applied sciences, especially for predicting aphid population development on crops in shaded areas.

Biography

I am a full professor at the Faculty of Biological Sciences, University of Zielona Góra, Poland. My scientific activity is focused on biochemical and behavioural aspects of aphid-plant interactions, especially aphid behavioural responses to plant allelochemicals, mechanisms of plant resistance to aphids, search for antifeedants against aphids, and probing behaviour of other-than-aphid herbivorous Hemiptera.

The functionary mechanism of a soybean gene *GmMCU1* in response to salt stress

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Salt stress is a key factor seriously limiting yield and quality of crops. Calcium as a second messenger, plays an important role in the process of responding salt stress in plant. MCU (mitochondria calcium uniporter) is reported an improtmant Ca2+ channel protein on mitochondrial inner membrane. We have isolated 10 soybean MCU genes, and found that the expression of GmMCU1 was significantly induced by Ca2+ and salt stress in the soybean root, and subcellular localization analysis showed GmMCU1 was a mitochondrial protein. The yeast and tobacco with heterologous over-expression of GmMCU1 showed a more salt-tolerant phenotype than control. These results suggest that GmMCU1 plays an importmant role in the reponse to salinity stress in plants.

Biography

Major Research Interests: Cloning and functional analysis of salt tolerant genes, the molecular mechanism and pathways of salt tolerant genes, salt tolerant plants planting technology research in saline land, genetic diversity of salt tolerant plants.

The expression of isoforms of type B methionine sulfoxide reductase in Norway maple (*Acer platanoides* L.) seeds

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Ewa M. Kalemba*, Ph.D., Institute of Dendrology, Polish Academy of Sciences, Parkowa 5, 62-035, Kórnik

How seeds perceive reactive oxygen species (ROS) signals and transmit them further at the protein level is not well understood. ROS are a major source of sulfur group oxidation in cysteine and methionine (Met) residues. The first oxidation step of Met to methionine sulfoxide (MetSO) is reversible. The R- and S-stereoisomers are reduced by the specific methionine sulfoxide reductases (Msrs) MsrA and MsrB, respectively.

Norway maple (Acer platanoides L.) is important tree species found in the temperate zone. Norway maple seeds become tolerant to desiccation at 18 weeks after flowering. Subsequently, these seeds can be slowly desiccated at ambient temperature until they reach a moisture content of 7–10% without a loss of viability. Norway maple seeds are clearly desiccation tolerant and belong to the orthodox category.

Norway maple seeds were analyzed during their development between 12 and 22 week after flowering and during subsequent dehydration of mature seeds. The level of ROS was monitored and redox potential was established to determine the phases of more oxidative environment in seed tissue. Using antibodies specific to AtMsrB1 and AtMsrB2 the two proteins were analyzed using Western blot and their tissue and cellular localization was demonstrated using confocal microscopy. The abundance of MsrB1 and MsrB2 synthesis is different in embryonic axes and cotyledons. Other B-type isoforms of Msrs are also present in the A. platanoides genome. They include genes homological to Arabidopsis thaliana MsrB1, MsrB2, MsrB4, MsrB7, and MsrB9 genes.

Both MsrB1 and MsrB2 are zinc binding enzymes involved in protein repair and response to oxidative stress. MsrB1 is selenoprotein reduced by the glutahione/glutaredoxin system whereas MsrB2 rely on the reduction system involving thioredoxins. MsrB1 is 13 kDa protein whereas MsrB2 is 17 kDa and undergo alternative splicing. Since majority of epidermal cells, parenchymal cells and developing vascular bundles contained both MsrB proteins we compared the MsrB1 and MsrB2 expression and distribution and discuss their possible roles in regulation of important developmental stages in Norway maple seeds including seed maturation and drying.

The research was financed by National Centre of Sciences, project nr 2015/18/E/NZ9/00729.

Take Away Notes:

- Seeds require extended protective mechanisms enabling their survival at important developmental stages.
- Methionine sulfoxide reductases are crucial element of enzymatic antioxidative system.
- Seed desiccation affects ROS production and MsrB2 alternative splicing.

Biography

Ewa Kalemba graduated from the Faculty of Biology at Adam Mickiewicz University in Poznań (Poland) with the M.Sc. degree in molecular biology and B.Sc. in bioinformatics and obtained the Ph.D. degree at Institute of Dendrology of Polish Academy of Sciences in Kórnik (Poland). Research: focus on regulation of seed physiology at important developmental stages including maturation, dehydration and desiccation, dormancy release and germination. Experience: research associate, the recipient of "Research in Paris" scholarship (post-doc at Sorbonne University), the author of 19 indexed articles, the principal investigator of 3 research projects.

Genome identification and transferability of microsatellite markers between Atriplex species

Correa, Francisco, BSc., INIA-Rayentue; Pérez-Díaz, Jorge, Ph.D., INIA-Rayentue; Rojas, Pamela, Ph.D., INIA-Rayentue; Torres, Claudia, MSc., Universidad de Chile, Paneque, Manual, Ph. D., Universidad de Chile, Bastias, Adriana*, Ph. D., Universidad Autónoma de Chile.

Species of the genus Atriplex (Chenopodiaceae) are halophytes and able to photosynthesize under low soil water availability and high temperatures. Several Atriplex species are known for their high biomass generation, which made them candidates for solid biofuels production. Besides, Atriplex sp. also can be used as animal forages, especially in drought periods.

Most of the 21 native Chilean species from Atriplex genus are endemic. They grow in arid areas of Chile's north, except a species that grow until the Estrecho de Magallanes.

The aim of this work is to develop microsatellite (SSR) markers from genome sequencing of A. deserticola and A. atacamensis, and study their transferability with other atriplex species.

We have generated and characterized genome sequences using Illumina technology, Hiseq2500 paired-end, specifically. A quality control and a pre-processing of the sequences including trimming and filtering were realized. Assembly of the nucleotide sequence reads was performed using the SOAPdenovo software. Finally, the software MISA was used to found microsatellite markers of A. deserticola and A. atacamensis.

In this work, we provided microsatellite markers from high throughput next generation sequencing of the A. deserticola and A. atacamensis genomic DNA. These SSR markers were compared and 100 SSR markers conserved between both, A. atacamensis and A. deserticola were evaluated in 11 different Atriplex sp. These markers could be used in germplasm analysis, accessing genetic diversity and linkage mapping of A. deserticola, A. atacamensis and other Atriplex species.

Take Away Notes:

- Use NGS to generate SSR markers
- To discover common SSR markers between two Atriplex species
- To identify highly transferable SSR among Atriplex species

Biography

Dr. Adriana Bastías Barrientos is a biochemist and received her doctorate in science major in plant genetic engineering in 2011 from Universidad de Talca, Chile. During her studies, she did research stays at Universidad Jaume I in Spain and Max Planck Institute of Molecular Plant Physiology (Potsdam-Golm, Germany), where he studied molecular plant physiology. Her thesis was focus in the role of transcription factor like AREB in primary metabolic pathways in tomato fruits. Currently, she is professor and researcher at Universidad Autónoma de Chile and is working in genomics and transcriptomics native plant of Chile.

Downregulation of PHOTOTROPIN 1 in *Solanum lycopersicum* L.

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Phototropin 1 (PHOT1) is a part of blue light sensory system in plants that fine-tune the efficient use of solar energy and modulate growth through a variety of responses including phototropism, chloroplast movement, leaf flattening and positioning, stomatal opening, and rapid inhibition of hypocotyl growth. We used amiRNA interference to generate transgenic phot1 tomato plants. Downregulation of PHOT1 caused distinct phenotype in plant height and number of trichomes on the leaf and stem surface compared to wild-type. Also, the serration of the leaf margin was reduced in phot1 and leaf flattening was altered which may be associated with changed level of transpiration and efficiency of the photosynthesis. The fruits of mutant plant were also affected by the downregulation of PHOT1 showing decreased number of seeds with the delayed germination rate. Moreover, the phot1 fruits were darker green compared to wild-type. Proteomic analysis of fruit pericarp showed changes in proteins connected with carotenoid biosynthesis pathway predicting the higher level of carotenoids such as lycopene, an antioxidant which is important component in human diet. The carotenoid content will be measured by high-performance liquid chromatography analysis. Subsequently, to examine the role of mutation in drought stress, various watering regimes (80% and 50% of field capacity and non-watering) were applied to wild-type and transgenic plants. Chlorophyll fluorescence and content, gasometric parameters, water potential, leaf temperature, gene expression and enzymatic activity (APX, SOD, CAT, POX) were measured in these plants.

Biography

Petra Hloušková graduated in Molecular and Cell Biology (Mgr.) at the Faculty of Science, Palacký University in Olomouc in 2013 with diploma thesis concerning the role of E3 ubiquitin ligase COP1 in boron-regulated hypocotyl elongation in Arabidopsis thaliana (L.) Heynh. Subsequently, she enrolled the doctoral study program in Biochemistry. The aim of her work is to study the blue light-induced de-etiolation in tomato and more precisely to uncover the role of 14-3-3 proteins, PHOT1 and cytokinins in this process.

Next generation transcriptome assembly for *Euterpe oleracea*

Maria Teresa G. Lopes, Ph.D., Univerdade Federal do Amazonas; Ananda V. de Aguiar*, Ph.D., Embrapa Fllorestas, Fernanda A. Gaiotto, Ph.D., Universidade Estadual de Santa Cruz; Annette Fahrenkrog, Ph.D., University of Florida; Flora Bittencourt, Ph.D., Universidade Estadual de Santa Cruz; Christopher Dervinis, Master, University of Florida; Bárbara S. F. Müller , Master, Universidade Fderal de Brasilia; Rodrigo F. dos Santos, Master, University of Florida; Regina C. Quisen, Ph.D., Embrapa Florestas; Matias Kirst, Ph.D., University of Florida

Euterpe oleracea, Arecaceae family, is used especially for fruit. Its natural habitat is Amazon rainforest. Here we used high throughput RNA sequencing (RNAseq) to obtain the reference transcriptome for this species, establishing a critical genomic resource necessary for future genetics studies. Leaves of one adult individual of E. oleracea were collected in the Amazon rainforest (Brazil). They were immediately frozen in liquid nitrogen and lyophilized. Total RNA was isolated and converted into cDNA prior to sequencing using an Illumina NextSeq platform. A total of 102,576,656 raw reads (pair-end read of 151 length) were filtered by quality using Trimmomatic and assembled into 193,487 transcripts with Trinity. The E. oleracea novo transcriptome assembly contains 153,805 unigene databases represented by 117 Mbp, with a median (mean) contig length of 334 bp (608 bp) and a GC content of 44.9%. The databases were annotated for their putative functions based on Arabidopsis thaliana transcriptme database resource. Total of 14,207 annotated unigene databases were categorized into 30 functional groups under Gene Ontology terms. In the biological process category, cellular processes (39.09%) and metabolic processes (35.92%) were the predominant groups. For the cellular component category, the predominant were cell parts (51.98%) and organelles (32.6%). The main distributions in the molecular function category were catalytic activity (36.33%) and binding (35.48%). This is a critical resource to be used for the development of new molecular tools for conservation genetics and evolutionary studies.

Take Away Notes:

- The audience can get a greater knowledge of the technology that helps to understand the genetic makeup of a species which is very important to human and animal foods.
- The study presents objectively modern and efficient techniques to reach its goals.
- Taking under consideration the conference theme, many of the participants will have similar objectives in their respective studies.
- The audience can use the results of this work for many purposes including: to comparing the transcriptome and genome other palm species around the world; to obtaining some marks as SNPs; further in depth studying about conservation, evolution and breeding palm species. This will help to obtain SNPs that will be used a variety of studies on genetic themes. RNA sequencing was the strategy to access the functional component, especially since it is a species without a reference genome. In the future, this set of SNPs can be used to design one chip for the palm species. This kind of information about this native's species quite possibly has an even greater significance to Brazilian researchers.

Biography

PhD in Genetics and Plant Breeding at Universidade Federal de Goiás and post-doctorate in forestry genomics at the University of Florida (2016). I am a Senior Researcher in Forestry and Genetic Resources at Brazilian Agricultural Research Corporation (EMBRAPA) and Professor of Forest Breeding and Genetic Conservation of Forest Species in graduate course at Universidade Estadual de São Paulo (UNESP). The area of expertise is focused on conservation, breeding and genomics with emphasis on forest species. The author also serves as a consultant to scientific funding agencies in Brazil and acts as a technical consultant in the pine tree breeding area for forestry companies in Brazil.

Phosphatidic acid, a signal molecule in wheat seedlings under stress conditions and *Trichoderma* presence

Przemysław Bernat[1]*, Justyna Nykiel-Szymańska[1], Ewa Gajewska[2], Sylwia Różalska[1], Paulina Stolarek[1], Julia Dackowa[1], Mirosława Słaba[1]

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Anomalies in environmental conditions activate in plants a series of processes that allow minimizing their negative impact. These factors, such as drought or dangerous pollutants may result in changing the profile of cytoplasmic membranes phospholipids and induce synthesis of the lipids signaling messenger, phosphatidic acid (PA).

In this work, we investigated the effect of drought and/or synthetic auxin herbicide, 2,4-dichlorophenoxyacetic acid (2,4-D), on the phospholipid profile of wheat (Triticum aestivum L.) seedlings, with the special emphasis on the PA level. Moreover, because Trichoderma spp. is known to offer a beneficial relationship with plants, the phospholipid composition in wheat roots and shoots under stress conditions in T. harzianum presence was observed.

Phospholipid differences between samples were analyzed using liquid chromatography/electrospray ionization–MS/MS.

In the group of 4-day-old seedlings exposed to the herbicide the inhibition of growth was observed (in the shoots and roots). Concurrently, in seedlings inoculated with T. harzianum and herbicide the growth inhibition was partly alleviated. Overall, the PA level was higher in the roots than in the shoots. The presence of the fungus did not increase the PA level in the plants, also the herbicide did not induce PA accumulation. On the other hand, a strong, 4-fold increase in the level of the lipid messenger was found in samples exposed to the insufficient water content.

The obtained results confirmed the important role of PA in plant stress signaling and beneficial relationship of T. harzianum with wheat.

This study was supported by the National Science Centre in Krakow, Poland (Project No. 2015/19/B/NZ9/00167).

Take Away Notes:

- The obtained results confirmed the important role of phosphatidic acid in plant stress signaling
- LC-MS/MS technique helps to determine the stress condition in plants
- Trichoderma sp. could alleviate abiotic stress in plants.

Biography

Przemysław Bernat is an Associate Professor at the University of Lodz (Poland). His Ph.D. in Biology was done at the University of Lodz. His research interest includes metabolomics (especially lipidomics) of microorganisms and their biodegradation ability. He is also interested in the interaction between microorganisms and plants, with a special focus on metabolomics. He is an author of more than 50 publications.

Behavior of Arsenic species in rice cultivated in soils with *Penicillium* sp. for mitigation

Fabiana Roberta Segura (Doctorate student)[a]; Ana Carolina Cavalheiro Paulelli (Doctorate student)[b]; Gilberto Úbida Leite Braga (Professor, Ph.D.)[b]; Walter dos Reis Pedreira Filho (Professor, Ph.D.)[c]; Fábio Ferreira Silva (Researcher, Ph.D.)[a]; Bruno Lemos Batista(Professor, Ph.D.)[a]*

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[c]Fundação Jorge Duprat Figueiredo de Segurança e Medicina do Trabalho, Ministério do Trabalho e Previdência Social, 05409-002 São Paulo – SP, Brazil

Rice grains are significant source of inorganic arsenic (i-As) for humans' diet. The Codex/FAO has few regulations for limits and mitigation of As in rice. Fungi isolated from rice's rhizosphere are potential tools for As-mitigation. The inoculation and management of native microorganisms isolated from rice paddy soils are a potential tool for bioremediation and mitigation of As contamination in rice grains once these organisms can uptake and storage As, convert i-As to less toxic organic forms, volatilize organic species and, improve grains yielding in rice plants, "diluting" the As-species accumulated in the grains. All these mechanisms are welcome for food safety once the rice is known for accumulating As 10-fold more than other cereals and the new regulations of Codex Alimentarius preconize the maximum limit of 200 and 350 μg Kg-1 of i-As in polished and husked rice grains, respectively. Here we used background soils (Bkg) and soils containing 5 mg As(V) kg-1 (Spk) and the addition of the fungus genera Penicillium sp. for rice cultivation at flooded conditions. The soils, roots, and grains were analyzed after complete plant maturation. For grains produced in Bkg, total As (t-As) increased in soils where the Penicillium sp. was added, due to the increase of organic As (o-As) and As(V). However, As(III), he most toxic form, decreased in the grains. In the Spk soils was observed significant reduction of t-As in grains. Penicillium sp. presented intermediary efficiency for As-mitigation. The non-retained As specie (NRAS) was detected. Rice grains yielding was improved by the addition of the fungus. Therefore, the use of fungus is an important mechanism to be used for As-remediation in rice, a valuable global cereal. The authors thank to Fundação de Amparo a Pesquisa do Estado de São Paulo (FAPESP grant 14/05151-0).

Take Away Notes:

- They will learn about rice regarding arsenic metabolism, mechanisms of mitigation and arsenic speciation.
- The experimentation can be reproduced using other microorganisms of interest or rice cultivars specific from the different countries. Trying to improve the method of mitigation, they can help for the decrease the arsenic exposure from food.
-

Biography

Graduate in Pharmacy (2004), Federal University of Alfenas, Brazil (2004). Master Scientist in Toxicology, Faculty of Pharmaceutical Sciences, University of Sao Paulo Ph.D. in Science (FCFRP-USP, 2012), where he worked with chemical speciation of arsenic in food, being part of this doctoral held at the University of Aberdeen, Scotland (Scotland, UK), with emphasis on the metabolism of arsenic by different rice cultivars and identification and quantification of phytochelatins by (HPLC / MS, ICP-HR / HR-ESI-MS). It has more than 52 articles published in analytical chemistry, toxicology, food analysis and metabolism. Currently professor at the Federal University of ABC, Brazil.

Wounding induces tomato Ve1 R-gene expression

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In tomato, Verticillium resistance is determined by the Ve-gene locus, which encodes two leucine-rich repeat-receptor-like proteins (Ve1, Ve2). The gene encoding Ve1 protein has two functional alleles; Ve1, encoding a resistance protein, and ve1, with a premature stop codon encoding a truncated product. In both resistant and susceptible plants, Ve1 is induced differentially while Ve2 is constitutively expressed throughout disease development. Contrary to their putative role in Verticillium resistance, these profiles have been observed even during compatible Verticillium interactions, colonization by some bacterial pathogens, and growth of transgenic tomato expressing the fungal Ave1 effector, suggesting broader roles in disease and/or stress. Here we have examined further Ve-gene expression in resistant and susceptible plants under abiotic stress, including drought, salinity and physical damage. Using qRT-PCR and label-free LC-MS methods, changes have been evaluated at both the mRNA and protein levels. The results indicate that Ve1-gene expression responds specifically to physical damage or plant wounding, resulting in a defense/stress cascade that resembles observations during Verticillium colonization. In addition, changes in Ve1 or Ve2 function also result in responses that occur with wilt pathogen and are consistent with an antagonistic relationship between the two genes. Mutational analyses also indicate the plant wounding hormone, systemin, is not required, while jasmonic acid appears to play a direct role in Ve1 induction.

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Shade levels and variety effects on tomato fruit yields

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Solar radiation receipts in greenhouse horticultural crops determine air and plant temperatures, which may result in undesirable effects such as low growth rates and inferior produce quality. Most horticultural crops exhibit the C3 photosynthesis (Ps) pathway and have optimum radiation requirements around 400-500 µmol/m²/sec, while the photosynthetic saturation point is reached at 600 to 800 µmol/m²/sec (Jones, 2007). However, according to Lorenzo et al., (2010), under greenhouse conditions, solar radiation levels may limit tomatoes' production even with PAR levels of 1200 mmol m-2 s -1 as light saturation is only experienced at the upper levels of the crop canopy. In the Central Valleys of Oaxaca (CVO) region, Mexico, located roughly at 17 ° N and 97 ° W, at a mean altitude of 1550 m, there are high radiation and temperature levels during March-May (late Spring), which may limit tomato production in greenhouses. This research aimed to evaluate the effect of four plastic covers on yields and physiological indicators of Lycopersicon esculentum Mill. varieties grown under greenhouse conditions in The Central Valleys of Oaxaca Region. Our results showed that at PAR levels in excess of 1000 µmol m-2s-1 Ps was reduced because of temperatures higher than 35° C, which resulted in a lower RH (< 40%) and Cs in Abril. Therefore, it is recommended to use plastic covers which do not transmit more than 800 µmolm-2s-1, as the largest fruit yields were obtained with plastics with those characteristics, which decreased air temperatures by 5 °C. It was concluded that solar radiation does not limit tomato fruit yields, but high air temperatures and low relative humidity.

Take Away Notes:

- According to their job category, they may implement changes for greenhouse management or use this results to re-design existing ones.

Biography

Jaime Ruiz-Vega is an agronomist with specialization in soil management with a PhD degree from Iowa State University in Agricultural Climatology and Crop Production. The following courses have been taught; from 1989 to 1991: Agroclimatologia, Programa de Maestría, ITAO No. 23, From 1991-2007 Fisiotécnia Vegetal, Programa de Maestría, ITAO No. 23, and from 2003 to date Agroecología. Programa de Maestría, CIIDIR OAXACA. He has been an agricultural researcher from 1976 to 1993 at the Instituto Nacional de Investigaciones Agricolas and a Profesor-Investigador at Instituto Politécnico Nacional (CIIDIR, U. Oaxaca) from 1993 to date. He has produced 54 refereed papers and 7 book chapters, four doctorate and 34 MSci thesis, and has attended 73 international meetings.

Impacts of titanium dioxide particles on photosynthetic performance and antioxidant system in *Raphanus sativus*

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The nanoparticles (NPs) have a particular effect on a certain plant, but this effect may differ in other species. Titanium dioxide (TiO_2) have generally positive effects on distinct parameter physiologic and productive in plants, but little has been evaluated its impact on photosynthesis and antioxidant system, and less yet in *Raphanus sativus*. This work aimed was to assess the effects of titanium dioxide particles on photosynthetic performance and antioxidant system in *Raphanus sativus*. The species was grown in a substrate (peat + perlite, ratio 2:1) in plastic boxes 1 L capacity. The substrate was moisturized at the begin of the assay with 250 mL box^{-1} of Hoagland solution. *R. sativus* was grew in a chamber under 100 µ*mol* m^{-2} s^{-1}, 23±2 ºC, 25 % RH, and 16/8 h photoperiod, for 30 days. The nanoparticles (NPs) and microparticles (µPs) of titanium dioxide (TiO_2) anatase were suspended in ultrapure water and applied by foliar way in 10 – 100 – 500 – 1000 – 1500 mg L^{-1} doses. As an absolute control was used ultrapure water and CuO as a positive control in 500 mg L^{-1} dose. Ti concentration on leaves was evaluated by ICP-MS, at the end of assay. The net photosynthesis and photochemical parameters were measured after 12 – 36 – 60 and 84 h of TiO_2 exposition, using a portable CO_2 infrared gas analyzer (Licor LR6400, LI-COR, Lincoln, NE, USA), and a portable pulse-amplitude modulated fluorimeter (FMS 2, Hansatech Instruments, King's Lynn, UK), respectively. The antioxidant system was evaluated at the end of the assay (84 h). The main results are associated with the entry of TiO_2 to the mesophyll, where Ti concentration was observed in concomitant relation with doses, especially in µPs where concentrations were higher than NPs. Doses of µPs 100, 1000 and 1500 mgL^{-1} were significantly ($p<0.05$) higher with respect to control in about 29-fold. A transient increase of net photosynthesis was observed, around 1.5-fold higher than control, especially at 60 h after treatments were applied. No differences were observed between doses for both, NPs and µPs. The same was observed in photochemical parameters, except for electron transport chain (ETC) and non-photochemical quenching (NPQ) with an inverse relation between them. There was no marked trend for the variables of the antioxidant system, except in total phenols concentration, that was higher for both NPs and µPs in the higher dose ($p<0.05$), over 1.3-fold than the positive control and 2.6-fold than the absolute control. Finally, it is suggested that µPs and NPs, of TiO_2 had a positive effect at the physiological level in *Raphanus sativus*, manifested mainly by the increased of the net photosynthesis and response of the antioxidant system.

Take Away Notes:

- The absorption and transport of particles at nanometric and micrometric scales in plants generate diverse effects, generally negative, but not for TiO2 on Raphanus sativus. Until now there was no evidence of this in this species. This work is the continuation of previous reports of different authors on in a few species of agricultural importance.
- The audience will know the first approach about to the more efficient photosynthetic performance in Raphanus sativus and will be possible discuss underlying mechanisms that provoke this phenomenon at physiological and biochemical level.
- Thus, the present work can open (together with earlier works of distinct authors) a window to contribute the solution to one of the principal problems of humanity, as is the need increase the efficiency energetic transformation.
- On this one of the first approach in this line, the discussion can be open and the audience can extrapolate these results and its futures perspectives related to bio products based on nanomaterials.

Biography

Ricardo Tighe-Neira is a Chilean of forty years old, Agronomist, Master of Science and academic of Department of Agricultural Sciences and Aquaculture of Natural Resources Faculty of the Universidad Católica de Temuco. Currently, is studying a Ph.D. in Ciencias Agropecuarias at Universidad Católica de Temuco, Chile. The present work is part of its doctoral researches, related to doctoral thesis that is titled "Evaluation of the effects of TiO2 nanoparticles on the efficiency of photosynthesis at the metabolic and molecular level in *Solanum lycopersicum*".

Drivers of alpha and beta vascular plant diversity in a continental archipelago (Ionian Islands, Greece)

Anna-Thalassini Valli[1], Konstantinos Kougioumoutzis[1,2], Eleni Iliadou[2], Maria Panitsa[2] and Panayiotis Trigas[1]*
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The Mediterranean Basin is one of the major global terrestrial biodiversity hotspots, while most of the Mediterranean Islands belong to the two Greek archipelagos, namely the Aegean and the Ionian. Although the factors affecting plant species richness and endemism are well studied in the Aegean Sea, regression modeling techniques have not been applied to disentangle the role of biogeographical factors in shaping plant assemblages in the Ionian archipelago. Moreover, the majority of biogeographical studies in the Greek Islands have been focused on alpha-diversity patterns, while there are only two macroecological studies investigating factors affecting beta-diversity in the Aegean archipelago. The aims of the present study in the Ionian archipelago are: 1) to investigate the drivers of native and endemic plant species richness, 2) to analyze beta-diversity and its separation into its two components (turnover and nestedness) and finally, 3) to identify if there are any islands that can be regarded as plant diversity hotspots. According to our results, area is confirmed as the most powerful single explanatory variable of island plant species richness for all species richness metrics, namely Native (N), Total Endemics (TE) and Ionian Endemic taxa (IoE). Mean annual precipitation and temperature, as well as shortest distance from the nearest island are also significant predictors of vascular plant diversity in the Ionian archipelago. Finally, our hotspot analysis revealed four small islands (i.e. Kalamos, Ereikousa, Antipaxoi and Atokos) with exceptionally high plant diversity, while the aforementioned islands belong to the "NATURA 2000" network of protected areas. In conclusion, the minimal isolation and the close proximity of the Ionian Islands to the mainland source have resulted in islands that still behave as parts of a continuous land mass. The rather strong environmental and the reduced dispersal filtering (due to the recent formation of the Ionian Islands) have led to islands with homogenized plant communities and to floras principally comprising common species, also explaining the low proportion of endemics. Kalamos island emerged as the most important diversity and endemism hotspot.

Take Away Notes:

- The knowledge on the factors shaping island plant assemblages greatly contributes towards understanding the underlying processes resulted to the enormous biodiversity of the islands worldwide. It also contributes towards an effective conservation management of the sensitive island biota.
- Unraveling the drivers of alpha and beta-diversity patterns in the Ionian archipelago would increase our knowledge on the factors shaping plant species assemblages on continental island systems.
- The identification of plant diversity hotspots in the Ionian Islands will contribute towards an effective management of the priority sites for plant conservation. /Our results underline the need to integrate more protected areas into the existing Ionian Management Agencies.

Biography

Panayiotis Trigas has a great interest in the origin, evolution and diversity of vascular plants, and in particular, how different factors may influence patterns of diversification. More specifically, he has been working with the vascular plant diversity of the Mediterranean region, focusing on the evolution, diversity and conservation of range restricted species. He is also pursuing research focusing on understanding biogeographic patterns and historical processes that have shaped distributions of vascular plants, especially on islands and mountainous areas. In addition, he is interested in the diversity of aromatic and medicinal plants and crop wild relatives in the Greek flora, focusing on the development and conservation of plant genetic resources.

Use of olive recombinant hydroperoxide lyases for synthesis of green leaf volatiles: Activation and stabilization of enzymes by selected additives

Sophie Vincenti
University of Corsica, France

Green leaf volatiles (GLVs), especially C6-aldehydes and C9-aldehydes, produced by plants, are responsible for the characteristic odor of cut grass, called “green note”. GLVs are widely used in flavor and food industries. Their production represents an important industrial stake. In addition, consumers’ distrust of chemical flavors leads to a strong growth in the natural flavor market. GLVs are synthesized naturally in plants during a lipid metabolic pathway called lipoxygenase pathway. First, lipoxygenase (LOX) catalyzes regiospecific dioxygenation at the carbon 9 or 13 of C-18 polyunsatured fatty acids, mainly linoleic and α-linolenic acids, to form the corresponding fatty acid hydroperoxides. Subsequently, HPL can act on these 9-hydroperoxides or 13-hydroperoxides of to form C9-aldehydes or C6-aldehydes and C9-oxoacids or C12-oxoacids, respectively.

Given the high demand for natural GLVs, biocatalytic processes using the enzymes of the LOX pathway have been developed for large-scale production. Plant extracts are used as a source of LOX and HPL to convert vegetable oils chosen for their fatty acid profile into natural GLVs. Soybean flour is successfully used as LOX source, while many plant extracts with HPL activities were tested (mint leaves, green bell pepper, or tomato leaves or guava fruit) and conversion yield remains very low. Large amounts of raw materials are required, which leads to dependence on environmental conditions, harvesting period, and plant heterogeneity. In addition, crude extracts contain other enzymes that use fatty hydroperoxides, leading to undesired products and loss of substrate. The use of recombinant HPLs in such processes constitute an interesting alternative to overcome drawbacks arising from the use of HPL from plant extracts.

We isolated a cDNA encoding for olive HPL named HPL full-length from black olive fruit (Olea europaea L., Leccino variety), and then, we deleted the N-terminal transit peptide to produce the matured HPL. Both enzymes was expressed in Escherichia coli, purified and characterized biochemically. We showed that olive recombinant HPLs (rHPLs) are promising efficient biocatalysts for the production of natural C6-aldehydes. However, the use of HPLs for bioconversion reactions is limited by their poor stability.

The stabilization and activation of olive rHPLs was investigated using selected chemical additives. Both olive rHPLs are relatively stable at 4°C, and enzyme activity can be preserved (about 100% of the rHPL activities are maintained) during 5 weeks of storage at −20 or at −80°C in the presence of 10% glycerol. Among the additives used in this study, 2.5% glycine, 0.5 M NaCl, and 0.25 M Na2SO4 provided the highest activation of HPL full-length activity, while the best matured HPL activity was obtained with 0.25 M Na2SO4 and 1 M NaCl. Results of C6-aldehyde production assays also showed that glycine, NaCl, and Na2SO4 are appropriate additives and that NaCl appears to be the best additive, at least for hexanal production.

Antioxidant activity, total phenolic and total flavonoid contents of the methanol extracts of the leaves and stems of milkweed, *Gomphocarpus physocarpus* (E.Mey)

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The antioxidant activity of the methanol extracts of the stems and leaves of Gomphocarpus physocarpus (E.Mey.) (Apocynaceae) were assessed to determine the medicinal potential of this South African milkweed. The possible phytochemical sources, of the antioxidant activity were also evaluated by measuring the total phenolic (Folin-Ciocalteu method) and Flavonoid contents (Aluminium chloride method). Histochemical tests were conducted to confirm the location of these compounds. The EC50 based on the DPPH radical scavenging activity was similar for the leaf (9.93±0.11 µg/ml) and stem (11.37±0.46 µg/ml) extracts which was significantly lower than the standard antioxidant, ascorbic acid (13.52±0.41 µg/ml). The total phenolic (8.7±0.41 mg GAE/g DW) and flavonoid contents (2.91±0.21 mg QE/g DW) of the stem extracts are possibly responsible for the strong antioxidant activity. Histochemical analyses and fluorescence microscopy revealed the location of phenol accumulation to be in the laticiferous and parenchymatic tissues of the stem cortex and pith. It is possible that the plant accumulates phenolic compounds as part of its chemical defense strategy against insect herbivory. This defense strategy may in fact be a major source of novel antioxidant compounds.

Take Away Notes:

- The leave and stem extracts of Gomphocapus physocarpus have strong antioxidant activity.
- This antioxidant activity is due to the high amount of phenolics and flavonoids found in the plant.
- Phenolic compounds are located in laticifer cells which is part of the plant defense strategy. This indicates that the plants chemical defense may serve as a source of novel medicinal 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, laticifers) in medicinal plant species and the phytochemistry and ethnopharmacology of selected southern African medicinal plants.

Study of tolerance to natural chilling stress in triploid citrus and potential impact on fruit quality

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Yann Froelicher (Ph.D. CIRAD UMR AGAP), Jérémie Santini (Ph.D. CNRS UMR 6134 SPE, University of Corsica Pascal Paoli),
Liliane Berti (Pr. CNRS UMR 6134 SPE, University of Corsica Pascal Paoli)

Mediterranean area allowed a Citrus production thanks to the pedoclimatic conditions. Climate change is a worldwide problem (global warming, significant temperature fluctuation, drought episode increasing…) that can affect negatively citrus production and reduce fruit quality. In Corsica, the agricultural activity is widely represented by the clementine production (25,000 t per year and 90% of Corsican production is exported). The main economic and environmental issues is the maintaining of citrus fruit production with nutritional and organoleptic quality despite climatic changes. Thus, the aim will be to segment market with production of innovative seedless fruits to answer to consumer expectations and diversify production when clementine isn't produced anymore.

Polyploidy is an important determinant in plant evolution, facilitating the capacity to successfully grow up in habitats characterized by strong fluctuating environmental conditions. Polyploid plants are for these reasons widely studied in vegetal production under environmental constrains.

Many studies demonstrated that tetraploid genotypes showed an enhance stress tolerance to abiotic stresses. However, few studies focused on the behaviour of triploid variety subjected to unfavourable environment. The use of triploid plants could improve tolerance to abiotic stress and allows the production of seedless fruits. In this study, we will compare the behavior of diploid and triploid citrus from the same crossing (Fortune x Tangor Ellendale). The response to natural chilling stress will be evaluated by measuring various physiological and biochemical parameters. Net photosynthesis, stomatal conductance, transpiration and chlorophyll rate will be monitored. Antioxidant defenses mechanisms will be characterized by monitoring the activities of superoxide dismutase, catalase, ascorbate peroxidase and the content in glutathione, ascorbic acid and proline. Cellular damages will also be recorded thanks to malondialdehyde, a marker of lipid peroxidation, and hydrogen peroxide. Genes sequences involved in stress management will also be identified thanks to nucleic and protein sequences basis and the complete clementine genome. These data will allow to identify oligonucleotide used as primers for PCR analysis. The impact of stress on citrus fruit quality will be evaluated through the determination of sugars and organic acids levels. Activities of the enzymes involved in primary metabolism (phosphofructokinase, phosphoenolpyruvate carboxylase, cytoplasmic isocitrate dehydrogenase) will also be monitored to clarify the biochemical pathways involved during abiotic stress.

Taken together, the excepted results will enable us to propose an alternative to improve stress tolerance, maintain and develop a sustainable and efficient citrus crops. The first results will be presented at the conference.

Take Away Notes:

- Studying of the behaviour of polyploid citrus in environmental and controlled conditions.
- Studying on the formation of triploid, characterization of genes involved in tolerance to abiotic stress and of biochemical pathways in fruits.
- Improving citrus crop productions under unfavourable environmental conditions and yielding the best organoleptic quality.
- Selecting innovative citrus varieties growing after the end of the clementine harvesting.

Biography

Radia LOURKISTI is a Ph.D. student in Plant Biochemistry and molecular Biology at the University of Corsica Pascal Paoli (France), with the collaboration of the French National Institute for Agricultural Research (INRA) and the French Agricultural Research Centre for International Development (CIRAD). She currently study the tolerance to natural chilling stress and deficit water of triploid citrus and consequences on fruit quality. The study focuses on the oxidative stress and antioxidant mechanisms from using a combined physiological, biochemical and molecular biological approaches. Her research is part of "InnovAgrumes" project, an unifying project, financed by European regional development funds. The main goal is to develop a sustainable and efficient citrus crop while proposing innovative citrus fruits with the best organoleptic quality, despite the climate change. She has published 2 articles in international peer reviewed journals such as Journal of Plant Physiology and Ecotoxicology.

Production and characterization of intergeneric hybrids between turnip and radish

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Zhe Liu, Master, Institute of Vegetable Crops, Jiangsu Academy of Agricultural Sciences, China
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Intergeneric hybridization was performed between Brassica rapa L. em. Metzg. subsp. rapa and Raphanus sativus following tissue culture of hybrid seeds. One allotriploid hybrid (3n=28) was created from crosses between seven radish and six turnip species and identified as highly sterile. Twenty-four intergeneric hybrids were produced from crosses between 12 turnip and eight radish species and confirmed to be amphihaploids, with 19 chromosomes in mitosis. All of the hybrids were pollen-sterile, had white petals, and were intermediate in most of their morphological traits with respect to their parents. Allotetraploid were created by using colchicine to double chromosome aiming at fertility recovery of the hybrids. These novel intergeneric hybrids of turnip and radish are very useful for enriching the gene pool of B. rapa and creating research materials to further understand the relationships and genomic structure of the two genera.

According to the content, there are several questions can be discussed during the presentation, which are list as below:

What kind of chemicals can used to accelerate fertilization? How to identify the real hybrids by morphological, cytological and molecular ways? what's the effective of the real intergeneric hybrids harvest? what's the function and application of these intergeneric hybrids are?

Take Away Notes:

- In the present study, Gly (100 mg/L), GA3 (60mg/L), NaCl (5%) solution was spreading on stigmas to overcome the pre-fertilization barriers.in the cross of turnip and radish sepsis, these chemicals solution could accelerate fertilization and improve development of ovaries and ovules. The effect of these chemicals on different crosses combinations were different.
- The hybridity of these hybrids can be confirmed by morphological observation, cytological and molecular characterization.
- Wide hybridization can be used as bridge materials to exploit and introgression of target genes for desirable agronomic traits between these two genera, thereby facilitating resistant and quality breeding in radish and turnip.
- This research will expand the knowledge of wide hybridization and lead to a considering of the relationship between Brassica rapa and Raphanus . Our successful intergeneric hybridization technics used in this study will be an examples for other genera.

Biography

Lina Lou, study as M.S. and Ph.D. from Nanjing Agricultural University during 2006-2012; and worked as Assistant Professor at Institute of Vegetable Crops, Jiangsu Academy of Agricultural Sciences.

The main publications are as below:

Production and characterization of intergeneric hybrids between turnip (Brassica rapa L. em. Metzg. subsp. rapa) and radish (Raphanus sativus L.). Scientia Horticulturae, 2017,220: 57-65

Production and identification of an allotriploid hybrid of radish (Raphanus sativus L.) × turnip (Brassica rapa L. spp. rapa). Jiangsu Journal of Agricultural Science, 2017,33(4) : 881-889

Research progress in distant hybridization between Radish (Raphanus sativus) and Brassica. Acta Agriculturae Jiangxi,2015, 27(9):21-27

Cell cycle regulation of the initial division events during de novo root organogenesis in arabidopsis

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Unlike animals, plants have remarkable abilities to regenerate and form an entire plant body from various tissues or organs, or even from a single somatic cell. Among the different types of plant regeneration, de novo organogenesis, in which adventitious roots and shoots form from wounded or detached plant tissues or organs, is frequently used in basic research. Previous researches have revealed some basic mechanisms underlying de novo root organogenesis in arabidopsis, among which the dispensable cell fate transition events can be represented by the expression of WOX11, WOX5 and LBD16. However, previous theories cannot illustrate how the initial cell division events are regulated. As is known, proper pattern of the very first division is absolutely important for the regeneration of adventitious roots, and our work fucusing on cell cycle regulation during de novo root organogenesis may give some new insights into the molecular basic of de novo root organogenesis in arabidopsis.

Here, we will make a brief introduction of the mechanism underlying the initial cell division events from three aspects as follows: First is about the pattern and progress of the initial cell division of 'competent cells'. Secondly, we will discuss about the relationship between cell fate transition and cell cycle regulation during the initial cell division events. At last, we will make a summary of the already known data underlying regulation of the initial cell division events and get a preliminary conclusion.

This presentation will provide new insights into plant regeneration benefits related research;

Our improved molecular model underlying de novo root organogenesis may better guide agricultural industry.

Biography

From year 1999 to 2003, I completed my study in Department of Horticulture of Shanghai Jiaotong University and achieved bachelor degree.

From year 2003 to 2006, I worked as a research assistant in Institute of Plant Physiology & Ecology, SIBS, CAS.

From year 2006 to 2016, I worked as a laboratory technician in Institute of Plant Physiology & Ecology, SIBS, CAS.

From 2016 to this day, I work as a senior laboratory technician in Institute of Plant Physiology & Ecology, SIBS, CAS.

Use of biocatalytic processes for the production of value-added compounds from vegetable oils

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The volatile compounds, responsible for the fresh odor of cut grass known as "green note", have a particularly interest for flavor and food industries. These compounds (hexanal, 3Z-hexenal and 2E-hexenal) are naturally synthesized in higher plants through the lipoxygenase pathway. The lipoxygenase catalyzes, first, the oxygenation of linoleic and linolenic acids to form fatty acid hydroperoxides, which are then cleaved by hydroperoxide lyase (HPL) to generate short-chain aldehydes and oxoacids.

Unfortunately, the amount of these compounds is too low to consider their extraction from raw plant, and the processes of production currently used are highly polluting or lead to a low yield. To overcome these drawbacks, the use of recombinant, or commercial enzymes, in such processes constitutes an attractive alternative because they would allow producing these molecules in a more effective way, while benefiting from the "natural" label.

The combined action of a Candida rugosa lipase and a soybean 13-lipoxygenase was performed on sunflower or linseed oils. The first one oil, which contains around 67 grams of linoleic acid for 100 grams of oil and traces of linolenic acid, was used to produce 13-hydroperoxides of linoleic acid. The second oil, which contains around 56 grams of linolenic acid and 15.5 grams of linoelic acid for 100 grams of oil, was used to produce mainly a large amount of 13-hydroperoxides of linolenic acid but a smaller amount of 13-hydroperoxides of linoleic acid is also produced.

There is no commercial 13-Hydroperoxyde lyase available, so we have produced and purified an olive recombinant 13-Hydroperoxyde lyase (HPLwt) and then used it in several experimental conditions. We have obtained conversion yields of 93 % and 73 % for hexanal and 3Z-hexenal productions respectively. The both steps of the process were optimized in a laboratory scale. In order to raise the quantities of green note compounds produced (for an industrial application), the optimization of a process combining the commercial lipase, the 13-lipoxygenase and the 13-hydroperoxide lyase will be conducted in a bioreactor. Furthermore, during enzymatic reaction, the hydroperoxide lyase products another compound, a bi-functional compound (oxoacids with 12 carbon atoms), particularly interesting for production of biolubricants and biomaterials. The ongoing research (PO FEDER AGRIEX project) aims to developing a biocatalytic process for production of these added-value compounds.

Biography

I'm a research engineer at the Laboratory of Biochemistry and Molecular Biology of Plant of the University of Corsica in the Joint Research Unit Environmental Science (UMR 6134) of CNRS (National Center for Scientific Research), Natural Resources project. Graduated of INSA (National Institute of Applied Sciences) of Lyon in 2012, I work at the current Laboratory since 2013. My works are based on studies of production of high value-added molecules with a biocatalytic process using metabolic pathway of plants. I'm also the referent of AGRIEX (PO FEDER 2014-2020) project.

Development and validation of InDel markers for *Capsicum spp* based on whole-genome re-sequencing

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Genome-wide detection of insertion/deletion length polymorphisms in Capsicum spp was performed by comparing whole-genome re-sequencing data from two Capsicum accessions, C.annuum cv. G29 and C.frutescens cv.PBC688, to the reference genome sequence of C.annuum cv. CM334. In total, we identified 1,664,770 InDel polymorphisms between CM334 and PBC688, 533,523 InDels between CM334 and G29, and 1,651,856 InDels between PBC688 and G29. From these, 1605 InDel polymorphisms of 3-49 bp in length between PBC688 and G29 were selected for experimental validation.1262 (78.6%) showed polymorphisms, 90 (5.6%) did not amplify a product, and 298 (18.6) showed no polymorphism. For future validation of these InDel polymorphisms, 288 InDels were screened across five accessions representing the five domesticated species. Of these assayed markers, 194 (67.4%) were polymorphic, 87(30.2%) were not polymorphic and 7 (2.4%) did not amplify a PCR product. At the same time, we tested the polymorphism of 288 InDel markers in C.annuum and C.frutescens, of which more than 90% amplified a PCR product. 36 (12.5%) showed polymorphism between the two C.annuum accessions and 38 (13.2%) between the two C.frutescens accessions. This set of novel PCR-based InDel markers will be a valuable resource for genetic studies and breeding programs in Capsicum spp.

Take Away Notes:

- We have shown the feasibility and facility of using genomic re-sequencing data to identify putative InDel polymorphisms.
- InDel markes may be assayed using the same separation and detection technologies as SSR markers.
- This set of novel PCR-based InDel markers will be a valuable resource for genetic studies and breeding programs in Capsicum spp.
- A comparison of morphological traits, including seeds, flowers, fruit color, shape and size in pepper is the simplest approach for the detection of genotypes and the assessment of genetic diversity. Nevertheless, phenotypic evaluation is influenced by environment and might not distinguish between closely related genotypes and morphological identification can often be problematic when the number of useful traits is limited. More recently, the application of DNA markers allowed to better discriminate the species in the existing complexes.
- InDel markers as a kind of codominant marker, which is known as a user-friendly marker type, will have wide application and are indeed useful in marker-assisted selection (MAS) breeding.

Biography

Dr. SB Wang has been with Institute of Vegetable Crops, Jiangsu Academy of Agricultural Sciences, China since 1984. He earned his Ph.D. in vegetable genetics and breeding at Nanjing Agricultural University, China. He serves as the principle investigator for pepper genetics and breeding. He conducts research to characterize the inheritance of economically important attributes in pepper. He bred more than 20 pepper varieties and published more than 100 articles. His research work was supported by the National Key R&D Program and Natural Science Foundation of China.

Comparative transcriptome analysis reveals key genes and pathways related to male sterile of eggplant (*Solanum melongena* L.)

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Male sterile (MS) is an effective tool for hybrid production. We have obtained eggplant male sterile lines from progenies of an interspecific hybrid (S. aethiopicum × S. melongena). To understand the mechanism for MS in eggplant, the comparative transcriptomic files of MS line and its maintainer line was analyzed with the RNA-seq technology. A total of 117695 unigenes were assembled and 19652 differentially expressed genes (DEGs) were obtained based on FPKM method. The results showed 1716 DEGs were shared in three groups. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis indicated that these DEGs were mainly involved in oxidation-reduction, carbohydrate and amino acid metabolism. Moreover, transcriptional regulatory was also the impact effector for MS and anther development. Weighted gene co-expressed network analysis (WGCNA) showed two modules might be responsible for male sterile. This study threw light on the molecular mechanism of MS and identifying several key genes related to male sterile.

Take Away Notes:

- We used newly synthetic eggplant MS line to perform investigation. The understanding of related mechanisms is useful for future eggplant breeding with MS lines.
- We identified some genes in metabolic pathways which were related to MS. The results provided useful information for future deeply study of pollen development in eggplant and other plant species.
- Our study found extremely complicated transcriptional regulation network in pollen development of eggplant. Further studies of some transcription factors will be beneficial to reveal the mechanisms of plant MS.

Biography

Dr. Zhuang has been with Institute of Vegetable Crops, Jiangsu Academy of Agricultural Sciences, China since 1996. He serves as the principle investigator for eggplant genetics and breeding. He conducts research to characterize the inheritance of economically important attributes in eggplant and develop improved breeding lines and cultivars. He earned his Ph.D. in vegetable genetics and breeding at Nanjing Agricultural University, China. His research work was supported by the National Key R&D Program and Natural Science Foundation of China , and Key R&D Program and Natural Science Foundation of Jiangsu Province.

Impact of harvest season on sensory and phenolic profiles of selected clones of *Cyclopia subternata* (honeybush)

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[2]Tshwane University of Technology, South Africa
[3]Stellenbosch University, South Africa

Cyclopia subternata (honeybush) is a commercially important South African fynbos plant used as a herbal tea. Some genotypes produce a bitter-tasting tea, contrary to the "sweet, honey-like" beverage, typically associated by consumers with honeybush tea. Furthermore, this species is a rich source of bioactive xanthones, benzophenones and flavanones. The objective of this study was to determine the impact of harvest season on the sensory and phenolic profiles of selected clones of C. subternata. Sensory and phenolic profiles are second tier criteria for selection of honeybush plant material for breeding purposes. Six clones were selected, based on biomass yield and the rooting and survival of cuttings. The plant material was processed, including "fermented", and a hot water infusion of the "tea bag fraction" subjected to sensory analysis entailing descriptive sensory analysis. Standardised protocols were followed for processing and sensory analysis. The data were analysed using univariate and multivariate statistical procedures. The phenolic content of the leaves (unprocessed) was determined by HPLC-DAD and analysed using the univariate ANOVA. The results showed that harvesting season significantly affected the phenolic content of honeybush. Harvesting in summer and winter resulted in infusions with the highest intensities of positive aroma attributes; however, no clear trend for harvest season could be established for taste modalities. The highest phenolic content was recorded in summer and autumn, whereas the opposite was evident in winter. Significant differences in terms of sensory attributes and phenolic content were observed between clones, with some clones less affected by harvesting season. The differences in harvest season and clones may guide selection of clones for breeding programmes aiming at improving herbal tea quality and/or nutraceutical value.

Take Away Notes:

- Audience will learn about the new crop and its use, learn about how season affects the quality of tea as described by the chemical compounds and sensory profile and about how the genotype also contributes towards the variation in tea quality.
- It will make the audience aware that harvest season/time influences the quality of tea and that it should be taken into consideration when deciding to harvest. Selections/genotypes differ in their reaction and may be used for different products e.g. nutraceutical production etc. This will therefore assist the audience to consider looking at other factors when dealing with the quality of a crop and improvement thereof. Such factors include, effect on harvest season, variation in genotype, inter-species variation etc. The methodology used in this study may also assist the audiences towards improving their research.

Biography

Gugu S. Mabizela was born in Newcastle (Madadeni), a small town in KwaZulu-Natal where she matriculated in 2006. After completing her undergraduate studies at the Tshwane University of Technology (TUT), she joined the Agricultural Research Council (ARC) as a PDP student in 2012. She received her M.Tech in Horticulture from TUT in May 2015 and is currently registered as a PhD student in the Horticulture Department of the Science Faculty at TUT. The title of her PhD study is "Metabolic profiling of Cyclopia subternata and C. genistoides in response to drought stress and seasonal variation" and aims to complete it in 2019. During her Master's studies, Ms Mabizela published an article in the South African Journal of Botany on the effect of growth media, plant growth regulators and clone on rooting potential of Cyclopia subternata stem cuttings at different planting dates. Ms Mabizela received a fellowship to attend and present at the International Conference on Women in Science, Technology, Engineering and Mathematics (STEM) in Sandton during November 2015 and presented at eight other conferences in South Africa. In 2016 she gave a poster presentation at the 20th Eucarpia General Congress at ETH in Zurich. In 2018 Ms Gugu Mabizela received full sponsorships from DowDuPont to cover all her expenses to attend the SA Plant Breeders Association Conference. She also had the privilege to present in the DowDuPont Plant Sciences Symposium, together with Dr Geoff Graham (DuPont Pioneer Research Vice President for Global Plant Breeding, DuPont Pioneer, and Des Moines, Iowa, USA) and three other sponsored students. At the end of her studies, Ms Mabizela would like to make a significant impact in the agriculture research community by applying her acquired skills and experience in this field. Ms Mabizela is currently residing in Stellenbosch, Western Cape where she is undertaking her research with the ARC Infruitec-Nietvoorbij.

Aluminum toxicity differentially affects carbohydrates concentration in *Vaccinium corymbosum* L. cultivars

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Starch is the main molecule of carbohydrate storage in plants, composed of glucose residues. It is commonly associated with storage organs such as roots, stems and leaves. Under stress, starch can be stored or degraded in plants, as well, remobilized to provide energy and carbon molecules when photosynthesis is limited or helping to generate organic acids and sugars. The aluminum (Al), at low pH, can be toxic (Al3+) to plants, altering the total carbohydrates, increasing organic acids and decreasing photosynthetic performance. Highbush blueberry is an important crop species cultivated in the south of Chile. The aim of this work was to determine the relation of starch with the concentration of soluble sugars, organic acids and photosynthesis, in highbush blueberry under 200 µM of AlCl3 at pH 4.5 in nutritive solution for 48h. The results showed significant differences ($p<0.01$). Brigitta, Star and Cargo cultivars decrease starch concentration in 30%, 69% and 30%, respectively to 48h in roots. In leaves, there are not significant differences; however, the trend is to increase to 24h and decrease to 48h, only in Duke decreases at 24 and 48h. The soluble sugars, glucose and fructose did not present significant differences in leaves and roots; however, Camellia increases glucose and fructose at 24 and 48h, and in Cargo glucose decreases at 48h in leaves. Respect to sucrose, the trend is to decrease under Al. Fumarate showed not significant differences ($p>0.05$), but its tendency is to decrease in roots under Al. Photosynthesis showed a decrease ($P<0.05$) in Brigitta, Star and Duke cultivars under Al3+. Further, there is a positive correlation of starch with glucose (0.36) and fumarate (0.06), and negative correlation with fructose (-0.48), sucrose (-0.23) and photosynthesis (-0.12) ($p<0.01$). Finally, it is suggested that aluminum decreases photosynthesis, the concentration of carbohydrates and fumarate in highbush blueberry. On the other hand, starch is related to concentration of soluble sugars, and its increased could decrease photosynthesis. Acknowledgments: Fondecyt Iniciación N° 11160355 and FONDECYT Regular N° 1171286 projects.

TOR signaling under abiotic stress in plants

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[2]Instituto de Fisiología y Recursos Genéticos Vegetales (IFRGV- CIAP- INTA), Córdoba, Argentina.
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Environmental stresses strongly limit crop yields, whose negative effects are increasing in the context of climate change. Therefore, understanding the defense response of plants against abiotic stress is an extremely important issue. Under unfavourable conditions a fine tuning and balance between growth and stress responses are required to survive. In eukaryotes, TOR (Target of Rapamycin) complex is a central hub that integrates external and internal inputs and regulates growth and development. Although the knowledge of the TOR signaling in plants has augmented considerably in recent years, its role under adverse conditions is not described. Thus, we studied the TOR complex 1 signaling in the plant model Arabidopsis thaliana under different abiotic stress. We performed physiological analysis, biochemical and molecular biology techniques in young seedlings of wild-type plants and in various TOR complex mutants (conditional mutant tor-RNAi, raptor1B and lst8.1). Taken together, the results point to the requirement of TOR signaling in the plant response to the diverse abiotic stress, however its regulation is different depending on the nature of the stress.

This work was supported by CONICET, ANPCyT, UNMdP (EXA841/17) and FIBA.

Biography

Chemistry Licentiate and PhD (Biological Chemistry) from University of Buenos Aires (Argentina). Career Investigator (Superior Investigator) of the Argentinean Research Council (CONICET), Full Professor, National University of Mar del Plata (Universidad Nacional de Mar del Plata). Research Field: Carbohydrate metabolism in plants, unicellular algae and cyanobacteria.

Gene exploring of downy mildew resistance from a Cucumis hystrix introgression line of cucumber (*C. sativus* L.)

Ji Li*(Ph.D.), Kaijing Zhang(Ph.D.), Qunfeng Lou(Ph.D.), Jinfeng Chen(Ph.D.)
College of Horticulture, Nanjing Agricultural University, Nanjing, China

Downy mildew is a major devastating disease of cucumber, causing significant economic losses of yield in up to 80 countries yearly. In previous study, an introgression line derived from interspecific hybridization between cucumber and the wild relative species cucumis hystrix Chakr. (2n = 24), IL52, was selected as highly resistant to downy mildew and has been used for genetic analysis of DM resistance. Here, with an objective of identifying candidate genomic regions and candidate genes responsible for downy mildew resistance, traditional QTL mapping and BSA-seq were performed with RIL populations from the same cross changchunmici × IL52. Through a combination of QTL-seq and conventional QTL mapping, a reliable major QTL dm5.2 was identified for downy mildew resistance in cucumber. QTL-seq approach identified 9 SNPs affected 9 candidate genes associated with downy mildew resistance in cucumber. Validation and identification of candidate genes for downy mildew resistance is underway.

Take Away Notes:

- Downy mildew (DM) and powdery mildew (PM) are two major foliar diseases in cucumber.
- IL52, an introgression line derived from interspecific hybridization between cucumber and the wild relative species Cucumis hystrix Chakr. (2n = 24), was originally selected as highly resistance to DM and has been used for genetic analysis of DMR.
- BSA-seq, which takes advantage of bulked segregant analysis (BSA) and high-throughput genotyping using NGS technology is proposed as an efficient strategy for rapid identification of QTLs/genes controlling quantitative and qualitative traits of interest.
- This study also sheds new light on the potential value of the Cucumis hystrix introgression line of cucumber for DMR breeding program.

Whole-transcripts studying of the synthetic allotetraploid Cucumis hytivus by Pacbio sequencing technique

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The importance of wild Cucumis species for cucumber (Cucumis sativus L.; 2n=2x=14) improvement has long been recognized because they possess resistance to pathogens not present in Cucumber crop. Cucumis hystrix Chakr. (2n=2x=24 chromosomes) is the only sister species grouped as Cucumis subgenus together with C. sativus. C. hystrix is cross-compatible with cucumber, but the odd diploid number of chromosomes leads to sterile in interspecific hybrid(2n=19; 7 from cucumber and 12 from C. hystrix). The fertility was restored by chromosome doubling via somaclonal, consequently a new allotetroploid(2n=38) was synthesized and named Cucumis hytivus J.-F Chen & J. H. Kirkbr. As the offspring of C. sativus and C. hystrix, C. hytivus confers critical roles for cucumis subgenus either in significantly enriching the gene pool of cucumber or in understanding the process of revolutionary and evolutionary changes triggered by hybridization and allopolyploidization among the cucumis species.

Take Away Notes:

- Genomics studies of C. hytivus were greatly hindered by the large and complex tetraploid genome. Genetic and molecular cloning study of valuable genes was limited by lack of genome information.
- In this study, Iso-seq (isoform-sequencing) technique was employed which was developed by Pacific Biosciences (PacBio), and capable of identifying new isoforms with extraordinary precision due to its long-read technology.
- Non redundant gene set of C. hytivus were generated which could serve as a transcripts database to discovery agricultural important genes and study the revolution of genes in cucumis subgenus.

Effect of different water conditions on phenolic compounds and tocopherols in mung beans

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Konkuk University, Seoul, Korea

The main object of the present study was to evaluate the influence of irrigation periods on the distribution of phenolic compounds (flavonoids and phenolic acids) and tocopherols (α-, β-, γ- and δ-tocopherol) in mung bean cultivars. Each mung bean seed was treated with one of three different irrigation treatments that represented different lengths of time between irrigation events (100 mL/3 days, 100 mL/6 days and 100 mL/ 9 days) from the July 2, 2017 to the August 30, 2017. The average total phenolic compounds contents of different irrigation events (100 mL/3 days, 100 mL/6 days and 100 mL/ 9 days) were shown 2912.0 μg•g-1 (100 mL/3 days), 3321.8 μg•g-1 (100 mL/6 days) and 3002.0 μg•g-1 (100 mL/ 9 days). The tocopherols in mung bean seeds were analyzed by GC instruments. The average total tocopherol compounds of 3 different days and 100 mL/ 9 days) were shown 112.1 μg•g-1 (100 mL/3 days), 85.1 μg•g-1 (100 mL/6 days) and 93.0 μg•g-1 (100 mL/ 9 days). Among 3 different irrigation events, 100 mL/3 days water controls showed the highest levels of total tocopherols concentrations.

Take Away Notes:

- This study provides valuable information for breeders about future conventional breeding programs for mung bean containing phenolics and tocopherols.
- This study demonstrates the secondary metabolites within mung bean of different environmental conditions.
- Future study are needed for water application strategies to improve product quality of mung bean cultivars.

Biography

My major is the crop science of agriculture. The secondary metabolites (phenolic compounds, tocopherols, fatty acids, etc) of legumes is my main research parts. These findings are published in the Journal of Agricultural and Food Chemistry, and many other papers published various international journals.

AtMYB44 acts as a repressor of Protein Phosphatase 2C Gene Transcription

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Seoul National University, Korea

Role of the Arabidopsis R2R3 MYB transcription factor AtMYB44 has been described in diverse hormonal signaling processes, including abscisic acid (ABA)-mediated tolerance to abiotic stress and seed germination, ethylene-modulating insect defense, and disease resistance mediated by salicylic acid and jasmonic acid. AtMYB44 appears to act as a repressor of gene transcription in ABA-mediated stress responses. In AtMYB44-overexpression (35S:AtMYB44) transgenic Arabidopsis, expression of a group of protein phosphatase 2C (PP2C) genes, including ABI1, ABI2, AtPP2CA, HAB1, and HAB2, was diminished under salt stress.

PP2C genes encode a group of protein phosphatases that counteract protein kinases, thereby inhibiting the ABA-mediated signaling process. Meanwhile, transgenic Arabidopsis, soybean, and rice seedlings overexpressing the AtMYB44 gene exhibit enhanced drought/salt-stress tolerance, presumably owing to the repression of PP2C gene transcription.

Sucrose non-fermenting 1-related protein kinases (SnRKs) and clade A PP2Cs act as positive and negative regulators of ABA signaling processes, respectively. PP2Cs physically interact with SnRK2s to form complexes, inactivating the kinases via dephosphorylation. Under abiotic stress conditions, the soluble ABA receptors PYR/PYL/RCAR capture ABA and consequently bind to PP2Cs, inhibiting phosphatase activity. SnRK2s are released from the PP2C–SnRK2 complex and phosphorylate ABA-responsive element binding factors (AREB/ABFs), which activate the expression of ABA-responsive genes.

A series of independent studies has suggested that AtMYB44 physically interacts with PYLs (PYL8 and PYL9) and blocks the interaction of PYLs with PP2Cs. In particular, it was reported that AtMYB44 physically interacts with PYL8 and represses ABA signaling in response to drought and senescence. In such cases, AtMYB44 acts as a negative regulator of ABA signaling and stress responses, in contrast to our previous observation of the positive role of AtMYB44 in ABA responses.

Additionally, several studies have described AtMYB44 as a phosphorylation-dependent positive regulator of ABA signaling. In particular, it has been proposed that AtMYB44 functions as a transcriptional activator of tolerance-enhancing factors rather than as a repressor of tolerance-diminishing factors. Moreover, a research group reported that AtMYB44 acted as a transcriptional activator of WRKY70 by directly binding to the promoter in the defense response against a necrotrophic pathogen.

We investigated the role of AtMYB44 as a repressive transcription factor regulating the expression of clade A PP2Cs, including ABI1, ABI2, and HAI1. We observed that AtMYB44 physically interacts with TPR corepressors through the EAR motif (LSLSL) in the C-terminal catalytic domain. AtMYB44 forms a complex with TPR corepressors and represses the transcription of PP2Cs via the promotion of histone deacetylation at the gene locus. These results support the role of AtMYB44 as a repressor of PP2C gene expression and a positive regulator of ABA responses. Finally, AtMYB44 binds to PP2C promoters in a signal-independent manner, but is released from these regions in response to external signals to liberate gene transcription. This may explain the roles of this transcription factor in diverse signaling processes.

Take Away Notes:

- The biological roles of the Arabidopsis transcription factor AtMYB44 have been described in diverse hormonal signaling processes.
- Its mode of action as a repressor or activator of gene transcription remains controversial.
- We demonstrate that AtMYB44 binds to the protein phosphatase 2C (PP2C; ABI1, ABI2, and HAI1) promoters, physically interacts with a TOPLESS-RELATED (TPR) corepressor.
- The AtMYB44-TPR complex recruits histone deacetylase, and subsequently suppresses PP2C gene transcription in a signal-independent manner.

Biography

Graduated from Seoul National University, Department of Agricultural Chemistry.

Researcher of the Korea Institute of Science and Technology (KIST).

Received Ph.D. degree from the University of Georgia (USA), (Department of Biochemistry).

Research Fellow in the Harvard Medical School (Department of Genetics) and Massachusetts General Hospital (Department of Molecular Biology).

Currently, Research Professor of the Seoul National University (Center for Food and Bioconvergence)

The influence of laser beams and light intensities on Jordan cultivated lentil (*Lens culinaris* Medik) and wheat (*Triticum aestivum* L.) growth and metabolism

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[2]Department of Physics, Faculty of Science and Arts, Jordan University of Science and Technology, Irbid, 22110, Jordan

Light is considered as an environmental signal that controlled plants growth and development mainly by supplying sufficient duration, quality and wavelength of light intensities that is responsible for triggering on/off many physiological reactions. The objectives of this study was to examine the role of gamma aminobutyric acid (GABA) shunt pathway specific response in two wheat (Triticum aestivum L.) cultivars (Hurani 75 and Um Qayes) and two lentils (Lens culinaris Medik) cultivars (Jordan 1 and Jordan 2) to blue LED laser (intensity= 1.48 W/cm2) and high intensity invisible ultraviolet light (intensity= 3.99 W/cm2) treatments separately, with respect seed germination, seedling growth, oxidative damage in term of reactive oxygen substances accumulation, GABA accumulation level, total proteins and total carbohydrates level and glutamate decarboxylase gene (GAD) expression. Our results showed a remarkable change of proteins contents, carbohydrates contents, chlorophyll level, dry and fresh weight, GABA accumulation, MDA level, and GAD m-RNA levels under blue LED laser and high intensity invisible ultraviolet light treatments; separately in the both wheat and lentils cultivars. Under all blue LED laser and high intensity invisible ultraviolet light treatments, respectively; there were no significant differences of root emergence in all cultivars. The concentrations of MDA increased in all cultivars under blue LED laser and high intensity invisible ultraviolet light treatments with increasing exposure durations. GABA levels increased and correlated significantly in all cultivars as the exposure duration of blue LED laser and high light intensity increased; separately. Our study showed that a significant deceased of chlorophyll a and b content under all laser and high intensity invisible ultraviolet light treatments. A significant difference was found in proteins content in all used cultivars in response to laser and high intensity invisible ultraviolet light treatments. Carbohydrates content in all cultivars used in this study were significantly decreased under laser treatments. The transcription level of GAD increased significantly under blue LED laser and high intensity invisible ultraviolet light in all used cultivars. Our results indicate that GABA shunt is a key metabolic pathway that allows wheat and lentil to adapt blue LED laser and high intensity invisible ultraviolet light treatments. Generally, based on our results; Hurani 75 and Jordan 2 have higher adaptation mechanism more than Um Qayes and Jordan 1, respectively in response to blue LED laser treatments. Hurani 75 and Jordan 1 could tolerate high intensity invisible ultraviolet light more than Um Qayes and Jordan 2, respectively.

Biography

Nisreen AL-Quraan graduated in 1998 with Bachelor of Science degree from the Department of Biological Sciences, Yarmouk University, Jordan. She joined the graduate program in the Department of Biological sciences, Yarmouk University and received her Master of Science degree in Plant Biochemistry and Molecular biology in 2001. After completion of her MS, she worked as research and teaching assistant for two years in the Department of Biological Sciences, Yarmouk University, Jordan. On May, 2004 she joined the Department of Biological Sciences, Auburn University, Alabama, USA to pursue her PhD degree in Plant Biochemistry and Molecular Biology working on the plant abiotic stress interaction and the role of GABA shunt pathway in plant stress tolerance. She obtained her PhD Degree in August, 2008 from Auburn University, Alabama, USA. Since September 2008, Nisreen AL-Quraan has been an professor in plant biochemistry and molecular biology at Jordan University of Science and Technology, JORDAN. Her research is focusing on investigating the pathways that enable plants to adapt and tolerate harsh biotic and Abiotic stress conditions. She is interested in using Biochemical and molecular biology techniques to study and characterize the GABA shunt metabolic pathway that is activated in response to the interactions between plants and its environments.

Research interest: Plant Biochemistry and Molecular Biology, Plant and Environment.

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)/GSK3β-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.

Tapetum PCD retardation is critical for amino acid biosynthesis and aliphatic metabolism during sesame anther development

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Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, China

Anther development and male fertility was critical for crop seed formation and yield production. Male sterile plants provide an efficient pollination control system for hybrid breeding. Sesame 95ms-5AB was a novel recessive genic male sterile two-type line controlled by a single RGMS gene. The male abortion of 95ms-5A was appeared after tetrad stage. iTRAQ analysis and Metabolomics analysis between sterile anthers (95ms-5A) and fertile anthers (95ms-B) were performed to unravel the mechanisms of 95ms-5 male sterility. iTRAQ analysis indicated that differential expressed proteins (DEPs) were mainly involved in programed cell death (PCD), amino acid biosynthesis and lipid metabolism. Tunnel analysis further confirmed that tapetal cell degeneration was delayed in male sterile plant. Callose staining analysis indicated that callose degradation was abnormal in sterile plants during anther development. Lipid staining analysis revealed that lipid accumulation was higher in sterile anthers as compared with fertile anthers. TEM observation further confirmed the delayed tapetum PCD and the pollen wall polymerization and patterning were disturbed in sterile anthers. Metabolomic analysis as well revealed that differential metabolites between sterile anthers and fertile anthers were mainly accumulated in amino acid biosynthesis and fatty acid metabolism. Comparing to fertile anthers, the content of amino acid was reduced in tetrad stage, while was increased in microspore stage in sterile anthers and the branched amino acids were mainly altered in sterile anthers. Metabolomic analysis also confirmed the lipid content, mainly the fatty acid content, was altered in sterile anthers as compared with fertile anthers. This study demonstrated that delayed tapetum PCD disturbed amino acid biosynthesis and fatty acid metabolism, leading to male gametogenesis inhibited in sesame.

Our study provides a first insight into the mechanism that result in genetic male sterility in sesame and contributes to a better understanding of the regulatory network involved in anther development in sesame.

Biography

Ting Zhou, female, Ph. D, graduated from Huazhong Agricultural University, working in Oil Crops Research Institute, Chinese Academy of Agricultural Sciences. The research field was mainly focus on gene cloning and functional verification of important agronomic traits of sesame. Published papers in molecular & cellular proteomics, plant molecular biology, BMC plant biology. Hosting a national natural science foundation youth fund.

Changes on growth and abscisic acid contents of *Medicago sativa* to drought at different growth stages

Liqiang Wan*, Professor, Institute of Animal Science (IAS) in Chinese Academy of Agricultural Sciences (CAAS);
Yue Li, Post-doctor, Institute of Animal Science (IAS) in Chinese Academy of Agricultural Sciences (CAAS);
Xianglin li, Professor, Institute of Animal Science (IAS) in Chinese Academy of Agricultural Sciences (CAAS);
Yufei Wang, assistant researcher, Institute of Animal Science (IAS) in Chinese Academy of Agricultural Sciences (CAAS);
Jing Cao, Master candidate, Institute of Animal Science (IAS) in Chinese Academy of Agricultural Sciences (CAAS);
Hongyu Xu, Ph.D. candidate, Institute of Animal Science (IAS) in Chinese Academy of Agricultural Sciences (CAAS)

The morphological and physiological responses in plants to water stress varies at different stages of growth as affected by hormones and their relative concentrations, leading to different outcomes for crop production. Cereal crops harvested for grain suffer severer yield reduction from water stress during the reproductive stage than at the vegetative stage. In contrast, forage crops, with vegetative tissues the harvested product, should examined differently to cereal crops in experiments on the effect of water stress on production. ABA is a hormone closely related to stresses and, therefore, can improve the tolerance of crops to various biotic and abiotic stresses. ABA accumulates in the leaves when plants are under water stress, and reduces stomata opening and water loss from stomata, thereby maintaining the balance of water uptake and loss in plants and increasing the adaptation of plants to dry environments. Previous studies on drought tolerance of alfalfa focused on responses of plant morphological traits, osmotic pressure regulatory substances and peroxide scavenging systems. The effect of water stress on ABA metabolism remains unclear. Alfalfa (Medicago sativa L.) is an important forage species with high nutritional quality and yield around the world. As a legume plant, alfalfa is capable of fixing nitrogen to nitrate in nodules, by establishing a symbiotic relationship with rhizobium in the root system, making it an ideal crop for sustainable agriculture. The response of eco-physiological index of alfalfa at different growth stages on water stress remains unclear. Therefore, a pot experiment was designed and conducted in a greenhouse with three alfalfa (Medicago sativa) cultivars, Aohan, Zhongmu No.1 and Sanditi, to examine the morphological and physiological changes and response of alfalfa to water stress. The response of alfalfa to water stress at different growth stages was generally similar, but varied between cultivars. At the branching, flowering and podding stages, the shoot biomasses of Aohan and Zhongmu No. 1 were greatly affected by water stress, and these cultivars responded quickly to water stress. The shoot biomass of Sanditi was not affected by mild water stress, but had a slight response to moderate and severe water stress. The root/shoot ratios in Aohan and Zhongmu No. 1 were more sensitive to water stress than in Sanditi, with the root/shoot ratio in Aohan increasing most significantly. At flowering, the root/shoot ratio the highest and the effect of water stress the greatest. The abscisic acid (ABA) concentration in the roots of Aohan and Zhongmu No.1 increased under water stress, while in Sanditi there was only a slight or delayed response in ABA concentration. The objective of this study is to investigate the effect of water stress at different growth stages of alfalfa on growth and ABA concentration in roots, and to help to provide a better understanding of stress ecophysiology of alfalfa to assistance in the selection of drought-tolerant cultivars.

Take Away Notes:

- To examine the morphological and physiological index of alfalfa under water stress at different growth stages and then quantify the changes on growth and ABA concentration in roots of alfalfa cultivars;
- To have a better understanding on stress ecophysiology of alfalfa to assistance in the selection of drought-tolerant cultivars;
- To compare the root/shoot ratio and ABA contents in roots indicating different drought tolerance of alfalfa cultivars under water stress at certain growth stages with the control.

Biography

Liqiang Wan is a researcher and currently professor at the Institute of Animal Science (IAS) in the Chinese Academy of Agricultural Sciences (CAAS) in Beijing of China. He has a particular interest in effects of environments and management on natural and cultivated grassland, with a special focus on the response of forage crop plants on stress and ecophysiology in adversity regions across China. His current research focuses on the establishment of drought-resistance characteristic manipulative models, effects or action mechanism of root-resourced signal and assessment of yields and drought-resistance. He is one of members of Chinese Grassland Society (CGS), the secretary general and executive member of council of forage and feed production of CGS, executive members of councils of Grassland Ecology and Grassland Science Education of CGS. He got the first prize of scientific and technological achievements in Chinese academy of agricultural sciences in 2001 and the third prize of science and technology progress in Yunnan province in 2016.

Functional deficiency of phytochrome B improves salt tolerance in rice

Choon-Tak Kwon, PhD., Kiyoon Kang, PhD., Nam-Chon Paek*, PhD
Seoul National University, Republic of Korea

Soil degradation affects agriculture worldwide. Soils with high salt can result from local geological conditions or accumulation of salt from irrigation. Salt limits water uptake and reduces crop yields; therefore, salt tolerance is an important trait for crops grown in high-salt soils. Here, we show that the rice (Oryza sativa) phytochrome B (osphyB) mutant has greater tolerance to salt stress than its parent japonica rice (cv. Dongjin). We found that the osphyB mutant showed a higher survival rate, fresh weight, and levels of total chlorophylls and carotenoids, as well as enhanced membrane integrity under salt stress compared to the wild type. OsPHYB transcripts increased in tissues of the wild type after salt treatment; OsPHYB expression in the leaf blade was much higher than that in the stem and root. The osphyB mutant accumulated less Na+ in the shoot and considerably more K+ in both the shoot and root, maintaining a significantly lower Na+ to K+ ratio, possibly due to a lower rate of Na+ uptake and a higher rate of K+ uptake. To elucidate the possible mechanism of salt tolerance in the osphyB mutant, we performed quantitative reverse transcription PCR analysis, which indicated that salt stress-associated genes, including transcription factors and high-affinity K+ transporters, are upregulated in the osphyB mutant under high-salinity conditions. Taken together, our findings show that the null mutation of OsPHYB contributes to a decrease in the Na+/K+ ratio and enhances cell membrane integrity through upregulation of salt stress-associated genes, resulting in improved tolerance to salt stress.ds).

Take Away Notes:

- Red light signal is associated with salt stress response in rice.
- Based on our results, red light is closely associated with environmental stress responses. The salt stress methodology can be beneficial who is interested in the plant stress biology.

Biography

I was born in 1962 in Seoul, South Korea. I have achieved BS and MS degrees at Seoul National University in 1985 and 1987 and then PhD degree at Texas A&M University in 1994. Then my posdoc research was conducted at Iowa State University and USDA-ARS from 1994 to 1997. Since 1998, I have worked as a faculty member in the Department of Plant Science at Seoul National University. If you are interested in my research, please check in PubMed "Paek NC", and then you will find my publication record.

A new method of de novo shoot organogenesis in Arabidopsis

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Plants have the capacity to regenerate when they are wounded. For example, the leaves cut off from the seedling can regenerate new roots, getting a new life then. Similarly, when we remove the aerial part of the seedling, including the cotyledons and the apical meristem(SAM), the remained hypocotyl can regeneration a new SAM on the section, though at a very low frequency. We found that overexpressing some genes functioning in root construction can increase the frequency. And the mutant of cytokinin transport gene can delete the capability of shoot regeneration. So we proposed that the shoot regeneration depends on the root construction genes, and the cytokinin plays important roles as well. It has been a long time to research the mechanism of de novo shoot organogenesis by a two-step regeneration method: first treatment of the explant is on an auxin-rich callus induction medium (CIM), followed by incubation on a cytokinin-rich shoot induction medium (SIM).

During incubation on CIM, the initial cell can give rise to callus, which is lateral root primordia-like cells, and then the competent cells in the callus formate the primordium and precede shoot development on SIM. Our results also imply that the new method and the traditional one of de novo shoot organogenesis might share a similar mechanism.

Take Away Notes:

- First, we introduce a new method of de novo shoot organogenesis in Arabidopsis, which is simple and time-saving, compared with the two-step regeneration method. Then, if you research in the mechanism of organogenesis, this method can give you a new viewpoint to know the ability of plant regeneration. Finally, if you study genetics, you can get some knowledge about gene functions.

Biography

Education: Bachelor of Biology in East China Normal University, 1994.09-1998.06
Working Experience: Working in Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences,1999.08-today Teaching in Guizhou Normal College,1998.11-1999.07

Morphological and pathogenic characterization of discolored resistant rice

Muhammad Ashfaq[1*], Muhammad Usman Majeed[1], Muhammad Ali[1], Muhammad Saleem Haider[1] and Urooj Mubashar[2]
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Rice is the second most important cereal crop in the world and important food grain of the World population. In Pakistan, on an average 6 million tons of rice is produced each year that is about 30% of the world's paddy rice. Rice grain discoloration disease (a bacterial/fungal disease) is emerging as a major threat in Pakistan that deteriorates grain quality and texture. With abrupt changes in climatic conditions in the country, the disease severity may be minor to major across different ecological zones. Grain discoloration affects the grain morphology (size and shape of the grain) and ultimately significantly lower yield of the crop. Grain discoloration also affects the drying, shelling, milling and processing of the rice due to weight loss. To meet the day by day increasing demand of food due to increase in population, the yield, quality and quantity of the major food crops should be improved. For this purpose, we have to grow high yielding rice varieties having greater yield potential. Rice grain discoloration and other environmental factors that directly affect the grain quality, grain formation, plant structure and significantly decreasing its yield potential of the crop. To overcome these losses we have to devise the strategies for the screening and development of disease free rice varieties on the basis of morphological and pathogenic characterization. For this purpose diverse rice germplasm will be collected from National and International rice research institute to study its genotypic and phenotypic traits. This project will equally beneficial for the researchers, farmers and scientist's community to start up a new research projects. On the other hand, a screening of disease free rice step forwarding towards strengthen the economy of the country.

Biography

He completed his PhD from Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan in 2011. He visited McGill University Canada in plant science department as a visiting scientist from 17-01-2010 to 10-08-2010. He also joined the USDA, Arkansas, USA as a visiting scientist from 11-08-2010 to 23-11-2010. Recently he completed training course "Bilateral Seminar on Hybrid Rice" in China from 21 July, 2017 to 10 August, 2017. Currently he is working as Assistant Professor in the Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan from 5-10-2011 to date. He has participated in many International conferences in different countries for presentation of papers. His main focus is on rice breeding and genetics and has been recognized in this field.

Total research Publications: 50 in well reputed journals in his credit Research projects completed: 8

Correlation of leaf chlorophyll content and ripening rate in rice under heat stress

Woonha Hwang*, Seung-Hyeon An, Jae-Heok Jeong, Han-Yong Jeong, Hyen-Seok Lee, Jong-Tak Yoon and Kyung-Jin Choi
National Institute of Crop Science, Korea

Heat stress greatly effect on rice quality and yield. Therefore the breeding of heat tolerance rice is important against to global warming. To breed heat tolerance rice, we have to wait until rice harvesting time to check rice yield and quality. In order to select rice with high temperature adaptability more effectively, it is necessary to develop a method of early and easy selection without waiting for harvest time. When plant meets environmental stress, reactive oxygen species is generated then badly effect on plant metabolism. Chlorophyll content and chlorophyll a and b ratio also changed according to reactive oxygen species content. We analyzed the changes in yield and quality at high temperature, means temperature was 28ºC and daily difference of temperature was 10º, using rice cultivars cultivated in Korea. Based on these results, we chose varieties which showing high or low quality and yield difference between normal and high temperature conditions. We sowed selected rice seeds and cultivated to make young rice plant. Then we analyzed the change of chlorophyll content in leaves according to temperature conditions in selected rice cultivars. Analyzing the results, rice cultivars with little change in yield and quality at high temperatures were found to have less chlorophyll changes in the leaves. And rice cultivars with more change in yield and quality at high temperatures were found to have more chlorophyll changes in the leaves. Analyzing the content of reactive oxygen species in rice cultivars, we found that the rice cultivars with showing less change of chlorophyll content also showed less reactive oxygen species content with high activity of antioxidant enzyme. Based on the above results, it was confirmed that it can be efficient to select the heat tolerance rice during ripening stage by analyzing the leaf chlorophyll content after high temperature using rice young plant.

Take Away Notes:

- Select of heat tolerance rice in early stage
- Understand of chlorophyll change in plant by heat stress
- How heat stress effect on rice yield and quality

Characterization of *Southern rice black streaked dwarf virus* in Korea

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National Institute of Crop Science, Korea

Southern rice black streaked dwarf virus(SRBSDV) is a novel virus treatening crop production in eastern Asia. SRBSDV was first discovered in China, in 2001. Since 2009, the viral disease has spread rapidly from south to north in the rice-growing areases of eastern Asia, including Vietnam, Chnia and Japan. Analysis results of assembled contigs seven contigs matched all segments, except for 1, 3, and 8, of the 10 segments of Southern rice black streaked dwarf virus (SRBSDV), a member of the genus Fijivirus (family Reoviridae) (Zhou et al., 2008). Among sixty samples, two collected one from Jeonnam and the other from Gyeongbuk provinces might be infected to SRBSDV. The nucleotide sequences of the 600bp RT-PCR product subjected to BLASTn search, it matched to the sequence of the contig and showed 99% similarity to the virus isolated from China. Three SRBSDV positive samples were further analyzed, resulting in positive to the other six segments. The seven contig sequences of SRBSDV were submitted to GenBank (Genbank accession no. MF356695~3556701). In this study, a duplex reverse transcription polymerse chain reaction(duplex RT-PCR) method was developed for the silmultaneous detection of RBSDV and SRBSDV. The duplex RT-PCR assay provided as a rapid tool for the detection and differention of rice black streaked dwarf virus (RBSDV) and SRBSDV. The duplex RT-PCR assay can be used in routine diagnostic of these two viruses in order to study the disease epidemiology in rice crops.

Take Away Notes:

- Occurrence of rice virus disease in Korea
- SRBSDV biological characteristics
- SRBSDV gene information
- SRBSDV diagnosis method

Biography

BC Lee has completed PhD at the age of 32 years from Hokkaido University in Japan and postdoctoral studies from Chonnam National University in Korea. She is the senier researcher of National Institute of Crop Science, RDA, Korea.

Treatment of pepper seeds with chitosan increases the activity of chitinase enzyme and enhances seedling emergence in cold test

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[2]Department of Biotechnology and Genetic Engineering, Faculty of Art and Science, P.O. Box 3030 Jordan University of Science and Technology, Irbid, 22110, Jordan
[3]Department of Horticulture, Virginia Tech, Blacksburg, VA 24061-0327, USA

Pepper (Capsicum annuum), as a warm-season crop, has low seed germination under wet and cold conditions due to susceptibility of seeds to fungal diseases. Treatment of pepper seeds with chitosan improved seed germination under cold conditions, which might be due to the induction of systemic acquired resistance in seeds by increasing chitinase activity. Therefore, the objective of this study was to test whether seed treatment with chitosan improved low temperature germination by increasing chitinase activity. Pepper seeds were imbibed in 0.01, 0.05, 0.1, 0.3, and 0.5% chitosan solutions, 1% acetic acid, or hydroprimed in distilled water. Seeds were also treated with 1% Benomyl [methyl 1-(butylcarbamoyl)-2-benzimidazole] fungicide for comparison with dry-untreated seeds. All seeds were slowly dried back to their original moisture content after treatment. Seeds were evaluated for germination, mean germination time, seedling length, and fresh weight in warm germination test, and for seedling emergence in cold test. Chitinase activity was measured for treated seeds and seedlings during germination. Seeds treated with chitosan or hydroprimed germinated faster and produced seedlings with higher length and fresh weight. Neither treatments had an effect on the final germination percentage in warm standard germination test (≥86%); however, seed treatment with chitosan or hydropriming improved seedling emergence in cold test. Seed treatment with chitosan increased the chitinase activity in seeds and seedlings compared with those from untreated-control treatment. In conclusion, seed treatment with chitosan increased chitinase activity. Greater chitinase activity would protect seedlings from fungal diseases at low temperature and enhance the ability of pepper to emerge under wet and cold conditions.

Biography

Dr. Samarah holds a permanent appointment as a Professor at the Department of Plant Production at Jordan University of Science and Technology (JUST) in Irbid, Jordan where he has also served in various leadership positions at JUST including Head of Department of Plant Production, Assistant and Vice Dean of Scientific Research, and Vice Dean of Graduate Studies. Dr. Samarah's research interests include the interaction effect of seed maturity and environmental conditions on seed quality of important field crops; the effect of drought stress on seed production of field crops; the biochemical and molecular processes of crops grown under stress; studying mechanisms to produce genetically modified crops that tolerate drought stress; acquisition of seed desiccation tolerance and vigor during seed development and maturation; cultural practices to improve crop productivity in rainfed Mediterranean regions; relationship of seed quality tests to field emergence under semiarid rainfed Mediterranean conditions; breaking seed dormancy, enhancing seed germination and seedling establishment of major crops in Jordan. Dr. Samarah consulted on multiple projects involving the seed industry including the "Conservation and Sustainable Use of Dry Land Agro-biodiversity in West Asia" project. He has received several distinctions during his academic career. He was the top of his class during his undergraduate studies and received a scholarship from JUST to pursue his MSc and PhD in the United States. Dr. Samarah also received the Sigma Xi Research Award, Research Excellence Award, Gamma Sigma Delta Award, Fulbright Scholarship for Sabbatical Leave at Iowa State University, the Abdul Hameed Shoman Award for Young Arabic Scientists, and the Arab Fund Fellowship. His research activities are reflected in his 51 scientific articles in international, peer-reviewed journals. Dr. Samarah has attended 28 international conferences and scientific meetings in crop and seed science and technology. Dr. Samarah received his BSc. in Plant Sciences from JUST in 1994, an MSc in Seed Science from Mississippi State University in the United States in 1997, and a PhD in Crop Physiology/ Seed Science and Technology from Iowa State University in the United States in 2000.

Research interest: Crop Physiology/ Seed Science and Technology

Application of bioregulators Acetylcholine and GABA enhancements yield in soybean plants under water deficiency

Braga, Inae[1]*; Luiz Gonzaga Esteves Vieira[2]; Gustavo Maia Souza[4]
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Water deficiency is an important factor in limiting crop productivity and production potential. Alternatively, the plants can be "prepared" to successfully tolerate abiotic stress conditions, such as water deficiency. The use of priming presents more effective opportunities for the studies of stress physiology. The use of bioregulators as primers is an emerging approach that can modify plant physiology and may play a crucial role in regulating plant growth, leading to a possible yield increase in food crops. Consequently, they are often used to increase both plant growth and yield, and could promote a potential stress reduction. Bioregulators, such as γ-aminobutyric acid (GABA) and Acetylcholine (Ach), act as a defense of plants in response to stress, playing an osmoprotective role and promoting the growth of the root system, respectively. The objective of this study was to analyze the exogenous application of these two bioregulators, Gaba and Ach, in different stages of development, and to study its effect on the regulation of soybean response processes to the water deficit. To achieve this, we combined the application of Gaba and Ach, at the dose of 2.0 mM in soybean plants cv. Intact under different water regimes. The factors studied were: 1) application of Gaba and Ach (i) in S-seeds; (ii) L-leaf; (iii) in the seed and leaf - SL; (iv) control without application - C; and (2) water regimes: (i) 100% field capacity (FC) and (ii) irrigation suspension (IS). Leaf gas exchange and biomass analyses were performed for the physiological characterization of the plants. In observation of water deficit treatments, a 93% decrease in photosynthetic capacity was noted on the sixth day after the suspension of irrigation, as well as biomass decrease. The treatments of GABA and Ach, regardless of the mode of application under water deficit, were characterized by a lower fall in photosynthesis, an increase in stomatal conductance, and growth parameters (such as root dry mass and leaf area). Additional characteristics also included; the parameters of production, number of pods, number of seeds and mass of seeds per plant. Based on the results obtained in the present study, we suggested that the combined exogenous application of GABA and Ach bioregulators acted synergistically, promoting an increase in the performance of cv. Intact, by means of a greater tolerance to the damages caused by water deficit conditions, as well as promoting a greater growth in general, independent of the environmental conditions tested. This indicates that there is a potential use of these bioregulators for agricultural success.

Take Away Notes:

- The use of priming presents more effective opportunities for studies of stress physiology in plants. The present work offers an innovative approach to this by combining two substances, which have different functions in plant metabolism, Gaba, non-proteinic amino acid with osmoprotective action, (which is accumulated in plants under stress situations), and Acetylcholine (Ach), a cholinergic substance composed of ester acetic acid and choline, (with action on root growth). The results obtained in the experiments with the exogenous application of Acetylcholine and Gaba, under conditions of water deficiency, indicates their potential use for crop production, as a result, improving the development of agriculture as a whole. Regarding this, we propose that more research should be done on the application of these substances in different plant species, under various conditions of abiotic stress (such as temperature, water stress, salinity, heavy metals, and different types of soils). Observing if synergism and the priming action between Gaba and Ach remains in adverse situations. Further study can clarify the mode of action of Gaba and Ach within the vegetable species. Which will in turn, help establish and understand the use of Gaba and Ach in agriculture.

Biography

Biologist, integrating from the research laboratory in Plant Physiology, CEVOP - Center of Study on Ecophysiology of Plants of the West Paulista, located in Presidente Prudente / SP, from 2013., graduated in 2009 by Universidade do Oeste Paulista, I started a Master's in Agronomy in the year 2010, there I developed research on the 'Differentiation of cultivars of Urochloa brizantha' by molecular markers of repetition of inter-simple sequence (ISSR). In 2014 I started my PhD in Plant Biology at the Paulista State University "Júlio de Mesquita Filho" (UNESP). During the PHD course, I developed studies related to the application of bioregulators as primers in the different stages of development of soybean, submitted to water deficiency. After completing my PhD in March 2018, I continued the research (through a post-doctoral course at the university) on application of the Gaba and Acetylcholine in soybeans when submitted to thermal stress.

S-locus diversity of sweet cherry cultivars in Tunisia

Azizi Thouraya
National Institute of Research in Rural Water and Forests Tunisia, Tunisia

Sweet cherry (Prunus avium L.) is a species that is characterized by gametophytic self-incompatibility (GSI), which determines the fruit set and, consequently, the tree fruit load. In this study, S-alleles have been identified for nine sweet cherry cultivars in north-western Tunisia. We genotyped 9 cultivars (five introduced unknown cultivars, three international ones and one local 'Bouargoub') and we found 2 new Tunisian sweet cherry S-haplotypes (S2 and S10) using polymerase chain reaction (PCR) based on length polymorphism detection of S-RNase and SFB genes. Most introduced sweet cherry cultivars are self-incompatible and cross pollination is necessary to ensure the fruit set. The local cultivar has long been known for gametophytic self-compatible based on the fruit set rate of our research. However, the belonging of S-haplotype (S2, S10) of this cultivar to an allegedly incompatible cultivar group XLII (from the literature) is surprising and emphasizes a hypothesis that the self-compatibility of this last cultivar is unrelated to S-locus. This result is original and can be used in breeding programs. The haplotypes S2 and S10 was less frequent, whereas S3 was the most frequent (44.44%) in the nine studied cultivars.

Effects of different nitrogen sources on germination and growth regulation in various nitrogen related mutant

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School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

Nitrogen (N) is an essential macro element required for the success of all known life forms. N acts as a key catalyst to support photosynthesis and other important biochemical reactions required for healthy growth in plant. Nitrogen exists as diversity form, such as nitrates, nitrites, ammonia and nitric oxide, in plant, soil and atmosphere. But there is lack of research on nitrogen circulation inside or outside of plants. To understand interactions and mechanisms mediated by nitrogen signaling, we investigated plant germination and growth regulation and expression level of N related genes using Arabidopsis after application of different nitrogen sources. We identified 11 Arabidopsis N related genes that were differentially expressed in response to CySNO through RNA-seq analysis. Of those 11 genes, exprsseion level of NRT1.9, nitrite reductase (NIR1) and nitric oxide associated 1 (NOA1) was significantly reduced in about 2 times compared to control, whereas that of NRT1.6, NRT2.1 was significantly increased. Based upon the results, we did germination test on two types of media, Ca(NO3)2 and (NH4)2SO4, with N-related mutants. The germination rate of the Col-0 was decreased in each medium, while the other two mutants, nitrate reductase 1 (nia1) and nia2, didn't affect the germination rate. But germination rate of S-nitrosoglutathione reductase1 (gsnor1) and nitrous oxide overexpressor1 (nox1) mutants, which were known to be high in NO content, was decreased. On the contrary, in case of NO associated 1 (noa1) with low NO content, germination rate was increased in N medium. And then, we checked the expression levels of the genes that were significantly reactive to NO in RNA-seq data set. Each gene showed different expression pattern; in Col-0 and noa1 mutants were increased while decreased in gsnor1 and nox1 mutants. In particular, NRT1.6 showed a dramatic increase in noa1 mutant on Ca(NO3)2 media. This study demonstrated that exogenously supplied nitrogen substrates were definitely contributed plant germination and development by affecting nitrate involved and transport related gene expression. Taken together, we can conclude that nitrogen is not only involved in physiological development also effect nitric oxide related signaling pathways. Additionally this study suggests different point of view of nitric oxide research and further ideas.

Take Away Notes:

- Overall study of Nitrogen cycle
- Role of various Nitrogen sources on plant growth
- Research of Nitric Oxide pathway in plant
- Nitrogen in the atmosphere is important for the life cycle of a plant that circulates in the atmosphere and soil with an action of nitrogen fixation, nitrification, and denitrification. Nitrogen absorbed through the soil is known to accumulate nitrate form (NO3-) in the plant and to be used as a nitric oxide source. Also NO has been reported to play an important role in plant metabolism such as growth and development, as well as seed formation and disease resistance. However, present research is limited to the shoot and root part of the plant. Therefore, there is a lack of integrated studies on the nitrogen cycle in the rhizosphere, soil, atmosphere, and plants.
- This study gives a chance to the role of nitrogen cycle through nitric oxide research in plant.

Biography

I have been interested in studying overall of agriculture, so I received an agricultural and economics bachelor's degree from Kyungpook National University. In the process, I felt that biotechnology is most important for its implications in health and medicine from food. After all, I chose to go on to study further in this field and enrolled in the doctor´s course. Currently I am working as Ph.D candidate and a researcher in diversity of national project at KNU. I'm focusing on NO-mediated plant defense system toward both biotic and abiotic stresses using bioinformatics approaches like transcriptome.

Acetylcholine induces down regulation in GmABA2 and GmLEA3 in soybean plants under water deficit

Braga, Inae[1]*; Alessandra Ribas[2]; Luiz Gonzaga Esteves Vieira[2]; Gustavo Maia Souza[4]
[1]Universidade Estadual Paulista "Júlio de Mesquita Filho" (UNESP), Instituto de Biociências, Biologia Vegetal, Rio Claro-SP. and [(1,2)]Universidade do Oeste Paulista (UNOESTE), Programa de Pós-graduação em Agronomia, Produção Vegetal; (3) Universidade Federal de Pelotas – UFPel, Departamento de Botânica, Campus Universitário, S/N, Cx. Postal 345, Pelotas-RS

Water deficiency is a particularly limiting factor for the development and production of diverse crops, which can have a significantly detrimental impact on agriculture. Some bioregulators can be used as priming to minimize the damaging effects of water stress. Bioregulators, such as Acetylcholine (Ach) act in the regulation of the stomatal movement and being considered as ABA antagonist, respectively. This is because the enzyme encoding the GmABA2 gene catalyzes the conversion of xanthoxine to abscisic aldehyde, the latter being converted to ABA, the expression of the GmABA2 gene can also be used as an indicator for studies on soybean drought responses. LEA genes are induced by ABA or through environmental stress, such as water deficiency. It is suggested that such proteins act on water retention in ion sequestration and have the ability to stabilize membranes and proteins. The objective of this study was to analyze different modes of exogenous application of Ach and to study its effect on the regulation of the relative transcriptional responses of the GmABA2 and GmLEA3 genes in soybean, induced by water deficit using RTqPCR. For this we used an application of Ach in the concentration of 2.0 mM in soybean plants cv. Intact under different water regimes. The factors studied were: 1) the application of bioregulators (i) in seeds- S (ii) in leaf -L ; (iii) in the seed and leaf - SL; (iv) control without application - C; and (2) water regimes: (i) 100% of field capacity (FC) and (ii) irrigation suspension (IS). The GmABA2 gene, for the treatments that were under water deficit, for the control treatment, when the bioregulators were not applied, its expression was 3.6 times higher (Log2 = 3.59), in relation to the control with 100% of field capacity. A low transcriptional level of this gene was observed for all treatments with Ach (S, SL and L), Log2 = 1.6, 0.8 and 1.8 fold in change, relative to the control treatment. The GmLEA3 gene exhibited a higher number of transcripts in the treatments under water deficit for the control treatment, without application of Ach, compared to the other treatments, presenting a value of Log2 = 5.9, an increase of approximately 5 times in the number of transcripts compared to treatment with 100% of field capacity. Regarding the application of Ach, it was observed that the treatments with leaf applications (SL and L) showed a down regulation of the gene expression, Log2 = 1.7 and 2.6, compared to the control under water deficit (Log2 = 5.9). The application of Ach in seed and leaf showed a down regulation of GmABA2 and GmLEA3 genes. In addition, LEA proteins are accumulated in plant tissues exposed to water deficiency, osmotic stress at high temperature in soybean and, thus, may indicate the level of stress present in plants treated and untreated with Ach. The difference in the transcriptional level of GmABA2 with and without Ach, in soybean plants under water deficit, suggests that in the present study, Ach played a role in the regulation of signaling, reducing the signaling and activation of genes responsible for ABA biosynthesis.

Take Away Notes:

- Water deficiency is an important factor in limiting crop productivity and limiting a crop's ability to reach full production potential. In plants, the water deficit promotes a complex pathway of responses from the perception of stress through the roots, therefore triggering a cascade of events at biochemical, physiological, cellular and molecular levels, with physiological and metabolic processes being reprogrammed during the drought. Genes involved in drought tolerance are induced or repressed during water stress, among them we find ABA and LEA.
- LEA genes are induced by ABA or environmental stress, these are often associated with dehydration tolerance, plant resistance to water deficiency, and salinity and high temperature stress. It has been suggested that such proteins act on water retention in ion sequestration and have the ability to stabilize membranes and proteins. ABA is synthesized in shoots, roots and also in guard cells, and plays an important role in various physiological processes, such as the development and regulation of stomatal function, and stomatal closure in response to abiotic stresses.
- Use of bioregulators is an emerging approach that can modify plant physiology by altering the levels of DNA, RNA, enzymes and finally their products, such as proteins, carbohydrates, and lipids, and can play a crucial role in the regulation of plant growth.
- Therefore, the present work offers a different approach to the use of bioregulators in plants. Little widespread, the substance used at work, Acetylcholine, has broad functions in plant metabolism. It has been suggested that the bioregulator Acetylcholine (Ach), can influence the stomatal movement, promoting stomatal opening, acting in an antagonistic way to ABA. This allows a greater use of CO2, increases in photosynthetic rates, leading to a

possible increase in yields, especially in food crops such as soybeans. Thus, we suggest that more research be done on other plant species, submitted to different conditions of abiotic stress, to observe whether the action of Ach as an antagonist to ABA will be the same in other species or not, especially in water deficient conditions, such studies could work to clarify the mode of action of Acetylcholine within the vegetable species.

Biography

Biologist, integrating from the research laboratory in Plant Physiology, CEVOP - Center of Study on Ecophysiology of Plants of the West Paulista, located in Presidente Prudente / SP, from 2013., graduated in 2009 by Universidade do Oeste Paulista, I started the Master's in Agronomy in the year 2010, which was developed a research of Differentiation of cultivars of Urochloa brizantha by molecular markers of repetition of inter-simple sequence (ISSR). In 2014 I started my PhD in Plant Biology at the Paulista State University "Júlio de Mesquita Filho" (UNESP). During the doctoral course I developed studies related to the application of bioregulators as priming in different stages of development of soybean submitted to water deficiency. After completing PhD in March 2018, the research on the application of the Gaba and Acetylcholine in soybeans submitted to thermal stress was continued through the pos-doctoral course of the Universidade do Oeste Paulista.

OsCDF8 Delays Leaf Senescence by Regulating JA Biosynthesis Pathway in Rice (*Oryza sativa*)

Yejin Shim* (Ph.D student, Seoul National University, College of Agriculture and Life Science)
Kiyoon (Ph.D, Seoul National University, College of Agriculture and Life Science)
Nam-chon Paek (Professor, Seoul National University, College of Agriculture and Life Science)

Leaf senescence is a final stage of leaf development. In cereal crop, leaf senescence occurs during grain filling and largely affects many agronomic traits and finally total yield, so it is important to understand the regulatory network of leaf senescence of main staple food crops including rice. Although many genetic factors regulating leaf senescence have been reported, large part of its precise mechanism is still unknown. Here we report that OsCDF8, one of DOF (DNA-binding One zinc Finger)-type transcription factors, acts as a repressor of leaf senescence in rice. The T-DNA insertional mutant oscdf8-D overexpressing OsCDF8 showed a stay-green phenotype during both age-dependent and dark-induced senescence. The stay-green phenotype was further confirmed with the detached leaves of transgenic rice overexpressing OsCDF8 by 35S CaMV promoter. To elucidate the molecular mechanism of leaf senescence in oscdf8-D mutants, we performed RT-qPCR analysis, revealing that genes involved in jasmonate biosynthesis pathway like OsLOX2, OsLOX8, OsHI-LOX, OsAOS1, and OsAOS2 were downregulated as well as senescence-associated genes (SAGs), Osl85 and Osl57, and chlorophyll degradation genes (CDGs), NYC1, NYC3, and SGR in oscdf8-D mutants during dark incubation. In addition, the detached leaves of oscdf8-D mutants were less sensitive to exogenous MeJA treatment, referring that OsCDF8 regulated not only biosynthesis of JA but also its signaling pathway. Taken together, our results demonstrate that OsCDF8 suppresses the induction of leaf senescence in rice during natural condition and dark incubation by downregulating genes involved in biosynthesis and signal transduction of methyl jasmonate, which is a strong senescence inducing hormone.

Take Away Notes:

- It's the very first report of DOF-type transcription factor to participate in leaf senescence in natural long day condition.
- How to induce leaf senescence artificially; dark or senescence-relating hormones (ABA, methyl jasmonic acid, ethylene etc) treatment of detached leaves.
- What parameters to be checked throughout the developmental stages to evaluate the symptom of leaf senescence.
- The list of genes whose expression level will be altered during leaf senescence.

Biography

Yejin Shim received her BS from Seoul National University in agronomy in 2016 and MS from Seoul National University in 2018. Currently, she keeps researching in the same lab, crop molecular genetics lab as a Ph.D student.

She mainly does her research about rice (Oryza sativa japonica) and her interest of research is regulatory networks of leaf senescence, hormone signaling, and abiotic stress tolerance of rice.

Melatonin as promoter of germination and development in soybean seeds under to osmotic stress

Moro, Adriana Lima*; Spolaor, Bruna Oliveira; Braga, Inae; Bertolli, Suzana Chiari
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Soybean (Glycinemax (L.) Merrill) is one of the world's major oil crops. The productive potential of the soybean crop can be impaired since the seeds are susceptible to several factors during the production process, with water deficiency a limiting factor. Studies suggest that plants can be prepared through specific chemical compounds, termed "priming" to be tolerant to different abiotic stresses. The use of "priming" is a promising field for the physiology of stress in plants, among them we find Melatonin. Melatonin (N-acetyl-5-methoxytryptamine) can alleviate the harmful effects caused by stress and increase its productive potential. Melatonin (MEL) acts in the process of reproduction, germination and growth, and promotion of primary and secondary rooting structures. The aim of this work was to analyze the effect of the exogenous application of melatonin on the initial development of the seedlings and protective action in soybean seeds under osmotic stress. The exogenous application was made of the MEL bioregulator at the dose of 10 μM in soybean cv. Intact under two osmotic conditions, with and without osmotic stress. The germination occurred under the osmotic potential of -1.0 MPa and the hydrated control treatment was established with distilled water (osmotic potential of 0 MPa), and the stress control with mannitol solution (osmotic potential of - 1.0 MPa). Were performed germination test and initial seedling development analysis. The data were analyzed by analysis of variance and the means compared by the Tukey test ($p < 0.05$). For the treatments without conditions of osmotic stress, the application of Mel at the dose of 10 μM presented increase in all parameters evaluated. For the treatments with osmotic stress (-1.0 MPa), the application of Mel presented positive values for all the analyzed parameters, with increase of 6.20% G (germinated), 48.88% GSI (germination speed index), 188% PR5 (root protrusion with 5 days), 16.20% PR8 (root protrusion with 8 day), 12.27% SNS (strong normal seedlings) and 26.17% WNS (weak normal seedlings) when compared to the stressed control. The action of Mel as priming occurs in gene expression in stress situations, as it is also related to the induction of genes involved in cell division and osmoprotective mechanism. These effects can be achieved by activating DNA replication and cell division related to specific genes. The Mel promotes the repair of DNA machinery, resulting in the activation of respiration and the production of ATP during the soaking stage of soybean seeds. The exogenous application of Mel in seeds stimulates the production of signaling molecules and transcription factors that are inactive. Causing a quick defense response when exposed to stress. Thus, Mel is indicated as an osmotic stress attenuator during germination and initial development of soybean seedlings.

Take Away Notes:

- Environmental changes such as water deficiency cause physiological changes that impact the rate of germination and development of new plants. Water deficit also affects the enzymatic properties of plant cells under abnormal conditions. Under stress, the cell wall of plants is affected by reactive oxygen species (ROS), free radicals formed and accumulated under stress conditions. Plant cells have intracellular regulation between the production of ROS and its elimination through the actions of these different enzymes. However, some other natural substances of the plant can also aid in its defense process. The so-called bioregulators are found naturally, and also, applied in plants cultivated for the mitigation of possible effects to the stress. The physiology of the plant can be transform with the exogenous application of these, and can play a decisive role in structuring the growth of plants. Bioregulators are able to alter the levels of DNA, RNA, enzymes and their products, such as proteins, carbohydrates, lipids, causing a possible increase in yield in agricultural crops. In this way, the use of a class of bioregulators such as melatonin can act as a rooting, plant growth promoting agent, increase in seed production and act as an antioxidant metabolite, thus reducing the possible effects caused by water deficit in plants and resulting in increased productivity.

Biography

Biologist, coordinator the research laboratory in Plant Physiology, CEVOP - Center of Study on Ecophysiology of Plants of the West Paulista from 2012. Graduated in 2005 by University State Maranhão, I started the Master's in Agronomy in the year 2006 at the Paulista State University "Júlio de Mesquita Filho" (UNESP), which was developed a research of development of a Waxy additive in processed cassava. In 2009 I continue at UNESP starting my PhD in Agronomy which was developed a research Relationship between silicon and water stress on biochemical and physiological aspects in rice. Work with culture physiology and biochemical metabolism of plants submitted to abiotic. Member of the Postgraduate Program in Agronomy of the UNOESTE (University of Western Paulista).

Evaluation of genetic diversity in industrially important Kewda (*Pandanus odorifer* (Forssk.) Kuntze) using ISSR and SSR markers

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Pandanus odorifer (Forssk.) Kuntze commonly known as Kewda is native to South Asia and is an industrially important plant mostly cultivated in the coastal regions of India. It belongs to a paleotropic genus Pandanus having Gondwanan origin and belongs to the family Pandanaceae. The male flowers are used for the production of various perfumery products like kewda oil (rooh kewda), kewda attar and kewda water through hydro-distillation. It is used for scenting purposes and as food flavouring agent. It supplies about 85-90% of country's kewda essence with estimated turnover of Rs. 35-45 crores. Till now molecular characterization of kewda is only restricted to few genotypes with random amplified polymorphic DNA (RAPD) primers. In the present study, we examined the genetic diversity among 84 kewda accessions from 12 different kewda growing regions of Odisha, India. Two DNA-based molecular marker techniques, viz., inter simple sequence repeat (ISSR) and simple sequence repeat (SSR) were used to assess the genetic diversity in kewda genotypes. A total of 15 ISSR and 57 SSR primers were examined out of which 43 primers (13 ISSR and 30 SSR) showed amplification and were used for this study. ISSR analysis of 84 accessions yielded 32 polymorphic alleles ranging from 2 to 5 per locus (mean 2.5) with the size of amplicons ranging from 300 to 3000 bp in size. The 30 SSR primers produced 127 polymorphic alleles ranging from 2 to 10 per locus (mean 4.2) with size of amplicons ranging from 110 to 1500 bp. The marker index, based on the effective multiplex ratio and expected heterozygosity, was calculated for both analysis (MI = 1.9 for SSR and MI = 0.61 for ISSR assays). The mean values of Nei's gene diversity (h), Shannon's information index (I), Polymorphic information content (h = 0.2488, I = 0.36, PIC = 0.48), generated using the SSR primers were higher than that with ISSR primers (h = 0.19, I = 0.30, PIC=0.34), thereby suggesting that the SSR system is more efficient than the ISSR system in assessing genetic diversity in various kewda accessions. Mean genetic similarities were 0.72, 0.73, and 0.73, as determined using ISSR, SSR, and combined ISSR/SSR, respectively. These results suggest that the genetic similarity among kewda accessions is very high. An unweighted pair-group method with arithmetic average (UPGMA) cluster analysis was used on the results of ISSR, SSR, and combined ISSR/SSR to separate the kewda accessions. These results have an important implication for characterization of available germplasm of kewda, conservation and future improvement of the taxa and assessment of their genetic diversity. It can be used for future breeding programs to meet the ever-increasing demand of kewda in the perfumery industry.

Take Away Notes:

- Kewda (Pandanus odorifer) is an economically important plant. It is an important natural bioresource because of the unique fragrance it possesses. To enrich the genetic pool of the species, screening and selection of genotypes is essential which can be achieved only through proper genetic diversity study.
- Different populations have different levels of genetic diversity and identification of populations with low and high genetic diversity is very crucial for long term management strategies. Hence two different molecular markers were used for the study of genetic diversity in kewda.
- The results suggest that both ISSR and SSR are easy, simple and reliable methods for analyzing genetic diversity between the species. It is more preferable to combine them in analysis for assessing the genetic relationships with high accuracy.
- The assessment of genetic diversity provides the basis for characterization, conservation and sustainable utilization of the plant genetic resources. Appropriate conservation strategy for improvement of kewda genotypes could be easily formulated with the knowledge of population genetic structure.

DAY 3

KEYNOTE FORUM

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

September 20-22, 2018
Rome, Italy

Technological advances for in vitro culture and genetic enhancement of horticultural crops

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

In vitro and molecular techniques are important biotechnological tools that can speed up production technologies in horticultural crops. Small fruits including Fragaria (strawberry; Rosaceae), Rubus (brambles: raspberry and blackberry; Rosaceae) and Vaccinium (blueberry, cranberry and lingonberry; Ericaceae) are commercially important health-promoting horticultural crops that are believed to have significant role in anti-tumor, anti-ulcer, anti-oxidant and anti-inflammatory activities. Lowbush blueberry (Vaccinium spp. L.), cranberry (V. macrocarpon Ait.) and lingonberry (V. vitis-idaea L.) are three berry crops important to Canadian cool climates. Wildberry production systems are changing to a more intensive cultivated system leading to an urgent need for developing new techniques for selecting and establishing high-yielding, quality crops which are well-adapted to diverse biotic and abiotic conditions. The presentation concentrates on: wild berry germplasm characterization at molecular, biochemical and morphological levels and their utilization in hybrid development using in vitro and molecular techniques. Technological advances in bioreactor micropropagation in a liquid medium and use of in vitro and molecular techniques in hybrid development of berry crops have been described in detail. Epigenetic studies in micropropagated plants and biodiversity analysis in wild germplasm will contribute significantly in planning future production and improvement programs of horticultural crops.

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 114 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.

Biography

Mr. Zheng Zheng is the distinguished professor of Fudan University and head of Basin Pollution Control Research Center of Fudan University. He has worked in watershed pollution control and ecological recovery for decades. He is the principal investigator for dozens of China's national and provincial projects including four Chinese National Science Foundation projects, two projects under the National Plan of Research and Development in High Technology (the 863 Plan), and three projects under the National Key Research Program in Water Pollution Control. So far, Prof. Zheng's research funding has exceeded 20 million U.S. dollars. He has got more than 40 national patents and 12 national, provincial, and ministerial awards for progress in science and technology.

Ecological restoration of plants and China's watershed pollution control

Zheng Zheng

Fudan University, China

With China's reform and opening up, rapid economic development, and improvement of people's living standards, industrial and domestic wastewater discharge as well as fertilizer and pesticide residues in agricultural runoff has increased drastically since 1980's, leading to the widespread eutrophication of its watersheds, the pervasive outbreak of algae blooms, and the degradation and collapse of its aquatic ecosystems. Therefore, pollution control and aquatic ecosystem recovery has become one of the most critical tasks faced by Chinese authorities.

The prevailing view is that only when water pollutant concentration is reduced to the level of the 1980's can a fundamental improvement in water quality and ecological restoration be achieved. However, the reality in China is that on the one hand pollutant loads have exceeded their environmental capacities in most watersheds, and on the other hand they are hard to reduce due to economic development. Furthermore, even if wastewater has been properly collected and treated so as to meet the strictest wastewater discharge standards in China, its pollutant concentrations far exceed the surface water quality standards (often exceed the Category III surface water quality standard by several or a dozen times). Nevertheless, previous study results have indicated that water quality needs to improve to Category II or better to control algae bloom effectively.

There is a loud opinion that exotic species should be eradicated from watersheds besides pollution control to achieve its ecological recovery. So far, China has approved such projects. The above situation seems to indicate that watershed pollution control and ecological recovery has fallen into a deadlock in China. We feel that effective watershed pollution control and ecological recovery in China requires new thinking.

First, adjust China's economy progressively to an environment-friendly industry structure with low emissions. Meanwhile, lifestyle in China should change gradually following the environment-friendly concept.

Secondly, solve the issue of current huge difference between China's sewage treatment discharge standards and surface water quality standards, including raising China's sewage treatment discharge standards.

Thirdly, gradually strengthen the construction of clean water networks by linking water bodies to form stream networks and recovering plant ecosystems so as to increase the carrying capacities and self-purification capabilities of watersheds as well as the health level of ecosystems.

Fourthly, we could not and should not pursue a complete restoration of plant communities in the watersheds to those in the 1980's, because situation changes with time. We should focus on advancing with time and carrying out ecological restoration to establish a new ecological balance.

Finally, our research group has conducted several years of research at the Dianchi, one of the most polluted and ecologically degraded lakes in China. In view of its poor water quality of worse than Category V, nearly none vegetation coverage, and highly polluted inflow which is mostly discharge from wastewater treatment plants with pollutant concentrations far exceeding surface water quality standards, we have proposed the concept of spatiotemporal configuration of plants, and have gradually realized the control of algae bloom and recovery of plant communities in our experimental area.

Take away notes:

- Serious watershed pollution and ecological degradation in China has been mainly caused by economic development.
- It is impractical to expect to reduce water pollution and restore plant communities in China to the level of 1980's. Current solutions to the issue have fallen into a deadlock.
- New thinking in watershed pollution control and ecological degradation in China has been proposed.
- Pioneering projects implementing the spatiotemporal configuration of plants, which not only facilitate water quality improvement but also establish new ecological balance, have been introduced.

DAY 3

SPEAKERS

2nd Global Conference on

PLANT SCIENCE AND MOLECULAR BIOLOGY

September 20-22, 2018
Rome, Italy

Yellow canopy syndrome in sugarcane is caused by a sink source imbalance

Frederik C Botha*, Ph.D., Sugar Research Australia and University of Queensland, Australia
Annelie Marquardt, Sugar Research Australia and University of Queensland, Australia
Kate Wathen-Dunn, Sugar Research Australia, Australia
Gerard Scalia, Sugar Research Australia

Yellow Canopy Syndrome (YCS) is a condition affecting sugarcane production in Australia. It is not evident whether biotic or abiotic factors trigger the onset of YCS development. The presentation will focus on the phenology of YCS development and the accompanying changes in physiology, the metabolome, transcriptome and proteome. Evidently, the development of YCS is a failure to export adequate amounts of sucrose and an inability to prevent sucrose accumulation in the leaf by redirecting carbon to starch. Expression of the sucrose transporters and SWEET proteins suggest that the failure to export sucrose is not linked to inadequate loading of the phloem. A conceptual model of the sequence of events occurring in leaf metabolism will be discussed. Early stages in sucrose accumulation triggers a reduction in CO2 fixation in the cytosol of the mesophyll cells through a reduction in PEPC expression and suppression of PEP regeneration by reducing PPDK in the mesophyll chloroplast. At the same time triose phosphate is preferentially allocated to starch synthesis. These reactions cause reduced electron flow through the ETC and increased ROS production. Initially it is primarily photosystem II in the mesophyll chloroplasts that are affected with most of the genes encoding the structural and function components of PSII downregulated. In addition to a redirection of carbon flow to starch, an upregulation of the phenylpropanoid and ascorbate synthesis pathways is a likely responseto reduce damage from ROS. As sucrose continue to build up in both the cytosol and apoplast, chloroplast metabolism in all compartments is suppressed and photoreaction centres are uncoupled from electron transport. This, linked to stomatal closure as a result of the increased sucrose levels, leads to elevated leaf temperatures, accelerated senescence and cell death.

Take Away Notes:

- An insight into the lack of feedback control of sucrose on C4 photosynthesis. Unlike C3 plants the C4 grasses have a limited ability to buffer against ‘sucrose overflow’ when sink demand decreases. This makes the highly efficient C4 species particularly vulnerable against conditions that slow the growth of the sink, culminating in reduced sink strength.
- Characterisation of the mechanisms underpinning feedback control of sucrose would be a valuable resource in teaching of plant biochemistry. This is imperative to understanding the difference in sensitivity of the decarboxylation mechanism in the bundle sheath cells.
- A new appreciation of the major gaps in knowledge about sink source relationships in the C4 grasses.
- Could inform approaches to identify and development of molecular markers to select for resistance against changes that are induced by sucrose accumulation in the leaf.

Biography

Frederik (Frikkie) Botha is the Executive Manager Technology at Sugar Research Australia and Honorary Professor at the University of Queensland, Australia. His research focus on the genetic and molecular control of carbon partitioning in the culm and leaves of sugarcane. The research aims to understand the control of carbon partitioning between the cell wall components, respiration and sucrose accumulation in the culm and the impact of this on sink strength. An early switch to sucrose accumulation reduces biomass accumulation and reduces sink strength. The limited capacity to buffer leaf sucrose through partition of carbon to starch requires maintenance of a strong sink demand to prevent induction of premature senescence in the canopy.

Salt tolerance mechanisms in grasses with salt excretion

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About 6% of land area affected by soil salinization that produce serious problems for world agriculture. Improving of salt tolerance in crops is a global challenge for the nearest future. Salt tolerance is a genetically and physiologically complex trait that causes the difficulties in breeding and genetic manipulations in salt-tolerant crops. For engineering the salt tolerance traits in crop, it is crucial to clarify the genetic and specific physiological backgrounds in different plant lineages. Among grasses, about 200 halophyte species were identified with over 70 different independent origins of salt tolerance (Bromham, 2015). About 30 grass species developed effective salt excretion system with one of them, Oryza (=Porteresia) coarctata, being close relative to cultivated rice. The focus of our study was the comparison of salt tolerance mechanisms in grasses with salt excretion evolved in different grass lineages. Oryza coarctata is a wild rice species which has high tolerance to salt with traits which are of interest for improving tolerance of rice growing under saline conditions. Spartina anglica is a serious invasive species in natural saltmarsh ecosystems, and Urochondra setulosa, native to northeastern Africa and southwestern Asia, grows in coastal sand dunes, salt marshes and estuaries. The leaf anatomy and ultrastructure of salt glands, pattern of salt excretion, features of gas exchange, accumulation of key photosynthetic enzymes, maintenance of water content, Na+ and K+ accumulation, and osmolality along with levels of some osmolytes and betaine aldehyde dehydrogenase expression, were compared in the three species grown without salt, with 200 mM NaCl, and with 200 mMKCl. Measurements of gas exchange showed photosynthesis was not affected by salt treatments. Stomatal conductance decreased under the salt treatments reducing water loss by transpiration with increase of water use efficiency (WUE). Despite differences in the type of photosynthesis (S. anglica and U. setulosa are C4 while O. coarctata is a C3 plant), the three species have a similar leaf anatomy; the adaxial side has distinctive ridges while the abaxial side is flat in S. anglica and O. coarctata and undulated in U. setulosa. All species have salt glands with distinctive difference in their distribution, excretion rates, anatomy and ultrastructure. S. anglica and U. setulosa have bicellular glands with basal and cap cells, however, O. coarctata has unicellular glands. In contrast to a previous report, our results show that the multiple unicellular trichomes in O. coarctata are not responsible for salt secretion. All three species accumulate compatible solutes with increasing osmolality but they differ in osmolyte composition and amount. In summary, O. coarctata, S. anglica and U. setulosa show high tolerance to salt based on function of photosynthesis, maintenance of leaf water content, synthesis of compatible solutes, and capacity for salt excretion from leaves; but, they have distinct differences in the salt excretion system and accumulation of osmolytes. In three species from different grass lineages, salt tolerance was evolved using similar principle reactions (increase of WUE, accumulation of osmolytes and establishment of salt excreting system) with variable mechanisms of their realization.

Biography

Nuria Koteyeva is a senior researcher in laboratory of Anatomy and Morphology, Komarov Botanical Institute, Russian Academy of Sciences. N. Koteyeva was graduated from St. Petersburg State University, Russia, where she was awarded a Master of Science degree in Plant Biology. Her PhD was in plant sciences and carried out at Komarov Botanical Institute; she received PhD degree in 1999 for the investigation of the structural basis of plant cell cold-tolerance. Koteyeva'srecent research interests are in two main areas: 1. Theevolution, development and maintenance of Kranz anatomy in C4 plants and 2. The stress tolerance mechanisms.

Effect of high light stress on the photosynthesis of a shade demanding plant: *Panax ginseng* C.A. Meyer

SEGRET Léa*, Ph.D. Student, France Ginseng, France
BERGER Monique, Ph.D,INP, EI Purpan
GALDIN Maxence, Master student, INP, EI Purpan
DAYDE Jean,Ph.D,INP, EI Purpan

Panax ginseng C.A. Meyer is a shade species. This plant optimal growth irradiance is comprised between 5% and 20% of full sunlight(Proctor & Palmer 2017; Li 1995; Parmenter & Littlejohn 1998). If receiving too much light, leaves could suffer from photoinhibition of photosynthesis. Growing *Panax ginseng* plants under too much light during prolonged period, could cause photobleaching and premature leaf death(Proctor & Palmer 2017). We investigated the photosynthesis responses in 3 years*Panax ginseng* C.A. Meyer plants. Two light levels were applied on greenhouse grown plants. Low : 35 µmol(photons).m^{-2}.s^{-1} corresponding to 5% of full sunlight; and high: between 100 and 150 µmol(photons).m^{-2}.s^{-1} corresponding to 15% of ambient light. This two levels corresponding to the levels used in literature to assess light effect on ginseng plants photosynthesis (Jang et al. 2015; Chen et al. 2016; Lee et al. 2012). They were combined in 4 treatments: Control (always Low); M1: High only during 2 weeks in June; M2 : High only during 2 days in July ; M3: High 2 weeks in June and 2 days in July. The 2 weeks of high light stress applied in June (early in the vegetal cycle) correspond to a pre-treatment in order to observe plant plasticity response to stress (M1 and M3).

The relationship between net photosynthesis assimilation (A_{net}) and photon flux density (PFD) was fitted to equation model from (Ye 2007) : $A_{net} = \varphi_{(Io\_Icomp)} \text{ x } [(1 - \beta \text{ x } I)/(1 + \Upsilon \text{x } I)] \text{ x } (I - I_{comp})$. With $\varphi_{(Io\_Icomp)}$ = quantum yield in the range of I_o to I_{comp} [µmol(CO$_2$).µmol^{-1}(photons)], β and ϒ = adjusting factor, I = photosynthetic photon flux density [µmol(photons).m^{-2}.s^{-1}], I_{comp} = light compensation point [µmol(photons).m^2.s^{-1}]. The quantum yield and light compensation point were estimated by the slope and intercept of the linear region of the light response curve respectively.

The maximum photosynthesis rate (P_{gmax})never exceed 2.4µmol(CO$_2$).m^{-2}.s^{-1} when plants were always grown at optimal irradiance (control). In plants grown at high light intensity in June and July (M3), net photosynthesis rate could not exceed 1.8µmol.(CO$_2$).m^{-2}.s^{-1}. A significant difference was observed between P_{gmax} of plants grown at high light intensity in June and July (M3) (1.8 µmol(CO$_2$).m^{-2}.s^{-1}) and P_{gmax} of plants grown at high intensity only in June (M1) (2.7 µmol(CO$_2$).m^{-2}.s^{-1}).For *Panax notoginseng* and *Panax ginseng* plants the same trends were observed (Chen et al. 2016; Jang et al. 2015), but the maximum photosynthesis rate found was higher for *Panax notoginseng*(between 4 and 5 µmol(CO$_2$).m^{-2}.s^{-1})than *Panax ginseng*(Chen et al. 2016). This could be due to the species or to the difference of temperature during measure period in Toulouse, France and Yunnan Province, China. Indeed *Panax ginseng* plants are very sensitive to high temperature (Lee et al. 2012). Thus, it seems that when strongly stressed in June, plants displayed some plasticity and then can have better or normal photosynthetic activity when return under optimal light. However, when stressed in June and July, ginseng plants couldn't adapt and thus have very low photosynthesis rate when return under optimal light.

The φ_{PSII} (PSII quantum yield) for low PFD: 50µmol(photons).m^{-2}.s^{-1} is significantly higher for the control plants (0.63 µmol(CO$_2$).µmol^{-1}(photons)) compared to plants which were stressed in June and July (M3) (0.31 µmol(CO$_2$).µmol^{-1}(photons)). Besides, NPQ (Non Photochemical Quenching) seems to be higher for M3 plants than for control plants and less stress plants (M1 and M2). Thus it seems that *Panax ginseng* plants suffer from photoinhibition when grown at high light level in June and July but not when grown under high light only in June (leaves plasticity).

Take Away Notes:

- How to preform light saturating curves for shade demanding plant on LI6400 (measure time, accuracy, detection threshold limit, improvement).
- The better model found in literature (among 12) to analyze light saturating curves on shade-demanding plant with Panax ginseng C.A. Meyer used as a model.
- How shade demanding plant responded to high light stress in terms of photosynthesis rate (plasticity response of plants) with Panax ginseng C.A. Meyer used as a model.
- Fluorescence variables measurement during light saturating curves run can give us information about photoinhibition status of the plant.

The morphology of the structural elements of Rhododendron and their taxonomic significance

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Botanical Garden-Institute FEB RAS, Vladivostok, Russia

The flora of the Russian Far East is attractive by its biodiversity and the fact that there are boundaries of the distribution of East-Asian species. Among them are Rhododendron mucronulatum Turcz., Rh. dauricum и Rh. sichotense. The specimens of the subsection Rhodorastrum are characterized by existence of convergent morphological traits, that, in turn, causes discussions concerning their taxonomic status. To discover questions related to taxonomy, leafs, pollens and seeds morphology were investigated, as well its correlation to different environmental factors. To do that, we applied methods of electronic scanning microscopy and geometric morphometry. The most significant features of pollens and seeds that are more steady and are not-related to climatic variables were obtained. The difference between species by their pollens is observed on the level of structural elements in the zone of apocolpium, mesocolpium and near the aperture space. For seeds the most significant taxonomical feature as a coefficient of elongation of the cell exotesta was pointed out. Population investigation of these features on the Primorsky krai territory showed the existence of areas where pollen grains and seeds combine structural elements of different species.

The obtained results demonstrate existence of variability of structural elements, that is caused by climatic variables, as well likely processes of hybridizations, because the territory of Primorsky kray is a zone of sympatric distribution of Rh. mucronulatum, Rh. dauricum, Rh. sichotense.

Take Away Notes:

- The obtained data shows a series of morphological features that could be used in taxonomy of close-related species. Moreover, it was shown, that processes of hybridizations could be identified by finding mixing of structural elements of different species in their pollens and seeds. Facts on relationship the leaf form and climatic variables could be used for another taxonomical complicated groups of plants that are characterized by high interspecies variability.
- The obtained data is a basis for further genetic investigations and could be used in evolutionary biology for understanding the formation and species migration in East Asia.

Biography

Koksheeva - leading researcher in laboratory of Introduction and selection, Botanical Garden-Institute FEB RAS, Vladivostok, Russia. I. Koksheeva was graduated from Eastern State University, Russia, where she was awarded a Master of Science degree in Plant Biology. Her PhD was in plant sciences and carried out at Botanical Garden-Institute FEB RAS; she received PhD degree in 2006 for the investigation of the reproductive biology of Rhododendrons during introduction in the South of Primorsky Krai. Recent research interests are related to the study of morphology of pollen, seeds and leaves, the taxonomy of rhododendron species.

Ethnobotanical study on the medicinal plants in the central-southern Apennine, (Italy)

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Piera Di Marzio, Professor of Vegetation ecology, Department of Bioscience and Territory, University of Molise, Pesche (IS), Italy
Paolo Maria Guarrera, Executive of Central Institute for the "Demoetnoantropologia", MiBACT, Rome, Italy
Maria Iorizzi, Professor of Organic chemistry, Department of Bioscience and Territory, University of Molise, Pesche (IS), Italy

During the presentation will be discussed the result of an ethnobotanical research planned in the Apennine territory (Italy) between 2011 and 2014. The focus was on wild and cultivated plants used in "folk medicine" in mountain villages in the central-southern Apennine, which are full of ancient traditions and rich in natural and fascinating environments. Field data were collected through semi-structured and open interviews with native People. The plants were identified and vouchers specimens were scanned to create a Virtual Herbarium that will be showed during the presentation.The inventory included 106 taxa belonging to 45 families; among these, 87 were wild species and 20 were cultivated speciesTheuse of several index such as the Ethnobotanicity Index (EI), the Relative Importance Index (RI) and the Fidelity Level Index (FL) will be discussed. It will be showed the plant part used, and the traditional method of preparation.The uses recorded were 429 totally and, among these, 69,1% of the uses concerned internal applications to treat digestive system disorders, infections and respiratory system disorders mainly, while 31,9% concerned external applications,especially to treat skin/subcutaneous cellular tissue disorders and injuries(sensu Cook 1995). In particular, 17 new uses compared with the international literature and 16 unusualand rarely mentionedplants are documented and will be showed. Finally, as example, to well understand the composition ofT. poliumused in folk medicine in the Apennine, the aerial parts were analysed through two extraction procedures. The first extraction was carried out with methanol and the second by a decoction preparation according to the traditional medicine. Both extracts were purified, and the composition of the secondary metabolites was compared and the results of this analysis will be discussed.

Take Away Notes:

- Knowing the expertise of the audience my slides will be very useful to:
  - » Clarify the steps of the project research that can be replicated everywhere.
  - » Underline the rule of the systematic botany in the field research of medicinal plants.
  - » To show the high level of floristic diversity of the Apennine (Italy).
- I would underline the importance of the basic research (Systematic botany, Floristics) in the collection of wild species in the fieldand in general on the uses of medicinal plants.
- The study on the use of the medicinal plants in the academics world as well as in the industry world is increasingin the last years.

Biography

I'm a professor of systematic Botany at the university of Molise (Italy) and the curator of the Herbarium IS. PhD in Botanic science at the University "La Sapienza" Rome in 1997.My researches are concentrated on natural vegetation and vascular flora: ecology, chorology, cenology, distribution and genetic aspects of the Apennines and Mediterranean region. The topics researches are in the study of intra- and interspecific variation in some critical genus of the Italian flora (Quercus, Rosa) using an integrated approach: macro and micro-morphology analysis, geometric morphometric analysis and molecular analysis. In the last years, I have focused my study on the medicinal plants, distribution, folk uses and metabolites collected in the Apennines (Italy).

Floral morphology and reproductive biology of Asarumsieboldii Miq

Svetlana Nesterova PhD
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Species of the genus Asarum (Aristolochiaceae) are perennial herbaceous plants grow mainly in Southeastern Asia and several species in North America and Europe. We chose the East Asian Asarumsieboldii for study. In the Russian Far East, the species grows in the southern part of region. The A. sieboldii flower is bisexual, trimerous, radial, mainly purple. The perianth is simple, gamophyllous, the form is almost spherical tube with a three lobes. The gynoecium consists of six carpels. Our research has shown that A. sieboldii has a half-inferior, six-locular ovary. The androecium from 12 stamens that do not fuse with gynoecium. It means that the gynostemium is not formed. The lifetime of single flower is 2-3 days. It turned out that flowering has three stages. At the first stage (female), anthers are closed, cross-pollination (xenogamy) with involving flies (Dolichopodidae, Diptera) and ants (Hymenoptera) is possible. At the second stage (bisexual), there is direct contact of anthers with the pistil stigma and self-pollination occurs. The final, third, flowering stage can be estimated by the drying and blackened lobes of stigma and anthers. We believe that A. sieboldii has two types of pollination: cross pollination, or xenogamy, which is assisted by dichogamy in the form of protogyny and extrorse opening of anthers, and autogamy in the form of contact autophilia. The fact of self-pollination was established by us experimentally using insulators and the fruit set was 89%. The agents of seed dissemination are ants: Leptothoraxacervorum and Myrmicaruginodis(Formicidae, Hymenoptera).

Take Away Notes:

- The issues of flowering and fruiting of A. sieboldii have not been considered so far. The results of studying the aspects of flower morphology and reproductive biology supplement the general information on the reproduction of the species and are also important in solving problems related to the plant taxonomy and preservation of the gene pool of valuable plants in situ and ex situ.

Biography

Svetlana Nesterova PhD, Leading Research Associate Laboratory of Flora, Associate Professor, Botanical Garden-Institute FEB RAS, Vladivostok, Russia. Svetlana Nesterova was graduated from Far Eastern State University, Russia. Topic of PhD thesis was "Seeds cryoconservation of the natural plants of Primorskii region". In 2004 she received PhD degree. Area of scientific interests is ontogeny, reproductive biology, conservation of biological diversity. She combines the scientific work with reading lectures at the Far Eastern Federal University (Vladivostok, Russia).

Alkaline/Neutral invertases: Involvement of cytosolic or organellar isoforms in abiotic stress responses in wheat and poplar

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Sucrose is a central metabolite in plant life. In recent years, novel functions have been uncovered for alkaline/neutral invertases (A/N-Invs), enzymes that irreversibly hydrolyze sucrose into glucose and fructose. A/N-Invs play important roles in growth, development, and stress response. They occur as different isoenzymes located either in the cytosol or inside organelles (e.g., mitochondria, chloroplasts). In wheat, A/N-Invs were shown to play an important role associated with a more efficient cytosolic sucrose hydrolysis during environmental stresses (e.g., water deficit and low temperatures). The availability of complete sequenced genomes allowed us to identify and characterize the members of the A/N-Inv family in wheat (Triticum aestivum) and poplar (Populus sp.), and then investigate the expression of different isoforms in plants subjected to different stress conditions. In wheat, four of the seven A/N-Inv genes (TaNIN) were predicted as encoding cytosolic isoforms, which turned out to be phylogenetic and structurally similar to their rice homologs. RT-PCR analysis revealed differential gene expression in leaves and roots of two contrasting wheat varieties (winter Baguette 31 and spring BioINTA 1005) subjected to low (chilling) temperature or water deficit. Remarkably, only the winter cultivar, with higher fructan content, exhibited up-regulation of two cytosolic isoforms in leaves, and of other two different forms in roots. Conversely, the response in leaves was similar for both cultivars exposed to water deficit, with the enhanced expression of another isoform. The contrasting expression between cultivars under low temperature led us to hypothesize that certain cytosolic isoforms could be involved in the intricate sugar-signaling pathway that senses chilling and resulting in low temperature tolerance. On the other hand, in poplar, we retrieved 12 A/N-invertase homologous sequences from the recent sequenced Populus tremula genome (Ptr-NINVs). Six of the 12 putative Ptr-NINV deduced proteins were predicted as cytosolic isoforms and grouped in the ß-clade together with characterized cytosolic proteins in other plant species. The 6 remaining Ptr-NINV sequences that grouped in the α-clade were characterized as putative mitochondrial and chloroplastic isoforms. To characterize the organellar location, we identified the transit peptide sequences, made PtrNINV::GFP constructs and carried out transient expression in tobacco leaf cells. Preliminary experiments to identify isoforms related to stress tolerance indicated that one of the mitochondrial isoform may be involved in cold and salt stress response. Taken together, our results show that either cytosolic or organellar A/N-Invs may be important in the response to abiotic stress.

Take Away Notes:

- This research helps to understand the importance of alkaline/neutral invertases as possible "molecular markers" of tolerance to abiotic stress. The results can be used to help breeders in obtaining new tolerant cultivars (for example, to chilling, drought or salinity).
- On the other hand, we demonstrate that the expression of the alkaline/neutral invertase isoforms in a given stress condition is not a general feature of the plant species (i.e. wheat), but depends on the cultivar.

Biography

Chemistry Licentiate and PhD (Biological Chemistry) from University of Buenos Aires (Argentina). Career Investigator (Superior Investigator) of the Argentinean Research Council (CONICET), Full Professor, National University of Mar del Plata (Universidad Nacional de Mar del Plata). Research Field: Carbohydrate metabolism in plants, unicellular algae and cyanobacteria.

Effects of magnetic field on Peroxidase activity and hardening of New Guinea impatiens explants

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Hassan Salehi, Professor of Horticultural Sciences, Shiraz University, Iran
Sasan Aliniaeifard, Assistant professor of Horticultural Sciences, Tehran University, Iran

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.

Take Away Notes:

- 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 student in Master of Science Degree in horticulture science (ornamental plants) in the Faculty of Agricultural Sciences, Tehran University. He was graduated from Shiraz University in horticulture science in June of 2017. He was accepted to Tehran University through an entrance exam in the same year. He has been working at Tissue Culture Institute of Shiraz University as a researcher for two years. Fardad Didaran was granted the third rank in Physics Olympiad in 2013. He is currently working on new projects in the mentioned. Fardad Didaran lives in Tehran, Tehran Province, Iran.

Microbial source of water for the desert plants

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Water scarcity is one of the greatest challenges and a matter for several recent researches. The water sources for the desert plants are still aim for many researches. Knowing of these sources will enable saving the water resources as well as using of un-confidential water sources in irrigation. Through this present investigation, the wild plant Bromus inermis grown in the EL-Esmayelia desert rod, Egypt, was noticed to keep 5% of moisture in its rhizosphere zone at 20 cm depth below the soil surface; therefore, this study aimed at identification of this source of water. The endophytic bacteria were isolated from the root of B. inermis and identified by the 16s-rRNA gene sequencing method. Furthermore, their specific respiration rate was determined by the TTC method. Thirteen bacterial isolates were isolated. Five of them showed the highest specific respiration rate after one and three hours (Alcaligenes faecalis, Acinetobacter johnsonii, Enterobacter tabaci, Bacillus pumilus and Enterobacter mori). Alcaligenes faecalis is a facultative chemoautotrophic hydrogen-fixer, where the hydrogen is fixed by this bacterium by hydrogenase enzymes as an energy source and the water is produced as an end product of hydrogen oxidation. So, the source of water's protons is from hydrogen gas. Since the Enterobacter sp. is hydrogen-producing bacterium, the hydrogen gas source for Alcaligenes faecalis metabolism is not only from air, but also the hydrogen production by Enterobacter spp., which were also among the isolated bacteria. Therefore, the relationship appeared to be triplicate. The Alcaligenes faecalis starts the process by hydrogen fixation and water production that enable the plant seeds germination, which in turn produces organic compounds in the root exudates that stimulate the Enterobacter spp. growth, which produce hydrogen gas to continue the cycle.

This study was extended for four years, where 17 plant samples were collected from three different desert locations at Egypt and identified. The hydrogenases were detected in all of the isolated bacteria as well as in the rhizosphere of the plants samples by detecting the Hox C gene that encode the large subunit of the regulatory hydrogenase (RH) of Alcaligenes sp. and hyp A and Hyp B genes that encode accessory proteins required for hydrogenase maturation and found in hydrogen-fixing (Alcaligenes spp.) and hydrogen-producing (Enterobacter spp.) bacteria. The Hox gene was successfully detected in the Alcaligenes sp, while the Hyp A was detected in Alcaligenes sp., Enterobacter sp. and Pantoea agglomerans and Hyp B was detected in Enterobacter cloacae. The detection of these genes in the plant sample showed that Hox C gene in the wheat grains and rhizosphere of Salicornia fruticosa and Zhyophylum decumbens. Hyp A was detected in wheat grains, while Hyp B in rhizosphere of the wild wheat plant. Presence of these genes in the rhizosphere and grains of wild plants strongly suggest that the hydrogen-fixing and hydrogen-producing bacteria are transferred from the root through the plant and stored in the grain/seeds to enable the seeds germination in any environment, in which, it will be fall-down.

Take Away Notes:

- The water source for some desert wild plants is produced by some soil bacteria.
- There is a synergetic relationship between the hydrogen-producing bacteria, hydrogen fixing bacteria to produce sufficient amount of water that enable seeds germination and plant growth.
- The hydrogenase enzymes have a great role in the water production process for the desert plants
- Knowing the factors that control this process may enable the desert cultivation and/or saving the irrigation water.
- This study requires support from other scientists for detection of hydrogenase enzymes in several other wild plants from different desert locations worldwide.
- The radioactive isotopes experiment is strongly required to calculate the water production rate by the isolated hydrogen-fixing bacteria as well as the hydrogen production rate by the isolated hydrogen-producing bacteria.
- The success in this experiment opens new horizon in agriculture and can be considered as one good solution for

the water security problem.

Biography

Bs.C. of Biochemistry (1995), Ms.C. of Biochemistry (2003), Ph.D. of Biochemistry (2007), Faculty of Agriculture, Ain Shams University, Egypt. A professor of biochemistry, college of biotechnology, Misr University for Science and Technology (MUST), Egypt. Shared in two international research projects: One for genetic modification of wheat plants to increase the drought resistance activity and another project for enzymatic biodegradation of azo dyes. Have a sum of 23 published research papers in the fields of drug discovery, plant biology and bioremediation and one published international book entitled: Discovery of new biochemical compounds, LAP, Germany and one patent for wide spectrum antifungal and antibacterial pharmaceutical formula.

Water hyacinths as phytoremidation and cyanobacterial bloom control

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Cyanobacterial blooms, one of the main characteristics of eutrophic waters, is harmful to aquatic ecosystems and poses risks to public health, especially when the bloom-forming species can release toxins. Phytoremediation is considered to be an emerging green technology in which plants are used for to removal of nutrients, organic compounds, toxic metals and cyanobacteria from wastewaters. It has advantages because plants are solar-driven, economical, and helpful to achieve a sustainable environment. Water hyacinths are free-floating perennial aquatic macrophytes with long and dense hairy root systems which are conducive to absorbing nutrients and a medium for the filtering out and attachment of particulate matter including cyanobacteria. In general, due to a wide tolerance to environmental conditions, water hyacinths grow well even in heavily polluted waters. Therefore, they can be well used for harmful cyanobacterial bloom control and phytoremediation in algae dominated waters. An eco-engineering project with water hyacinths planted in large-scale enclosures was conducted as meteorological and hydrographical conditions in Lake Dianchi, and the results confirmed the great potential to use water hyacinths for phytoremidation and cyanobacterial bloom control in lakes with great amount of algae. Additionally, the pilot test suggested that water hyacinths achieved high efficiencies (over 90%) on algal and chlorophyll a removal from urban wastewater by using self-designed experimental devices. Furthermore, over 80% cyanobacterial N could be assimilated by water hyacinths. These results show a new strategy for cyanobacterial bloom control, phytoremidation and environmental restoration in eutrophic waters.

Comparative proteomic analyses of two clonal *Fusarium verticillioides* MRC 826 strains that differ in fumonisin production in maize

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Fusarium verticillioides is a plant pathogenic fungus that causes ear rot disease of maize and produces the carcinogenic fumonisin mycotoxins. The fumonisins are hazardous to both human and animal health and are associated with oesophageal and liver cancer in humans and have been classified as Group 2B (potentially carcinogenic to humans) by the International Agency for Research on Cancer. The association between fumonisin-contaminated maize and maize products and human disease raised food safety and public health concerns worldwide. With a worldwide research focus centred on the reduction of mycotoxin exposure to humans and animals, the current study investigated the molecular mechanisms associated with fumonisin biosynthesis of the fungus in maize to identify potential targets for prevention. Several genetically homogeneous subcultures have been shown to produce varying amounts of the fumonisins in maize cultures. These subculture strains are therefore unique and present ideal opportunities to investigate the molecular regulatory basis of fumonisin production.

Differential protein expression in a high (MRC 826-E) and a low (MRC 826-J) fumonisin producing strain were analysed in maize patty cultures using label-free LC-MS/MS at 7, 14 and 21 days of incubation. Eleven of the fumonisin biosynthesis proteins were detected, with significantly up-regulation in MRC 826-E after days 14 and 21. Fum1p, Fum6p and Fum8p, where significantly upregulated in MRC 826-E, 4.7-, 4.6- and 4.2-fold on day 14 and 3.7-, 3.1- and 1.7-fold on day 21, respectively. Quantitative real-time PCR of the FUM1, FUM6 and FUM8 genes confirmed the LC-MS/MS data with a 5.2-, 3.1-, and 4.5-fold increase in gene expression levels in MRC 826-E, respectively, which correlated with higher fumonisin production. No significant difference in FUM21 expression, a fumonisin transcription factor, was observed between the two strains, while the Fum21p was also not detected in either of the F. verticillioides proteomes. In addition to the Fum-specific proteins, a number of other proteins involved in various biological processes, metabolic functions as well as cellular components were significantly differentially expressed. Of specific interest was the up-regulation of proteins involved in the oxidation reduction processes and antioxidant activity associated with fungal metabolic processes related to FB production and fungal virulence via the involvement of cytochrome P450. Systematic analyses of these protein networks could provide new insight into the fumonisin production phenotype by elucidating novel molecular factors contributing to fumonisin biosynthesis in maize and could identify specific targets for the development of future control strategies.

- Findings of the current investigation provided important clues regarding the ability of F. verticillioides to regulate the production of fumonisins and specific targets were identified that could have important implications to devise resistant maize cultivars to the benefit of the maize industry
- A better understanding of the genetic composition and genomics (transcriptomics and proteomics) associate with F. verticillioides virulence and environmental factors determining plant susceptibility governing pathogen-host interactions using molecular and genomic tools, might lead to the development of novel disease management practices that prevent Fusarium ear rot and fumonisin contamination of maize.

Biography

Dr Lilly obtained her PhD degree at the University of Stellenbosch in 2004 on the metabolic engineering of Saccharomyces cerevisiae for optimum aroma compound production. Postdoctoral fellowships included genetically modifying yeast for metal bioremediation and research on the bioprospecting for novel enzymes for cellulose degradation and biofuel production through metatranscriptomic cDNA library construction. In 2014 she joined the Institute of Biomedical and Microbial Biotechnology (IBMB) at Cape Peninsula University of Technology as a Researcher and her current research focus is on the proteomic and transcriptomic analyses of molecular mechanisms associated with fumonisin production by Fusarium verticillioides in maize. Dr Lilly's current major research interests include gene expression studies using quantitative Real-time PCR and proteomic analysis.

Gating plant immunity and cell at the nuclear pore

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Effector-triggered immunity (ETI) is a major form of plant innate immunity. Using a combined genetic, genomic and proteomic approach coupled with advanced fluorescence-EM imaging, we discovered a novel transmembrane component of the nuclear pore complex (NPC), CPR5. We found that CPR5 is an immune-responsive NPC structural modular that coordinates permeabilized central channel selective barrier during ETI activation and results in simultaneous influx of massive stress-related signaling cargos into the nucleus required for ETI execution. In addition, we found that CPR5-dependent NPC conformational change leads a non-canonical activation of core cell cycle signaling components. Activation of this signaling pathway is essential to drive ETI transcriptional responses, suggesting that conserved cell cycle regulators have evolved important roles in defense activation. Together, this work uncovered a critical gating mechanism for immunity and death at the nuclear pore.

Take Away Notes:

- The most recent advances in the molecular mechanism of plant innate immune responses
- The discovery of a novel component of nuclear pore complex, one of the most important macromolecular protein complex in eukaryotic cells
- New tools with promising potentials in crop resistance engineering

Biography

Dr. Yangnan Gu received his Ph.D. in Molecular Cellular and Developmental Biology from Indiana University Bloomington in USA. He then moved to Duke University and Howard Hughes Medical Institute for his postdoc training. He is now an Assistant Professor at Tsinghua University in China. Dr. Gu's study focuses on the molecular mechanism of one of the most important form of plant immune responses, termed effector-triggered immunity (ETI). His research led to the discovery of a key signaling pathway controlled by the nuclear pore complex downstream of NB-LRR immune receptors during ETI activation.

Estimation of nuclear genome size and its correlation with Ty1-copia like LTR retrotransposon and cell phenotypic traits

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Bioenergy crops are often regarded as an important contributor in the mitigation of global climate change and energy security. Pongamia pinnata, Jatropha curcas, Ricinus communis and Mesua ferrea are four well known biofuel crops with versatile socio-economic values. The potentialities of these crops are dependent on extensiveness of knowledge of their genome structure. Thus, flow cytometric estimation of nuclear DNA content of these plants was made using propidium iodide (PI) as the DNA stain. The 2C DNA values were estimated to be 0.86 pg, 1.01 pg, 1.4 pg and 2.49 pg for Jatropha, Ricinus, Mesua and Pongamia respectively. Variation in genome size was observed among the plants collected from different geographic locations in Assam and was attributed mainly to climatic differences, along with the reverse transcriptase-RNase H (RT-RH) domains of the Ty1-copia retrotransposons. Dot blot analysis revealed that Ty1-copia accounts for 2 %, 6.21 %, 9.66 % and 2.5 % of total haploid nuclear genome of Jatropha, Ricinus, Mesua and Pongamia. Phylogenetic analyses showed that the RT-RH sequences were heterogeneous and resolved into distinct groups. Subsequently, environmental changes affecting phenotypic traits that are unswervingly responsible for growth and yield were studied. Inverse relationship of genome size with stomatal pore size, guard cell length, epidermal cell area and cell volume was observed whereas a linear relationship with stomatal density was seen. This comprehensive study effectively contributes to our understanding about genome organization and will provide valuable information for its utilization in future. Further, the information obtained from present study could be utilised for the development of new strategies to improve the existing genotypes.

Take Away Notes:

- The present study revealed the presence of different lineages of Ty1-copia that exists in plants.
- Copia elements contain high sequence heterogeneity.
- Due to high copy number these elements can be utilized for marker development.
- Genome studies along with extensive study on the phenotypic characters of biofuel crops can be helpful to search a potent trait in this field.

Biography

Dr Latha Rangan is currently Professor at the Department of Biosciences and Bioengineering, Indian Institute of Technology Guwahati. She obtained her PhD in 2001 and had post-doctoral stints on rice transformation in United Kingdom. Her main focus of research has been on in areas of Applied Biodiversity with special reference to bioresources of Northeast India using an integrative approach. Prof. Rangan has been successful in combining the old with the new, because nature is our prototype. The work has laid foundation for new ways to detect, authenticate, protect and exploit biodiversity, for instance as resource for sustainable agriculture taking the case of the useful medicinal plants. In brief applied biodiversity research has helped in tapping bioresources from wilderness to mining 'OMICS'. She has published over 90 articles as scientific papers, book chapters, conference proceedings and reviews. She is an Elected Fellow of National Academy of Sciences, India and recipient of awards such as Prof Hiralal Chakravarty Award of Indian Science Congress, Women Scientist Award of Biotech Research Society of India, Young Scientist Award of Society for Chemist and Biologist and Dr J N Baruah Science Award for her significant contributions in are of Plant Sciences.

Organic fertilization of fresh market peppermint grown under greenhouse in a newly reclaimed land middle Egypt

Sherif G. Salem*, Prof. Dr. Mahassen M.A. Sidky, Dr. Mohamed M.I. Afifi,
Agricultural Research Center, Egypt

Peppermint (Mentha piperita L.) a perennial plant, is among the largest exported medicinal and aromatic crops which have the potential to boost the Egyptian exports of high-quality, added-value crops. It is mainly grown by many smallholder farmers, particularly in the middle-Egypt region under open-field conditions. In recent years, the market for organic fresh-cut herbs including mint is increasing substantially. In reality, however, several constraints are limiting the production of sufficient quantities and high quality of Fresh Market Peppermint. The narrow fertile soil of Nile valley only 4 % of Egypt's total area, the extreme cold during winter months drastically reduces mint growth and yield, as well as the extensive application of chemical fertilizers, are the most critical barriers to the production of fresh organic herb.

Numerous studies have investigated the effects of fertilizer level and source on the growth and yield of Peppermint. However, Egypt has no research-based information about off- season organic production of fresh-cut Peppermint herb under low tunnel greenhouse conditions in a newly-reclaimed desert land.

In 2014 and 2015, a field experiment was conducted over two successive seasons using a completely randomized block design with three replicates in promising desert areas for future agricultural development planning located in the western desert of Samalout city, El Minya Egypt.

The objective of this study is to evaluate the effects of two cultivation methods [e.g., low- tunnel greenhouse (LTGH) vs. open-field conditions (OF)] and to determine the appropriate organic sources of nitrogen fertilizer to sustain soil fertility, maintain crop productivity and profitability. The effects of three different organic sources of nitrogen fertilizer [e.g., composted chicken manure (CHIM), Farmyard manure(FYM), Plant compost (PC)] were investigated as an alternative source for chemical nitrogen fertilizer (CNF)

The results of the experiment demonstrated that peppermint plant adapted best to the low tunnel greenhouses. Significant (P 0.05) increase of plant height by 169 and 122%, yield of fresh weight by 212 and 115%, dry weight by 229 and 118 %, as well as the essential oil yield significantly augmented by 235 and 119%, were observed in the first and second harvest respectively, comparing to those were cultivated in OF conditions. About the effects of different sources of nitrogen fertilizer, the treated plants with CNF has resulted in the highest records followed by CHIM, PC, and FYM treatments respectively, in both cultivation environments. Within these treatments, CNF treatment has significantly (P 0.05) increased plant Height, fresh weight, dry weight, essential oil yield, and nitrogen content of peppermint plants in comparison to FYM and PC. However, no significant differences detected between CNF vs. CHIM treatments. The results imply that high-quality, added- value peppermint products could be produced in sufficient quantities using the LTGH method and CHIM organic fertilizer in the newly-reclaimed desert land middle Egypt and similar agro-climatic zones.

Accordingly, this study proposes a novel technique that can readily be implemented in present Peppermint production systems to fulfill markets demands of such products.

Take Away Notes:

- Peppermint plant adopted best low tunnel cultivation method for off-season production of fresh-cut peppermint
- Organic production of medicinal plant mainly mint plant can be achieved using local organic fertilizer, e.g., composted chicken manure (CHIM) as an alternative organic source for chemical nitrogen fertilizer (CNF) followed by Plant residues compost (PC) under the experimental conditions.
- Western desert of the Samalout City of El Minya is proposed to be one of the promising areas for future agricultural development planning, in particular, medicinal plant production.
- Some of the audience will accept the idea, and they will try to implement it.
- Specialists scientists can apply this detailed information in their research.
- Some other audience will explore the idea of organic fresh-cut herbs under low tunnel greenhouse from another

perspective, e.g., economically, physiological studies.

- Other might use the information of this investigation in their extension work.
- The ideas can readily be implemented and explored for off-season herbal plant production.
- The results should motivate another researcher to expand the work to overcome the production limitation and might help local policymakers to set programs for extending organic production in this newly reclaimed land.
- The data assumed that there is a possibility to reduce nitrogen pollution and to sustain soil fertilizer using organic fertilizer as an alternative for the chemical counterpart.
- The research is providing a novel solution for the limitation decreases mint plant production and quality during winter months.
- This study should encourage local researcher to investigate another aspect regarding land reclamation and crop production of this spot area of the western Samalout city, El Minya

Biography

Mr. Sherif Salem is an Egyptian agronomist working for Agricultural Research Centre since 2003. He received his bachelor and master from Minya Univ., during his master education Mr. Salem explored the influences of composts, P-dissolving bacteria and N-fixing bacteria on yields and chemical compositions of organically produced cumin plant. During his research in 2011 at Technical Univ. of Denmark, he investigated the short-term effects of biochar and ash on soil nutrient dynamics, greenhouse gas emissions and plant growth.

Currently, Mr. Salem is investigating nutrient budgets/balances and flows of the organic farming in Egypt as well as he is exploring a novel techniques for sustainable nutrient management and off-season crop production in a newly reclaimed soil, a Ph.D. project at Copenhagen Univ., Denmark.

Bioassays Guided Fractionation of Ageratum conyzoides for Identification of Natural Antifungal Compounds against Macrophomina phaseolina

Arshad Javaid
Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan

Macrophomina phaseolina is a soil-borne fungal pathogen causing diseases in more than 500 plant species. The present study aimed to identify possible antifungal constituents in different parts of an asteraceous weed Ageratum conyzoides for the control of M. phaseolina through bioassays guided fractionation. Different parts of the weed were extracted in methanol and antifungal bioassays were carried out using different concentrations (1, 2, …5%) of the extract. Stem extract caused the highest inhibition in fungal biomass (20-83%) followed by leaf extract (16-67%). Methanolic stem extract was partitioned using four organic solvents. Bioassays carried out with different concentrations (3.125 to 200 mg mL-1) of the sub-fractions of methanolic stem extract revealed the highest antifungal potential of chloroform sub-fraction with 56-93% reduction in fungal biomass followed by n-butanol, ethyl acetate and n-hexane sub-fractions causing 24-76%, 7-75% and 5-70% reduction in fungal biomass over control, respectively. Chloroform sub-fraction with the highest antifungal potential was analyzed by GC-MS. Out of 10 compounds identified in this sub-fraction, 2H-1-benzopyran, 6,7-dimethoxy-2,2-dimethyl was the most abundant followed by hexadecanoic acid, methyl ester with peak areas of 27.58% and 18.85%, respectively. Other dominant compounds were 9,12-octadecanoic acid (Z,Z)-, methyl ester (13.67%) and 11-octadecenoic acid, methyl ester (15.28%).

Biography

Dr. Arshad Javaid is working as Associate Professor at Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan. His field of specialization is biofertilizers and natural pesticides. He has published 314 research papers on these topics. He is the author of 8 chapters in international books. He supervised 25 M.Phill. and 8 Ph.D. students. He is editor of various scientific journals including Mycopath, International Journal of Agriculture and Biology, Plant Protection, and Pakistan Journal of Phytopathology.

Investigation on population fluctuation, spatial distribution and sampling plans of Tetranychusurticae Koch. in common bean (*Phaseolus vulgaris*) fields in North Lorestan Province-Iran

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Two spotted spider mite, Tetranychusurticaekoch. is one of the most important pests of common bean in most of areas of Iran, including Lorestanprovince.The population Fluctuation, spatial distribution and Fixed precision sequential sampling plans of Two spotted spider mite were investigated in common bean Fields in Borujerd, Dorud, and Azna in 2008. T. urticae attacked common bean fields in the third decade of June. This pest had two certain peaks of population density on August 15 and 21. 2008 in Borujerd, on August 8 and 21.2008 in Dorud and on August 15 and 29.2008 in Azna. In this study two patterns of movement in the field (X shape and zigzag) was used. Statistical analysis showed that there was no significant difference between these two patterns, in related to CV, RV and RNP parameters. Results showed that, sampling should be done from top, middle and bottom of plant height. In addition, comparison of three sample units, 1.5 leaves per plants (a half leaf from each plant height), 3 leaves per plants (a leaf from each plant height) and 6 leaves per plants (two leaves from each plant height) showed that there is no significant difference between CV and RV of each female, nymph and egg populations with related to CV, RV and RNP parameters. But sample unit 1.5 leaves with the highest amount of RNP, showed significant difference comparison to two that of 3 and 6 leaves.Based on this research, sample unit with 1.5 leaves (three half leaves of left and right consecutively from three plant height) is recommended in sampling of T.urticae populations in common bean fields.

Take Away Notes:

- Based on R-square of regression analysis, Taylor's power law generally provided more adequate description of variance - mean in comparision to Iwao's patchiness regression model for all life stages of pest. Taylor's b and Iwao's were significantly >1 for all the life stages which were sampled by use of 1.5leaves, 3 leaves and 6 leaves sample units indicated that T.urticae populations were aggregated. Fixed precision sequential sampling plans (Green's Model) were also designed to estimate different life stages ofT.urticae density at four fixed precision levels (D=0.15, D=0.2, D=0.25, D=0.3). validity of this models for each life stage was studied by use of 15 independent data sets. To achieve a precision of 0.25 in Green's model and to sample of adult, nymph and egg populations density; 55, 55 and 87 (sample unit of 1.5 leaves), 46, 73 and 77 (sample unit of 3 leaves) and 25, 56 and 41 (sample unit of 6 leaves) respectively are required. The sequential sampling plans will be useful to researchers for quantitive assessment of integrated pest management (IPM) strategies, via rapid estimation of T. urticae population density per leaf. Therefore, Green's fixed precision sequential sampling plan (by use of 1.5 leaves) that has the least cost and the highest ASN, was the most preferred and suitable sample size for sampling of T. urticae in common bean fields. Also, to survey of relationship among infected plant ratios and pest population density in sample units, Wilson and Room models was used. Application of these models leads to save much more time and be great help in counting T. urticae population density.

Biography

I am holding a Master's degree in Entomology from ShahidChamran University of Ahvaz- Iran, which is one of the best universities in Iran. I have also a good research background and publications in insect ecology and Integrated Pest Management. Besides, I have further empirical activities in mass production of beneficial insects, biological control programs, insecticide application, behavioral ecology, and entomology.

Revisiting the past: A case of indigenous vegetables in Africa

Samuel Darko-Koomson*, Instak Agro Enterprise, Ghana (Chief Executive Officer), Africa Agribusiness Management Institute (Training Coordinator)
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Sankofa, a word from the Akan tribe in Ghana symbolizes bringing into the present what is good from the past to make the future better. Commercialization of indigenous vegetables has largely been ignored in Africa and Keyser (2013) states that improved farmer access to quality seeds is likely many years away due to capacity limitations and legal obstacles. Obel-Lawson (2006) identified non-appreciation of African traditional vegetables and urbanization as leading factors that contribute to peoples' preference for exotic vegetables as against indigenous ones. Vegetable production in sub-Saharan Africa has emerged as an important business for smallholder farmers especially those in the urban and peri-urban areas as it serves as their main source of livelihood. Popularly cultivated species comprise exotic vegetables such as lettuce, cabbage and cucumber, and indigenous African vegetables including bito (Hibiscus sabdariffa), berese (Hibiscus cannabinus), bento (Vigna unguiculata)) and alefu (Amaranthus cruentus).

Indigenous species have adapted to local conditions over time, are highly diverse and evolve as reliable performers in their localities. Generally regarded as low yielding, their desirable traits still make them sought after by some indigenous communities. The focus on exotic high yielding vegetable species, has rendered unexploited indigenous vegetable species to extinction (Shei, 2008). Varietal lines for most indigenous vegetables have become inferior due to inbreeding depression, which further threatens their extinction. Availability and accessibility of quality and well adapted indigenous vegetable seeds have become a major challenge. Loosing these qualities through the loss of indigenous varieties potentially threatens food security of indigenes. The UNs SDG 15 seeks to take urgent steps to halt biodiversity loss, protect and prevent the extinction of threatened species.

Africa trails behind in the use of modern varieties making it ever more difficult to compete with food imports from the global market (Keyser, 2013). It is important to understand the nutritional value of indigenous vegetable varieties to see how best they can be modernized. A major obstacle for the success of the vegetable sector is unavailability of well adapted seeds. There is an urgent need to conserve and save seeds of these species for current and future generations. Breeders can multiply these saved landraces and further improve them through genetic engineering without losing quality and other preferable attributes of the indigenous vegetables. These approaches have the potential to prevent extinction of local vegetable species, increase nutrient availability and preserve biodiversity to achieve SDG Goal 15.

Improving farmers' access to quality seeds for indigenous vegetables and introducing them to good agronomic practices can increase yield and decrease post-harvest losses, thereby reducing food insecurity for local indigenes. People from indigenous communities are moving to cities but they still have indigenous tastes implying that latent demand exists for indigenous vegetables. Majority of farmers are smallholders with little resources so prices of improved indigenous vegetable seeds must not be a disincentive for adoption. Seed sales could create jobs for unemployed individuals from rural communities who have migrated to urban areas.

The main objective of this study is to identify and preserve lines of indigenous vegetable varieties in Africa, giving rise to the following research questions:

- What are the varietal lines for common indigenous vegetables in Africa?
- What is the current commercialization level of indigenous vegetables in Africa?
- Which characteristics of indigenous vegetables are important to consumers and what can be done to improve the quality of these vegetables in Africa?
- At what price will African farmers be willing to buy seeds of improved indigenous vegetables?

The research adopts a cross-country approach to purposively sample study sites across a number of African countries including Nigeria, Kenya, Ghana and Tanzania.

Take Away Notes:

- The presentation is expected to increase the awareness of the audience on the following;
- Potential for genetic engineering of indigenous vegetables in Africa

- Possibility of research collaboration to improve quality of indigenous African vegetables
- Possibility on developing consortium to commercialize indigenous African vegetables
- This presentation shall
- Allow the research and business community to refocus on an important but often overlooked area under biotechnology, preserving indigenous African vegetables species
- Demonstrate to the audience a pragmatic approach to reduce the loss of biodiversity by providing a basis for building technological capacity of research institutions to develop improved indigenous vegetable seeds

Biography

Samuel Darko-Koomson has over 5 years of experience in multi-disciplinary research, including fieldwork in Agricultural Economics projects, and training of individuals in academia and business in data analysis. His volunteer group, ResearchENCLAVE, formed in 2014 along with 6 other researchers trained over 70 people within the first 2 years of establishment. Darko-Koomson is the Chief Executive Officer at Instak Agro. Since 2017, he has been the Training Coordinator at Africa Agribusiness Management Institute, a private organization based in Accra-Ghana, with a focus on training and capacity building of industry players in the agribusiness sector in Africa. Samuel has experience working on projects with International Institute of Tropical Agriculture (IITA) under CGIAR. He has been trained as a Competency Based Training Facilitator/Assessor under the GIZ-CAADP ATVET Project. His current research interests comprise agriculture and rural development.

Diversity of edible and inedible macrofungi in Turgo tropical forest ecosystem Mount Merapi national park

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The macrofungi exploration in Turgo tropical forest ecosystem of Mount Merapi National Park aimed to document the diversity and distribution of edible and inedible macrofungi in that region. Macrofungi sampling was distinguished by different forest elevations ie Turgo forest, Tritis forest, and Bingungan forest using adaptive sampling method of plot making. Data collection was conducted in May-June where the month is categorized as the wettest month in Turgo area. The total number of macrofungi obtained 133 specimens, in the Turgo forest found 48 species, in the forest Bingungan got 36 species and in the forest Tritis got 49 species. Species with a high level of macrofungi diversity based on the Shannon-Weiner index is owned by Tritis forest with the lowest elevation among the three is 2.521 followed by the Bingungan forest with an index value of 2.51 and the last of the Turgo forest is worth the index of 2.01 which means the three tracks have a moderate-high level of diversity. Comparing similarity between the three tracks based on the Sorenson index value found that the three tracks have a much different similarity. Judging from the important values, the highest value morphogroups are owned by macrofungi agarics group with 82% -169% value, followed by other groups ie jelly, polypore, cup, club, coral, and tooth which are calculated based on relative frequency and relative density values. Found 8 species that are edible, 12 species are inedible 6 species are medicinal 106 still remaining unknown.

Take Away Notes:

- The Audience will be able to use this method research to measure rapidly the diversity of macrofungi in a recent location, especially in tropical forest ecosystem.
- To detect important macrofungi species in ecosystem, this method is properly using.
- By plot making, we help to keep our focus on our chosen tracks.
- Inedible and edible wild macrofungi has high value for conservation and local economics.
- Mapping the distribiution is highly recommended for the future research as basic where macrofungi fruiting and dispersing differentiated by time and places. Monitoring for some uniqe or important species connected macrofungal conservation and continuing study to develop sustainable macrofungi in National Park and others conservation area.

Biography

Dwiki Prasetiya is biological science student at Yogyakarta State University, Indonesia. His interest comes to fungus and related to microbial phenomena, and he has joined to Biospelology Studien Gruppen also as a founder of Molecular and Microbiology Study Club . His two paper still under reviewed by AIP proceeding. He has experience in International Conference on Biological Sciences before. Now, he is doing his funding projects about Coprinoid mushrooms taxonomy, and Xylaria spp. polymorphisms based on molecular genetics.

Phenotyping of segregating generations derived from sunflower interspecific crosses (*H.annuus*) and (*H. argophyllus*)

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Limited water availability suggests that in future water insufficiency will be norm which leads to the major losses in yield and yield components. Management under these conditions as compare to unlimited water availability may result in reducing yield losses. Study was started to improve crop production by introgression of drought tolerant traits from wild sunflower to cultivated type of sunflower resultantly material of filial generations F1, F2, and F4 is analyzed on the basis of some phenotypic and physiological indicators. When compare to parents UCA-16 and Argo-5-IV these segregating populations have mean value in F1 and when compared by leaf parameters like leaf rolling, hairiness, leaf colour and waxes produced by cuticular layers behaved differently. In selected material of successive generations on cell membrane injury, achene yield and single head type will be further grown by keeping ultimate objective of drought tolerant inbred line.

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